

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: December 22, 2005, 02:28:47 ; Search time 51.4286 Seconds
(without alignments)
153.783 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEEDQFSQNPISCFE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29122	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 3;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 2						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 4;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 3						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 4;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 4						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 4;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 5						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 4;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 6						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 7						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 8						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 9						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 10						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 11						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 12						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 13						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 14						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 15						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				
RESULT 16						
ID	ABU8041	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	US2003027163-A1.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 93;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;				

DE Human PRO polypeptide #99.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 7
ID ABU8046 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 8
ID ABU84361 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 9
ID ABR66235 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 10
ID ABR65625 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 11
ID ABU99565 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 12
ID ABU8041 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 13
ID ABU59119 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO994.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 14
ID ABU82631 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 15
ID ABU82804 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
100.0%; Pred. No. 2.1e-07;
RESULT 16
ID ABU89925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036147-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 22
ID ABO2787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 30
ID ABU9450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 36
ID ABO33958 standard; protein; 229 AA.

DE Human secreted/transmembrane protein PRO994.
PN US200309013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 46
ID ABO11532 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID 198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 80
ID ABU59266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 81
ID ABU85371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 82
ID ABU89061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 83
ID ABU83141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 84
ID ABU94997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 85
ID ABU90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 86
ID ABU84056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 87
ID ABU93707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 94
ID ABU57029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 95
ID ABU85981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 96
ID ABU82268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;

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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human secreted polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 107
ID ABR6540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
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RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 128
ID ABU9650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.


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PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 147
ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
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RESULT 157
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 166

ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003050471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 180
ID ABM77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 181
ID ABM27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 182
ID ABM06155 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 183
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 184
ID ABM35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 185
ID ABM26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 190
ID ABM11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 191
ID ABM02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 192
ID ABM16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 194
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 194
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ID ABM29094 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 222
ID ABM04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 223
ID ABM08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
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PD 27-FEB-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 251
ID ABO4312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 252
ID ABO5942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 258
ID ABR8823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 93; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 270
ID ABM02441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.
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PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 298
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
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PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 310
ID ABM77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 312
ID ABM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 93; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 326
ID ABO51791 standard; protein; 229 AA.
```


DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 355
ID ABR73111 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;

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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 365
ID ABO30653 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 367
ID ABM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 368
ID ABM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 369
ID ABM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 371
ID ABM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 375
ID ABM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 383
ID ABM26959 standard; protein; 229 AA.
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DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US200304924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

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PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 403
ID ABM03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 404
ID ABM19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 405
ID ABM19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 414
ID ABM01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 415
ID ABM02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 417
ID ABM12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 418
ID ABM30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 419
ID ABM24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 421
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 422
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DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 443
ID ABO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
  RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 465
ID ABO41075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 466
ID ABO36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 467
ID ABO37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 470
ID ABO46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 474
ID ABM31839 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 478
ID ABM32449 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 481
ID ABM31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 482
ID ABM30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 498
ID ADC82448 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 499
ID ADD05671 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 500
ID ADD08628 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 501
ID ADD06877 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 502
ID ADC83124 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 503
ID ADD55231 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 504
ID ADD36052 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 505
ID ADD56189 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 506
ID ADD54627 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 507
ID ADE26781 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 508
ID ADE26248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 509
ID ADF67185 standard; protein; 229 AA.
DE Human PRO994 amino acid sequence SEQ ID NO:258.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 510
ID ADG01053 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 511
ID ADG08606 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 512
ID ADG02666 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 513
ID ADG01373 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 514
ID ADF95548 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 515
ID ADF95227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 516
ID ADG12363 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;


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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 535
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
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ID ADH57383 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 544
ID ADI35439 standard; protein; 229 AA.

DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.


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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 627
ID ADH02205 standard; protein; 229 AA.
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DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 636
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 644
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
  RESULT 645
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
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PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 646
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 647
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 648
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 649
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 650
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 651
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 652
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 653
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 654
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 655
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 656
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 657
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 658
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 659
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 660
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 661
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 662
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 663
ID ADM37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
RESULT 664
ID ABO00725 standard; protein; 232 AA.
DE Novel human polypeptide #312.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 46.2%; Score 43; DB 6; Length 232;
Best Local Similarity 66.7%; Pred. No. 78;
RESULT 672
ID AAU31159 standard; protein; 1058 AA.
DE Novel human secreted protein #1650.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 46.2%; Score 43; DB 4; Length 1058;
Best Local Similarity 69.2%; Pred. No. 4.4e+02;
RESULT 673
ID AAR71333 standard; protein; 1110 AA.
DE Deduced sequence encoded by Wilson's disease gene cDNA.
PN WO9506714-A1.
PD 09-MAR-1995.
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 46.2%; Score 43; DB 2; Length 1110;
Best Local Similarity 69.2%; Pred. No. 4.6e+02;
RESULT 675
ID AAE36368 standard; protein; 149 AA.
DE Human neuron-restrictive silencer factor repressor splice variant.
PN WO200297044-A2.
PD 05-DEC-2002.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match
Best Local Similarity 45.2%; Score 42; DB 6; Length 149;
Best Local Similarity 53.3%; Pred. No. 70;
RESULT 676
ID AAM58345 standard; protein; 222 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30450.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 45.2%; Score 42; DB 4; Length 222;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 677
ID ABU03573 standard; protein; 222 AA.
DE Human expressed protein tag (EPT) #239.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 45.2%; Score 42; DB 6; Length 222;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 678
ID AAR99364 standard; protein; 252 AA.
DE Human REST protein DNA binding domain.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 45.2%; Score 42; DB 2; Length 252;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 679
ID AAR99388 standard; protein; 428 AA.
DE Human REST protein (aa9-436).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 45.2%; Score 42; DB 2; Length 428;
Best Local Similarity 53.3%; Pred. No. 2.3e+02;
RESULT 680
ID AAR99367 standard; protein; 468 AA.
DE Human REST protein partial sequence (aa73-540).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 45.2%; Score 42; DB 2; Length 468;

Query Match
Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
RESULT 664
ID ADRI4507 standard; protein; 229 AA.
DE Human NF-kappaB pathway-associated protein SeqID508.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 665
ID ADY77743 standard; protein; 229 AA.
DE Neoplastic disease detection protein PRO994.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 93; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 666
ID AEA39511 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #141.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 667
ID ABM85216 standard; protein; 230 AA.
DE Mouse protein sequence MCP5099.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 75.3%; Score 70; DB 7; Length 230;
Best Local Similarity 72.2%; Pred. No. 0.0018;
RESULT 668
ID ABB60457 standard; protein; 410 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8163.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 48.4%; Score 45; DB 4; Length 410;
Best Local Similarity 53.3%; Pred. No. 68;
RESULT 669
ID AAW15074 standard; protein; 420 AA.
DE M. leprae gyrase intein.
PN FR2739859-A1.
PD 18-APR-1997.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 47.3%; Score 44; DB 2; Length 420;
Best Local Similarity 46.7%; Pred. No. 1e+02;
RESULT 670
ID ABU35713 standard; protein; 1249 AA.
DE Protein encoded by Prokaryotic essential gene #21240.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 47.3%; Score 44; DB 6; Length 1249;
Best Local Similarity 46.7%; Pred. No. 3.6e+02;
RESULT 671
ID AAW15078 standard; protein; 1273 AA.
DE M. leprae gyrA precursor.
PN FR2739859-A1.
PD 18-APR-1997.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 47.3%; Score 44; DB 2; Length 1273;

Best Local Similarity 53.3%; Pred. No. 2.6e+02;
RESULT 681
ID AAR93387 standard; protein; 487 AA.
DE Human REST protein (aa41-527).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 487;
Best Local Similarity 53.3%; Pred. No. 2.7e+02;
RESULT 682
ID AAR93370 standard; protein; 538 AA.
DE Human REST protein partial sequence (aa1-538).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 538;
Best Local Similarity 53.3%; Pred. No. 3e+02;
RESULT 683
ID AAW02288 standard; protein; 678 AA.
DE Human neuron restrictive silencer factor (partial sequence).
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 678;
Best Local Similarity 53.3%; Pred. No. 3.9e+02;
RESULT 684
ID ABG19842 standard; protein; 875 AA.
DE Novel human diagnostic protein #19833.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 42; DB 4; Length 875;
Best Local Similarity 46.7%; Pred. No. 5.2e+02;
RESULT 685
ID AAW02289 standard; protein; 976 AA.
DE Mouse neuron restrictive silencer factor.
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 5.9e+02;
RESULT 686
ID ADU80835 standard; protein; 1082 AA.
DE Murine NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1082;
Best Local Similarity 53.3%; Pred. No. 6.7e+02;
RESULT 687
ID AAR93365 standard; protein; 1097 AA.
DE Human REST protein.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 688
ID ADU80860 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v6.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 689
ID ADU80870 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v8.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;

RESULT 690
ID ADU80863 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v1.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 691
ID ADU80868 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v6.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 692
ID ADU80867 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v5.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 693
ID ADU80861 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v7.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 694
ID ADU80866 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v4.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 695
ID ADU80859 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v5.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 696
ID ADU80862 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v8.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 697
ID ADU80869 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v7.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 698
ID ADU80858 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v4.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 699

ID ADU80864 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v2.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 700
ID ADU80833 standard; protein; 1097 AA.
DE Human NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 701
ID ADU80857 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v1.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 702
ID ADU80865 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v3.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 703
ID ABG32157 standard; protein; 1281 AA.
DE N-methyl D-aspartate (NMDA) receptor related protein #1.
PN WO200264772-A1.
PD 22-AUG-2002.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 45.2%; Score 42; DB 5; Length 1281;
Best Local Similarity 46.7%; Pred. No. 8.1e+02;
RESULT 704
ID AAU02944 standard; protein; 1350 AA.
DE Angiotensin converting enzyme (ACEV) splice variant protein #44.
PN WO200136632-A2.
PD 25-MAY-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 45.2%; Score 42; DB 4; Length 1350;
Best Local Similarity 46.7%; Pred. No. 8.6e+02;
RESULT 705
ID AAR66039 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit 2A protein.
PN WO9424284-A1.
PD 27-OCT-1994.
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 706
ID AAR55529 standard; protein; 1464 AA.
DE Human NMDA R2A receptor subunit.
PN WO9411501-A1.
PD 26-MAY-1994.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 707
ID AAR80970 standard; protein; 1464 AA.
DE Human excitatory amino acid receptor modulatory protein NR2A-1.
PN EP674003-A2.
PD 27-SEP-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 708
ID AAW85576 standard; protein; 1464 AA.

DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US5849895-A.
PD 15-DEC-1998.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 709
ID AAY56113 standard; protein; 1464 AA.
DE Human NMDAR2A subunit protein sequence SEQ ID NO:11.
PN US5985586-A.
PD 16-NOV-1999.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 710
ID AAB26215 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US6111091-A.
PD 29-AUG-2000.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 711
ID ABB56507 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO 11.
PN US6316611-B1.
PD 13-NOV-2001.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 712
ID AAO18063 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO: 11.
PN US6376660-B1.
PD 23-APR-2002.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 713
ID ABG32158 standard; protein; 1464 AA.
DE N-methyl D-aspartate (NMDA) receptor related protein #2.
PN WO200264772-A1.
PD 22-AUG-2002.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 714
ID ABU65878 standard; protein; 1464 AA.
DE Human N-methyl D-aspartate receptor subunit associated protein #1.
PN US2002161215-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (ELLI/) ELLIS S B.
PA (LIAW/) LIAW C W.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 715
ID ABU61423 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor subunit #5.
PN US2002161193-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 716
ID ABU03575 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #241.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;

Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 717
ID ABU03578 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #244.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 718
ID ABU03574 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #240.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 719
ID ABU03577 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #243.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 720
ID ABU03572 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #238.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 721
ID ABU03579 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #245.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 722
ID ABU03571 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #237.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 723
ID ABU03576 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #242.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 724
ID ABU03580 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #246.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 725
ID ABU03570 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #236.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 726
ID ABU03573 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #241.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 727
ID ABO43070 standard; protein; 1464 AA.
DE Human NMDA receptor subunit NMDAR2A.
PN US2003013866-A1.
PD 16-JAN-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 728
ID AAE39234 standard; protein; 1464 AA.
DE Human NMDA receptor subunit, NMDAR2A protein.
PN US6521413-B1.
PD 18-FEB-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 729
ID ABU16324 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #1851.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 44.6%; Score 41.5; DB 6; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.3e+02;
RESULT 730
ID ADW94654 standard; protein; 355 AA.
DE Proliferation-required gene SAV0920 protein, SEQ ID 594.
PN US2005026189-A1.
PD 03-FEB-2005.
PA (WANG/) WANG L.
PA (ZAMU/) ZAMUDIO C.
Query Match 44.6%; Score 41.5; DB 9; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.3e+02;
RESULT 731
ID AAW48794 standard; protein; 117 AA.
DE Homo sapiens sprouty 1 cysteine rich protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 44.1%; Score 41; DB 2; Length 117;
Best Local Similarity 58.3%; Pred. No. 79;
RESULT 732
ID AAB41184 standard; protein; 139 AA.
DE Human ORFX ORF948 polypeptide sequence SEQ ID NO.1896.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 44.1%; Score 41; DB 3; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 733
ID ADE83550 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 11168.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 734
ID ADE58772 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 4658.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match
Best Local Similarity 44.1%; Score 41; DB 7; Length 139;
RESULT 735
ID ADN95257 standard; protein; 139 AA.
DE Human BEC/LEC-related protein sequence SeqID179.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match
Best Local Similarity 44.1%; Score 41; DB 7; Length 139;
RESULT 736
ID ADG47835 standard; protein; 139 AA.
DE Human sprouty-1 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 8; Length 139;
RESULT 737
ID ADJ95402 standard; protein; 139 AA.
DE Human sprouty-1 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 8; Length 139;
RESULT 738
ID AAW48793 standard; protein; 140 AA.
DE Homo sapiens sprouty 1 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match
Best Local Similarity 44.1%; Score 41; DB 2; Length 140;
RESULT 739
ID AAY87596 standard; protein; 156 AA.
DE Human SPROUTY protein short consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 156;
RESULT 740
ID AAY87595 standard; protein; 167 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:9.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 167;
RESULT 741
ID ADP29852 standard; protein; 188 AA.
DE Human secreted protein SEQ ID #619.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 8; Length 188;
RESULT 742
ID AAY87597 standard; protein; 288 AA.
DE Human SPROUTY protein long consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 288;
RESULT 743
ID AAY87592 standard; protein; 294 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:3.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.

Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 294;
RESULT 744
ID AAY87593 standard; protein; 295 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:5.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 295;
RESULT 745
ID AAU69508 standard; protein; 315 AA.
DE Human purified secretory polypeptide #77.
PN WO200162918-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 4; Length 315;
RESULT 746
ID AEB51826 standard; protein; 318 AA.
DE Human Sprouty-1 protein.
PN WO2005065686-A1.
PD 21-JUL-2005.
PA (UYQU) UNIV QUEENSLAND.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
Query Match
Best Local Similarity 44.1%; Score 41; DB 9; Length 318;
RESULT 747
ID AAY87591 standard; protein; 319 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:24.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 44.1%; Score 41; DB 3; Length 319;
RESULT 748
ID AAB64377 standard; protein; 319 AA.
DE Amino acid sequence of human intracellular signalling molecule INTRA9.
PN WO200077040-A2.
PD 21-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 4; Length 319;
RESULT 749
ID AAM38688 standard; protein; 319 AA.
DE Human polypeptide SEQ ID NO 1833.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 4; Length 319;
RESULT 750
ID ADY16807 standard; protein; 319 AA.
DE PRO polypeptide SEQ ID NO 2613.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 9; Length 319;
RESULT 751
ID AAM40474 standard; protein; 326 AA.
DE Human polypeptide SEQ ID NO 5405.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 44.1%; Score 41; DB 4; Length 326;
RESULT 752
ID ABB84246 standard; protein; 335 AA.
DE Human germinal protein 36.85.
PN CN1339486-A.
PD 13-MAR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

Query Match 44.1%; Score 41; DB 5; Length 335;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 753
ID ADE08605 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #760.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 7; Length 336;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
RESULT 754
ID AAY87594 standard; protein; 338 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:7.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 338;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 755
ID AAG30407 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
RESULT 756
ID ABB92109 standard; protein; 449 AA.
DE Herbicidally active polypeptide SEQ ID NO 1320.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 5; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
RESULT 757
ID AAG30406 standard; protein; 466 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 466;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 758
ID AAG41728 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51953.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 474;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
RESULT 759
ID AEA18817 standard; protein; 496 AA.
DE Amino acid sequence of E3 ubiquitin ligase murine Cbl-3.
PN WO2005044840-A2.
PD 19-MAY-2005.
PA (CBRB-) CBR INST BIOMEDICAL RES INC.
Query Match 44.1%; Score 41; DB 9; Length 496;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
RESULT 760
ID AAG41727 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51952.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 497;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
RESULT 761
ID AAG41726 standard; protein; 512 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51951.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 512;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
RESULT 762
ID ADN20612 standard; protein; 597 AA.
DE Bacterial polypeptide #3265.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 44.1%; Score 41; DB 8; Length 597;
Best Local Similarity 88.9%; Pred. No. 5e+02;
RESULT 763
ID ADU80837 standard; protein; 1068 AA.
DE Rat NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 44.1%; Score 41; DB 8; Length 1068;
Best Local Similarity 58.3%; Pred. No. 9.8e+02;
RESULT 764
ID ABU26822 standard; protein; 792 AA.
DE Protein encoded by Prokaryotic essential gene #12349.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 43.5%; Score 40.5; DB 6; Length 792;
Best Local Similarity 37.5%; Pred. No. 8.5e+02;
RESULT 765
ID AAY35218 standard; protein; 797 AA.
DE C. pneumoniae protein involved in metabolism of amino acids.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 43.5%; Score 40.5; DB 2; Length 797;
Best Local Similarity 37.5%; Pred. No. 8.5e+02;
RESULT 766
ID ADB65067 standard; protein; 158 AA.
DE Human protein encoded by clone SMINT20049920.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 43.0%; Score 40; DB 7; Length 158;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
RESULT 767
ID AAU23341 standard; protein; 204 AA.
DE Novel human enzyme polypeptide #427.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.0%; Score 40; DB 4; Length 204;
Best Local Similarity 44.4%; Pred. No. 2.2e+02;
RESULT 768
ID ADO24768 standard; protein; 281 AA.
DE Cat TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
RESULT 769
ID ADO24766 standard; protein; 281 AA.
DE Dog TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
RESULT 770
ID ADY11675 standard; protein; 358 AA.
DE Plant full length insert polypeptide seqid 67490.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 43.0%; Score 40; DB 8; Length 358;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
RESULT 771
ID ABU11564 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 511.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 772
ID ABU11734 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 681.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 773
ID ADO20208 standard; protein; 421 AA.
DE Human PRO polypeptide #557.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 43.0%; Score 40; DB 8; Length 421;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 774
ID ABP99229 standard; protein; 430 AA.
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 45.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
RESULT 775
ID ABP76709 standard; protein; 430 AA.
DE Streptomyces viridochromogenes AViGT1.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
RESULT 776
ID ABR39814 standard; protein; 600 AA.
DE Human SCAP polypeptide-Incyte Id. 33632254CD1.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.5e+02;
RESULT 777
ID ADR58983 standard; protein; 600 AA.
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 86.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.
Query Match 43.0%; Score 40; DB 8; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.5e+02;
RESULT 778
ID ABG20261 standard; protein; 633 AA.
DE Novel human diagnostic protein #20252.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 43.0%; Score 40; DB 4; Length 633;
Best Local Similarity 58.3%; Pred. No. 8e+02;
RESULT 779
ID ABG72972 standard; protein; 735 AA.
DE Lactococcus raffinolactis alpha-galactosidase.
PN WO200281674-A1.

PD 17-OCT-2002.
PA (UYLA-) UNIV LAVAL.
Query Match 43.0%; Score 40; DB 6; Length 735;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
RESULT 780
ID ADH22524 standard; protein; 971 AA.
DE Human transporter & ion channel (TRICH) protein SeqID22.
PN WO2003093444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 43.0%; Score 40; DB 8; Length 971;
Best Local Similarity 58.8%; Pred. No. 1.3e+03;
RESULT 781
ID ADZ80808 standard; protein; 1500 AA.
DE Amino acid sequence of human homologue of Drosophila gene CG1886.
PN WO2005039635-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 43.0%; Score 40; DB 9; Length 1500;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
RESULT 782
ID AEB28167 standard; protein; 1500 AA.
DE Human MNK protein.
PN WO2005062055-A2.
PD 07-JUL-2005.
PA (CANC-) CANCER RES TECHNOLOGY LTD.
Query Match 43.0%; Score 40; DB 9; Length 1500;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
RESULT 783
ID AEB86597 standard; protein; 1581 AA.
DE Human copper transporting ATPase ATP7A.
PN WO2005075632-A2.
PD 18-AUG-2005.
PA (CELL-) CELLZOME AG.
Query Match 43.0%; Score 40; DB 9; Length 1581;
Best Local Similarity 58.8%; Pred. No. 2.3e+03;
RESULT 784
ID AAY27134 standard; protein; 1591 AA.
DE Human munc13 (Hmunc13) polypeptide.
PN WO9931134-A1.
PD 24-JUN-1999.
PA (SILV/) SILVERMAN M.
PA (SONG/) SONG Y.
Query Match 43.0%; Score 40; DB 2; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 785
ID AAE14921 standard; protein; 1591 AA.
DE Human ubiquitous Munc13-2 protein mutant (W376R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 786
ID AAE14911 standard; protein; 1591 AA.
DE Mouse ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 787
ID AAE14912 standard; protein; 1591 AA.
DE Human ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 788
ID ADJ68886 standard; protein; 1591 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID692.

PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 43.0%; Score 40; DB 7; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 789
ID AAE14913 standard; protein; 1622 AA.
DE Rat ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1622;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 790
ID AAE14922 standard; protein; 1622 AA.
DE Rat ubiquitous Munc13-2 protein mutant (W387R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1622;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 791
ID AAE14914 standard; protein; 1985 AA.
DE Rat brain-specific Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1985;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
RESULT 792
ID ABP76679 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 43.0%; Score 40; DB 6; Length 19938;
Best Local Similarity 58.3%; Pred. No. 4e+04;
RESULT 793
ID AAU61252 standard; protein; 87 AA.
DE Propionibacterium acnes immunogenic protein #22148.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 41.9%; Score 39; DB 4; Length 87;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
RESULT 794
ID ABM57771 standard; protein; 87 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22447.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 41.9%; Score 39; DB 6; Length 87;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
RESULT 795
ID ADT58157 standard; protein; 114 AA.
DE Plant polypeptide, SEQ ID 8234.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 41.9%; Score 39; DB 8; Length 114;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
RESULT 796
ID ABB58677 standard; protein; 152 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2823.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 152;
Best Local Similarity 41.2%; Pred. No. 2.4e+02;
RESULT 797
ID ABU00656 standard; protein; 165 AA.
DE S. pneumoniae type 4 strain protein from coding region #223.

PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 6; Length 165;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 798
ID ABU44451 standard; protein; 198 AA.
DE Protein encoded by Prokaryotic essential gene #29978.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 198;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
RESULT 799
ID AAU36069 standard; protein; 215 AA.
DE Klebsiella pneumoniae cellular proliferation protein #57.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 215;
Best Local Similarity 43.8%; Pred. No. 3.5e+02;
RESULT 800
ID AAW38623 standard; protein; 238 AA.
DE S. pneumoniae BSCelABCD NCBI gi: 895746.
PN WO9743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 41.9%; Score 39; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
RESULT 801
ID ABU31150 standard; protein; 266 AA.
DE Protein encoded by Prokaryotic essential gene #16677.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 266;
Best Local Similarity 43.8%; Pred. No. 4.4e+02;
RESULT 802
ID AAY93593 standard; protein; 268 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 268;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
RESULT 803
ID ABU45046 standard; protein; 271 AA.
DE Protein encoded by Prokaryotic essential gene #30573.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 271;
Best Local Similarity 43.8%; Pred. No. 4.5e+02;
RESULT 804
ID AEB06770 standard; protein; 277 AA.
DE E. coli xanthosine phosphorolysis enzyme SEQ ID NO:10.
PN JP2005151962-A.
PD 16-JUN-2005.
PA (KOKU-) KOKURITSU DAIGAKU HOJIN NARA SENTAN KAGA.
Query Match 41.9%; Score 39; DB 9; Length 277;
Best Local Similarity 54.5%; Pred. No. 4.6e+02;
RESULT 805
ID AAY93568 standard; protein; 288 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 288;
Best Local Similarity 63.6%; Pred. No. 4.9e+02;

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RESULT 806
ID ABG25942 standard; protein; 300 AA.
DE Novel human diagnostic protein #25933.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 41.9%; Score 39; DB 4; Length 300;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
RESULT 807
ID AAB36504 standard; protein; 320 AA.
DE Human short phosphodiesterase protein SEQ ID NO:3.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.5e+02;
RESULT 808
ID ADJ58906 standard; protein; 320 AA.
DE Human cyclic nucleotide phosphodiesterase protein #2.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.5e+02;
RESULT 809
ID ABB67466 standard; protein; 328 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29190.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 328;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
RESULT 810
ID ADY50214 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain SEQ ID NO:23.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 811
ID ADZ46770 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain, SEQ ID NO: 23.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 812
ID AAY86040 standard; protein; 341 AA.
DE S. pneumoniae derived protein #249.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Query Match 41.9%; Score 39; DB 2; Length 341;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
RESULT 813
ID AAU08676 standard; protein; 391 AA.
DE Human phosphodiesterase type 7B #2.
PN WO200162940-A2.
PD 30-AUG-2001.
PA (MERE ) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 391;
Best Local Similarity 63.6%; Pred. No. 6.9e+02;
RESULT 814
ID AAY93569 standard; protein; 450 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 815
ID AAU08675 standard; protein; 450 AA.
DE Human phosphodiesterase type 7B #1.
PN WO200162940-A2.
PD 30-AUG-2001.
PA (MERE ) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 816
ID AAG78915 standard; protein; 450 AA.
DE Human type 7B phosphodiesterase, PDE7B.
PN JP2001238680-A.
PD 04-SEP-2001.
PA (TANA ) TANABE SEIYAKU CO.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 817
ID ADP79549 standard; protein; 450 AA.
DE Human phosphodiesterase 7B nucleotide sequence.
PN WO2004044196-A1.
PD 27-MAY-2004.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match 41.9%; Score 39; DB 8; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 818
ID AAB36503 standard; protein; 502 AA.
DE Human long phosphodiesterase protein SEQ ID NO:1.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 819
ID ABB09005 standard; protein; 502 AA.
DE Human phosphodiesterase-1.
PN WO200198471-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 41.9%; Score 39; DB 5; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 820
ID ADJ58904 standard; protein; 502 AA.
DE Human cyclic nucleotide phosphodiesterase protein #1.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 821
ID ADX65729 standard; protein; 518 AA.
DE Plant full length insert polypeptide seqid 36572.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 518;
Best Local Similarity 52.9%; Pred. No. 9.5e+02;
RESULT 822
ID ADS42354 standard; protein; 524 AA.
DE Bacterial polypeptide #20784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 524;
Best Local Similarity 54.5%; Pred. No. 9.6e+02;
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RESULT 823
ID ADS21971 standard; protein; 576 AA.
DE Bacterial polypeptide #11004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 576;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
RESULT 824
ID ADK47528 standard; protein; 659 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4043.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 659;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 825
ID ADR95065 standard; protein; 661 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3700.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 826
ID AEA58935 standard; protein; 661 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3700.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 41.9%; Score 39; DB 9; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 827
ID ADX87416 standard; protein; 739 AA.
DE Plant full length insert polypeptide seqid 50080.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 739;
Best Local Similarity 37.5%; Pred. No. 1.4e+03;
RESULT 828
ID ABM84355 standard; protein; 810 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 829
ID ABM84354 standard; protein; 810 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 830
ID ADT56766 standard; protein; 999 AA.
DE Plant polypeptide, SEQ ID 6843.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 41.9%; Score 39; DB 8; Length 999;

Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 831
ID AAY58717 standard; protein; 1001 AA.
DE Arabidopsis ran1-1 mutant protein.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 832
ID AAY58677 standard; protein; 1001 AA.
DE Arabidopsis RAN1 copper transporter.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 833
ID AAY58718 standard; protein; 1001 AA.
DE Arabidopsis ran1-2 mutant protein.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 834
ID ABP99398 standard; protein; 1001 AA.
DE Arabidopsis thaliana polypeptide SEQ ID NO 81.
PN WO200266660-A2.
PD 29-AUG-2002.
PA (META-) METANOMICS GMBH & CO KGAA.
Query Match 41.9%; Score 39; DB 5; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 835
ID ADJ70318 standard; protein; 1328 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2124.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 41.9%; Score 39; DB 7; Length 1328;
Best Local Similarity 64.3%; Pred. No. 2.8e+03;
RESULT 836
ID ABP27518 standard; protein; 1368 AA.
DE Streptococcus polypeptide SEQ ID NO 4212.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 5; Length 1368;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
RESULT 837
ID AAR72343 standard; protein; 1411 AA.
DE Wilson disease protein ATP7B.
PN WO9508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1411;
Best Local Similarity 64.3%; Pred. No. 2.9e+03;
RESULT 838
ID AAR70419 standard; protein; 1456 AA.
DE Rat homologue of human Wilson disease gene ATP7B.
PN WO9508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1456;
Best Local Similarity 64.3%; Pred. No. 3.1e+03;
RESULT 839
ID AEB86598 standard; protein; 1464 AA.
DE Human copper transporting ATPase ATP7B.
PN WO2005075632-A2.
PD 18-AUG-2005.
PA (CELL-) CELLZOME AG.

Query Match
Best Local Similarity 41.9%; Score 39; DB 9; Length 1464;
RESULT 840
ID AAU71957 standard; protein; 1513 AA.
DE Human bone marrow tissue polypeptide #35.
PN WO200179447-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 41.9%; Score 39; DB 4; Length 1513;
RESULT 841
ID ABB65616 standard; protein; 2271 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23640.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 41.9%; Score 39; DB 4; Length 2271;
RESULT 842
ID AAU75351 standard; protein; 2291 AA.
DE Drosophila Rotkehlchen, ROT, protein.
PN WO200200864-A2.
PD 03-JAN-2002.
PA (AVET) AVENTIS CROPSCIENCE GMBH.
Query Match
Best Local Similarity 41.9%; Score 39; DB 5; Length 2291;
RESULT 843
ID AAU33909 standard; protein; 346 AA.
DE Staphylococcus aureus cellular proliferation protein #185.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 4; Length 346;
RESULT 844
ID ADG48173 standard; protein; 355 AA.
DE Staphylococcus aureus COL fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 7; Length 355;
RESULT 845
ID ADG48213 standard; protein; 355 AA.
DE Staphylococcus aureus fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 7; Length 355;
RESULT 846
ID AAU36919 standard; protein; 388 AA.
DE Staphylococcus aureus cellular proliferation protein #1089.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 4; Length 388;
RESULT 847
ID ABM72178 standard; protein; 390 AA.
DE Staphylococcus aureus protein #1418.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 6; Length 390;
RESULT 848
ID AAW89800 standard; protein; 393 AA.
DE Staphylococcus aureus protein SEQ ID #5248.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 2; Length 393;

Best Local Similarity 34.6%; Pred. No. 8.4e+02;
RESULT 849
ID ABB65474 standard; protein; 438 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23214.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 4; Length 438;
RESULT 850
ID AAU12171 standard; peptide; 15 AA.
DE Human NPAT protein 12 N-terminal sequence.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 15;
RESULT 851
ID AAY59902 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 10.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 70;
RESULT 852
ID AAY59907 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 15.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
RESULT 853
ID AAY59914 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 22.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 70;
RESULT 854
ID ADP07825 standard; protein; 84 AA.
DE Human secreted protein, seq id 308.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 84;
RESULT 855
ID AAY11056 standard; protein; 100 AA.
DE H. pylori ORF hp2el0911_24804577_c3_104 cellular protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR) ASTRA AB.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 100;
RESULT 856
ID AAU74692 standard; protein; 110 AA.
DE Human NPAT protein 12.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 110;
RESULT 857
ID ADC24809 standard; protein; 140 AA.
DE Human breast specific polypeptide (BSP) DEX0238_130, SEQ ID NO:130.
PN WO2003020900-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 140;
RESULT 858
ID AAW89800 standard; protein; 393 AA.
DE Staphylococcus aureus protein SEQ ID #5248.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 41.4%; Score 38.5; DB 2; Length 393;

RESULT 858
ID ADQ65969 standard; protein; 140 AA.
DE Novel human protein sequence #942.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 8; Length 140;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
RESULT 859
ID ADR99381 standard; protein; 142 AA.
DE Chlamydia pneumoniae protein #13 for treating Chlamydia infections.
PN WO2004074318-A2.
PD 02-SEP-2004.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Query Match 40.9%; Score 38; DB 8; Length 142;
Best Local Similarity 47.1%; Pred. No. 3.2e+02;
RESULT 860
ID ADQ08608 standard; protein; 173 AA.
DE Ciona intestinalis nervous system associated protein SegID10.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 40.9%; Score 38; DB 8; Length 173;
Best Local Similarity 40.0%; Pred. No. 4e+02;
RESULT 861
ID ADJ48525 standard; protein; 178 AA.
DE Oil-associated gene related protein #25.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 40.9%; Score 38; DB 8; Length 178;
Best Local Similarity 46.7%; Pred. No. 4.2e+02;
RESULT 862
ID AAG19526 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21361.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 215;
Best Local Similarity 61.5%; Pred. No. 5.2e+02;
RESULT 863
ID AAU43540 standard; protein; 217 AA.
DE Propionibacterium acnes immunogenic protein #4436.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 4; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 864
ID ABM40059 standard; protein; 217 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4735.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 6; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 865
ID ADH61297 standard; protein; 270 AA.
DE INTSIG protein 7519192CD1, SEQ ID 14.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 270;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
RESULT 866
ID AAY35206 standard; protein; 291 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN WO9927105-A2.
PD 03-JUN-1999.

PA (GEST) GENSET.
Query Match 40.9%; Score 38; DB 2; Length 291;
Best Local Similarity 47.1%; Pred. No. 7.3e+02;
RESULT 867
ID AAG54677 standard; protein; 296 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69755.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 296;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;
RESULT 868
ID ABU17283 standard; protein; 302 AA.
DE Protein encoded by Prokaryotic essential gene #2810.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 40.9%; Score 38; DB 6; Length 302;
Best Local Similarity 77.8%; Pred. No. 7.6e+02;
RESULT 869
ID ABG18959 standard; protein; 325 AA.
DE Novel human diagnostic protein #18950.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 40.9%; Score 38; DB 4; Length 325;
Best Local Similarity 41.2%; Pred. No. 8.3e+02;
RESULT 870
ID ADY50213 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain SEQ ID NO:22.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 8.5e+02;
RESULT 871
ID ADZ46769 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain, SEQ ID NO: 22.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 8.5e+02;
RESULT 872
ID ABB07912 standard; protein; 336 AA.
DE Human PDE7a3 splice variant polypeptide.
PN WO200183772-A1.
PD 08-NOV-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 40.9%; Score 38; DB 5; Length 336;
Best Local Similarity 54.5%; Pred. No. 8.6e+02;
RESULT 873
ID AAR54070 standard; protein; 339 AA.
DE Prod. of gene participating in homologous recombination.
PN JP06141863-A.
PD 24-MAY-1994.
PA (MORI/) MORITA T.
PA (MATS/) MATSUSHIRO A.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 874
ID AAR78183 standard; protein; 339 AA.
DE Human RAD51 protein, involved in DNA repair.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOCO KK.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 875
ID AAR78181 standard; protein; 339 AA.
DE Mouse RAD51 protein, involved in DNA repair and recombination.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOCO KK.


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Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 339;
RESULT 876
ID AAW62523 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 339;
RESULT 877
ID AAW62522 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 339;
RESULT 878
ID AAY87918 standard; protein; 339 AA.
DE Human Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 3; Length 339;
RESULT 879
ID AAY87917 standard; protein; 339 AA.
DE Mammalian Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (RHOB-) RHOBIO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 3; Length 339;
RESULT 880
ID ABB07642 standard; protein; 339 AA.
DE Human RAD51 protein sequence.
PN WO200208432-A2.
PD 31-JAN-2002.
PA (RHOB-) RHOBIO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 339;
RESULT 881
ID ADK67821 standard; protein; 339 AA.
DE Human RAD51 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 339;
RESULT 882
ID ADQ07009 standard; protein; 339 AA.
DE Mouse Rad51 protein SEQ ID NO:2.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 339;
RESULT 883
ID ADQ07011 standard; protein; 339 AA.
DE Human Rad51 protein SEQ ID NO:4.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 339;
RESULT 884
ID ADY15466 standard; protein; 339 AA.
DE PRO polypeptide SEQ ID NO 1272.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 339;
RESULT 885
ID ADZ09769 standard; protein; 339 AA.
DE Human breast cancer marker RAD51 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 339;
RESULT 886
ID ADQ67649 standard; protein; 340 AA.
DE Novel human protein sequence #2315.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 340;
RESULT 887
ID ADR46211 standard; protein; 354 AA.
DE Human phosphodiesterase 7A truncation polypeptide 2.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 354;
RESULT 888
ID ADR46209 standard; protein; 359 AA.
DE Human phosphodiesterase 7A truncation polypeptide 1.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 359;
RESULT 889
ID ABU01155 standard; protein; 361 AA.
DE S. pneumoniae type 4 strain protein from coding region #728.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 40.9%; Score 38; DB 6; Length 361;
RESULT 890
ID AAG19525 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21360.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 40.9%; Score 38; DB 3; Length 363;
RESULT 891
ID ADX88971 standard; protein; 365 AA.
DE Plant full length insert polypeptide seqid 51635.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 365;
RESULT 892
ID ADR66273 standard; protein; 368 AA.
DE Human prostatic carcinoma derived protein SEQ ID 127 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 368;
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Best Local Similarity 70.0%; Pred. No. 9.5e+02;
RESULT 893
ID ADR66834 standard; protein; 368 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 127 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 368;
RESULT 894
ID ADK16327 standard; protein; 369 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #139.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 369;
RESULT 895
ID ADN42042 standard; protein; 369 AA.
DE Amino acid sequence of human polypeptide #8.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 369;
RESULT 896
ID ADN42014 standard; protein; 370 AA.
DE Amino acid sequence of human polypeptide #1.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 370;
RESULT 897
ID AAG19524 standard; protein; 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21359.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 40.9%; Score 38; DB 3; Length 378;
RESULT 898
ID ADN42040 standard; protein; 380 AA.
DE Amino acid sequence of human polypeptide #7.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 380;
RESULT 899
ID ADN42029 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #2.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 381;
RESULT 900
ID ADN42038 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #6.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 381;
RESULT 901
ID ADN42030 standard; protein; 382 AA.
DE Amino acid sequence of human polypeptide #3.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 382;
RESULT 902
ID ADN42036 standard; protein; 383 AA.
DE Amino acid sequence of human polypeptide #5.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 383;
RESULT 903
ID ADN42031 standard; protein; 384 AA.
DE Amino acid sequence of human polypeptide #4.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 384;
RESULT 904
ID AAR88225 standard; protein; 395 AA.
DE Transcription factor BTF2 complex p44 subunit.
PN WO9529245-A2.
PD 02-NOV-1995.
PA (ASRE-) ASSOC DEV RECH EN GENETIQUE MOLECULAIRE.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 395;
RESULT 905
ID ADN05016 standard; protein; 395 AA.
DE Antipsoriatic protein sequence #688.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 395;
RESULT 906
ID ADQ19648 standard; protein; 395 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2467.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 395;
RESULT 907
ID ADP55553 standard; protein; 395 AA.
DE Human PRO protein sequence SEQ ID NO:1529.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 395;
RESULT 908
ID ADY18147 standard; protein; 395 AA.
DE PRO polypeptide SEQ ID NO 3953.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 395;
RESULT 909
ID ADC94935 standard; protein; 400 AA.
DE E. faecium protein sequence SEQ ID 4562.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 400;
RESULT 910
ID AAU79713 standard; protein; 424 AA.
DE Human phosphodiesterase, PDE7A3 splice variant.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
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PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 424;
RESULT 911 54.5%; Pred. No. 1.1e+03;
ID AAU79727 standard; protein; 424 AA.
DE Human cyclic nucleotide phosphodiesterase, PDE8A variant #3.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 424;
RESULT 912 54.5%; Pred. No. 1.1e+03;
ID ABM83119 standard; protein; 425 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3368.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 425;
RESULT 913 54.5%; Pred. No. 1.1e+03;
ID AAE24528 standard; protein; 426 AA.
DE Mouse PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 426;
RESULT 914 54.5%; Pred. No. 1.1e+03;
ID AAE24527 standard; protein; 426 AA.
DE Human PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 426;
RESULT 915 54.5%; Pred. No. 1.1e+03;
ID AAE24529 standard; protein; 426 AA.
DE Rat PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 426;
RESULT 916 54.5%; Pred. No. 1.1e+03;
ID AAE24533 standard; protein; 428 AA.
DE Rat PDE7a protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 428;
RESULT 917 54.5%; Pred. No. 1.1e+03;
ID AAU16967 standard; protein; 432 AA.
DE Human novel secreted protein, SEQ ID 208.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 4; Length 432;
RESULT 918 54.5%; Pred. No. 1.1e+03;

ID ABM83118 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3367.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 437;
RESULT 919 54.5%; Pred. No. 1.2e+03;
ID ABM83121 standard; protein; 441 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3370.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 441;
RESULT 920 54.5%; Pred. No. 1.2e+03;
ID ABR40577 standard; protein; 445 AA.
DE Human secreted protein #SEQ ID 327.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 445;
RESULT 921 60.0%; Pred. No. 1.2e+03;
ID AAE24532 standard; protein; 446 AA.
DE Human PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 446;
RESULT 922 54.5%; Pred. No. 1.2e+03;
ID AAR97669 standard; protein; 448 AA.
DE Chicken Yes proto-oncogene associated protein YAP65.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match
Best Local Similarity 40.9%; Score 38; DB 2; Length 448;
RESULT 923 58.3%; Pred. No. 1.2e+03;
ID AAE24530 standard; protein; 456 AA.
DE Mouse PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 456;
RESULT 924 54.5%; Pred. No. 1.2e+03;
ID ADO21910 standard; protein; 456 AA.
DE Human CAMP phosphodiesterase PDE7a2 protein.
PN WO2004044229-A2.
PD 27-MAY-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 456;
RESULT 925 54.5%; Pred. No. 1.2e+03;
ID ADY18172 standard; protein; 456 AA.
DE PRO polypeptide SEQ ID NO 3978.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 456;
RESULT 926 54.5%; Pred. No. 1.2e+03;
ID ABM83120 standard; protein; 468 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3369.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 468;
RESULT 927 54.5%; Pred. No. 1.3e+03;

ID ABR40523 standard; protein; 477 AA.
DE Human secreted protein #SEQ ID 273.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 5; Length 477;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
RESULT 928
ID AAE24531 standard; protein; 482 AA.
DE Human PDE7A1 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 929
ID ADO40842 standard; protein; 482 AA.
DE Human phosphodiesterase 7a1, PDE7a1.
PN WO2004044235-A1.
PD 27-MAY-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 8; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 930
ID ADR46207 standard; protein; 482 AA.
DE Human phosphodiesterase 7A.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 931
ID ADY18092 standard; protein; 482 AA.
DE PRO polypeptide SEQ ID NO 3898.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 932
ID AAW00094 standard; protein; 498 AA.
DE CAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).
PN US5527896-A.
PD 18-JUN-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 2; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 933
ID AAY49808 standard; protein; 498 AA.
DE Human glioblastoma cell cAMP phosphodiesterase pTM22 protein.
PN US5977305-A.
PD 02-NOV-1999.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 2; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 934
ID AAB20619 standard; protein; 498 AA.
DE pTM22 human glioblastoma cell insert protein sequence SEQ ID NO:20.
PN US6100025-A.
PD 08-AUG-2000.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 3; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 935
ID ADR66097 standard; protein; 498 AA.
DE Human prostatic carcinoma derived protein SEQ ID 293 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 6; Length 548;
Best Local Similarity 58.3%; Pred. No. 1.5e+03;
RESULT 943
ID ADJ50318 standard; protein; 558 AA.
DE Oil-associated gene related protein #1818.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
Query Match 40.9%; Score 38; DB 8; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 936
ID ADR66439 standard; protein; 498 AA.
DE Human prostatic carcinoma derived protein SEQ ID 293 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 937
ID ADY25040 standard; protein; 507 AA.
DE Plant full length insert polypeptide seqid 72824.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 40.9%; Score 38; DB 8; Length 507;
Best Local Similarity 47.1%; Pred. No. 1.4e+03;
RESULT 938
ID ABM8992 standard; protein; 525 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7238.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 40.9%; Score 38; DB 7; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.4e+03;
RESULT 939
ID AAB42693 standard; protein; 529 AA.
DE Human ORFX ORF2457 polypeptide sequence SEQ ID NO:4914.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 40.9%; Score 38; DB 3; Length 529;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
RESULT 940
ID ADU80839 standard; protein; 529 AA.
DE Xenopus NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEO) GEN HOSPITAL CORP.
Query Match 40.9%; Score 38; DB 8; Length 529;
Best Local Similarity 46.7%; Pred. No. 1.4e+03;
RESULT 941
ID ADY70504 standard; protein; 529 AA.
DE Human beta-amyloid precursor protein, MGC4022.
PN WO2005023858-A1.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 40.9%; Score 38; DB 9; Length 529;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
RESULT 942
ID ABU29965 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #15492.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 40.9%; Score 38; DB 6; Length 548;
Best Local Similarity 58.3%; Pred. No. 1.5e+03;
RESULT 943

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PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 558;
RESULT 944 58.3%; Pred. No. 1.5e+03;
ID ADN72631 standard; protein; 558 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 526.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 558;
RESULT 945 58.3%; Pred. No. 1.5e+03;
ID ABR40445 standard; protein; 591 AA.
DE Human secreted protein #SEQ ID 195.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 40.9%; Score 38; DB 5; Length 591;
RESULT 946 60.0%; Pred. No. 1.6e+03;
ID ADY80077 standard; protein; 607 AA.
DE Amino acid sequence of murine pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP ) INST PASTEUR.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 607;
RESULT 947 41.2%; Pred. No. 1.7e+03;
ID ADY80065 standard; protein; 633 AA.
DE Amino acid sequence of human pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP ) INST PASTEUR.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 633;
RESULT 948 41.2%; Pred. No. 1.8e+03;
ID ABR42418 standard; protein; 653 AA.
DE Human potassium channel Kv1.4.
PN WO2003035690-A2.
PD 01-MAY-2003.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match
Best Local Similarity 40.9%; Score 38; DB 6; Length 653;
RESULT 949 50.0%; Pred. No. 1.8e+03;
ID ADA83742 standard; protein; 653 AA.
DE Human KCNA4 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match
Best Local Similarity 40.9%; Score 38; DB 6; Length 653;
RESULT 950 50.0%; Pred. No. 1.8e+03;
ID ADE57786 standard; protein; 653 AA.
DE Human Protein P22459, SEQ ID NO 3651.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 653;
RESULT 951 50.0%; Pred. No. 1.8e+03;
ID ADE63497 standard; protein; 653 AA.
DE Human Protein P22459, SEQ ID NO 9441.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 653;
RESULT 952 50.0%; Pred. No. 1.8e+03;
ID ABO59441 standard; protein; 653 AA.
DE Human genome derived single exon protein #5675.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 653;
RESULT 953 50.0%; Pred. No. 1.8e+03;
ID ADE63495 standard; protein; 655 AA.
DE Rat Protein CAA34133, SEQ ID NO 9439.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 655;
RESULT 954 50.0%; Pred. No. 1.8e+03;
ID ADE57784 standard; protein; 655 AA.
DE Rat Protein P15385, SEQ ID NO 3649.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 655;
RESULT 955 50.0%; Pred. No. 1.8e+03;
ID ADY80071 standard; protein; 664 AA.
DE Amino acid sequence of rat pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP ) INST PASTEUR.
Query Match
Best Local Similarity 40.9%; Score 38; DB 9; Length 664;
RESULT 956 41.2%; Pred. No. 1.9e+03;
ID ADM04783 standard; protein; 667 AA.
DE Human protein of the invention SEQ ID NO:3468.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 667;
RESULT 957 41.2%; Pred. No. 1.9e+03;
ID ADJ38278 standard; protein; 670 AA.
DE Plastid division-related Arc5 orthologue protein 60.
PN WO2004001003-A2.
PD 31-DEC-2003.
PA (UNMS ) UNIV MICHIGAN STATE.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 670;
RESULT 958 50.0%; Pred. No. 1.9e+03;
ID ABO75000 standard; protein; 700 AA.
DE Pseudomonas aeruginosa polypeptide #7175.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 40.9%; Score 38; DB 7; Length 700;
RESULT 959 43.8%; Pred. No. 2e+03;
ID ADS23975 standard; protein; 712 AA.
DE Bacterial polypeptide #13008.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 40.9%; Score 38; DB 8; Length 712;
RESULT 960 38.5%; Pred. No. 2e+03;
ID ADS43873 standard; protein; 757 AA.
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DE Bacterial polypeptide #22303.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 757;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
RESULT 961
ID AAE03804 standard; protein; 772 AA.
DE Schizosaccharomyces pombe RAD 15 protein.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Query Match 40.9%; Score 38; DB 4; Length 772;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
RESULT 962
ID ADN19422 standard; protein; 772 AA.
DE Bacterial polypeptide #2075.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 772;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
RESULT 963
ID ABM84550 standard; protein; 793 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4799.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 793;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
RESULT 964
ID ADT55566 standard; protein; 811 AA.
DE Plant polypeptide, SEQ ID 5643.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 40.9%; Score 38; DB 8; Length 811;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
RESULT 965
ID ADS24019 standard; protein; 822 AA.
DE Bacterial polypeptide #13052.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 822;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
RESULT 966
ID ABB58526 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2370.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 40.9%; Score 38; DB 4; Length 882;
Best Local Similarity 38.9%; Pred. No. 2.6e+03;
RESULT 967
ID ADN19659 standard; protein; 886 AA.
DE Bacterial polypeptide #2312.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 886;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
RESULT 968
ID ABO75893 standard; protein; 940 AA.
DE Pseudomonas aeruginosa polypeptide #8068.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 40.9%; Score 38; DB 7; Length 940;
Best Local Similarity 63.6%; Pred. No. 2.8e+03;
RESULT 969
ID ABM90649 standard; protein; 981 AA.
DE M. xanthus protein sequence, seq id 9848.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 40.9%; Score 38; DB 9; Length 981;
Best Local Similarity 42.9%; Pred. No. 2.9e+03;
RESULT 970
ID ADX05670 standard; protein; 998 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 235.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 40.9%; Score 38; DB 9; Length 998;
Best Local Similarity 60.0%; Pred. No. 3e+03;
RESULT 971
ID AAR43341 standard; protein; 1068 AA.
DE p110.
PN WO9321328-A1.
PD 28-OCT-1993.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 972
ID AAR43342 standard; protein; 1068 AA.
DE Human p110.
PN WO9321328-A1.
PD 28-OCT-1993.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 973
ID AAR46294 standard; protein; 1068 AA.
DE PtdIns 3-kinase 110 kD catalytic subunit.
PN WO9403609-A1.
PD 17-FEB-1994.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 974
ID AAU09687 standard; protein; 1068 AA.
DE Human p110alpha isoform of PI3-kinase.
PN WO200185986-A2.
PD 15-NOV-2001.
PA (ICOS-) ICOS CORP.
Query Match 40.9%; Score 38; DB 5; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 975
ID ADH68169 standard; protein; 1068 AA.
DE PI3K-alpha protein.
PN US2003182669-A1.
PD 25-SEP-2003.
PA (ROCK/) ROCKMAN H A.
PA (PRAS/) NAGA PRASAD S V.
PA (LAPO/) LAPORTE S A.
PA (BARA/) BARAK L S.
PA (CARO/) CARON M G.
Query Match 40.9%; Score 38; DB 8; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;

RESULT 976
ID ADU06422 standard; protein; 1068 AA.
DE Novel bronchial cancer-associated human protein SeqID646.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 40.9%; Score 38; DB 8; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 977
ID ADZ00491 standard; protein; 1068 AA.
DE p110-beta.
PN WO2005031341-A2.
PD 07-APR-2005.
PA (PFIZ) PFIZER HEALTH AB.
Query Match 40.9%; Score 38; DB 9; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 978
ID AAG70814 standard; protein; 1276 AA.
DE S cerevisiae apoptosis associated protein YPL090C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 40.9%; Score 38; DB 4; Length 1276;
Best Local Similarity 70.0%; Pred. No. 3.9e+03;
RESULT 979
ID AAR11465 standard; peptide; 15 AA.
DE Lepidoptera allostatatin polypeptide analogue.
PN EP421935-A.
PD 10-APR-1991.
PA (SANO) SANDOZ LTD.
PA (KRAM/) KRAMER S J.
PA (NOVS) NOVARTIS AG.
Query Match 40.3%; Score 37.5; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 980
ID ABP72616 standard; peptide; 15 AA.
DE Manduca sexta allatostatin.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 40.3%; Score 37.5; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 981
ID ADE14702 standard; peptide; 15 AA.
DE DMGPCR binding ligand #150.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 982
ID ADL83598 standard; peptide; 15 AA.
DE Manduca sexta allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 983
ID ADY80079 standard; protein; 392 AA.
DE Amino acid sequence of murine pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.

Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 984
ID ADY80073 standard; protein; 392 AA.
DE Amino acid sequence of rat pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 985
ID ADY80067 standard; protein; 392 AA.
DE Amino acid sequence of human pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 986
ID ABM70582 standard; protein; 806 AA.
DE Photorhabdus luminescens protein sequence #3679.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 40.3%; Score 37.5; DB 6; Length 806;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
RESULT 987
ID ABB91321 standard; protein; 838 AA.
DE Herbicidally active polypeptide SEQ ID NO 532.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 40.3%; Score 37.5; DB 5; Length 838;
Best Local Similarity 56.2%; Pred. No. 2.9e+03;
RESULT 988
ID ABG22709 standard; protein; 29 AA.
DE Novel human diagnostic protein #22700.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 29;
Best Local Similarity 42.9%; Pred. No. 79;
RESULT 989
ID AAM16024 standard; protein; 42 AA.
DE Peptide #2458 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 990
ID ABB35016 standard; peptide; 42 AA.
DE Peptide #2522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 991
ID AAM28525 standard; protein; 42 AA.
DE Peptide #2562 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 992
ID AAM68206 standard; protein; 42 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28512.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 993
ID AAM55833 standard; protein; 42 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27938.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 994
ID ABG49853 standard; peptide; 42 AA.
DE Human liver peptide, SEQ ID NO 28501.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 995
ID AAM03755 standard; protein; 42 AA.
DE Peptide #2437 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 996
ID ADZ40090 standard; peptide; 48 AA.
DE HIV-1 gp41 ectodomain peptide variant, Seq 2.
PN WO2005034842-A2.
PD 21-APR-2005.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 9; Length 48;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
RESULT 997
ID ADU80332 standard; peptide; 50 AA.
DE HIV transmembrane envelope glycoprotein GP41-based peptide, SEQ ID 2.
PN WO2004103312-A2.
PD 02-DEC-2004.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 50;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
RESULT 998
ID AAY12353 standard; protein; 55 AA.
DE Human 5' EST secreted protein SEQ ID NO:384.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 39.8%; Score 37; DB 2; Length 55;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
RESULT 999
ID ABP43919 standard; protein; 64 AA.
DE FLJ20040 fis clone COL00417.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 5; Length 64;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
RESULT 1000
ID ADH32550 standard; protein; 70 AA.
DE Yeast smORF338-encoded polypeptide, SEQ ID NO:1008.
PN WO200268593-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 5; Length 70;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
RESULT 1001
ID AAM85399 standard; protein; 74 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:12992.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 74;

Best Local Similarity 53.8%; Pred. No. 2.3e+02;
RESULT 1002
ID AAB45011 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 1003
ID AAB45012 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 1004
ID ABP07339 standard; protein; 85 AA.
DE Human ORFX protein sequence SEQ ID NO:14660.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 5; Length 85;
Best Local Similarity 27.8%; Pred. No. 2.7e+02;
RESULT 1005
ID ADI67220 standard; protein; 104 AA.
DE Lactobacillus rhamnosus polypeptide sequence #94.
PN US2004009490-A1.
PD 15-JAN-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 39.8%; Score 37; DB 8; Length 104;
Best Local Similarity 41.2%; Pred. No. 3.4e+02;
RESULT 1006
ID ABB97814 standard; protein; 107 AA.
DE Human secretory polypeptide (SPTM) 66.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 107;
Best Local Similarity 46.2%; Pred. No. 3.5e+02;
RESULT 1007
ID ADY22702 standard; protein; 120 AA.
DE Plant full length insert polypeptide seqid 70486.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 120;
Best Local Similarity 53.8%; Pred. No. 4e+02;
RESULT 1008
ID AAG05261 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1600.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 149;
Best Local Similarity 47.1%; Pred. No. 5.1e+02;
RESULT 1009
ID ABG06103 standard; protein; 163 AA.
DE Novel human diagnostic protein #6094.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 163;
Best Local Similarity 41.2%; Pred. No. 5.6e+02;
RESULT 1010
ID AAG59595 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77099.
PN EP1033405-A2.

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PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 166;
RESULT 1011
ID AAG07269 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4358.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 166;
RESULT 1012
ID AAR57031 standard; protein; 178 AA.
DE Serotonin receptor encoded by human PCR S10 clone.
PN WO9414957-A2.
PD 07-JUL-1994.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 2; Length 178;
RESULT 1013
ID AAG10820 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9294.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 181;
RESULT 1014
ID AAG06866 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3798.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 181;
RESULT 1015
ID AAG54822 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70045.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 185;
RESULT 1016
ID AAG06865 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3797.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 193;
RESULT 1017
ID AAG10819 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9293.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 193;
RESULT 1018
ID AAG05260 standard; protein; 194 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1599.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 194;
RESULT 1019
ID AAG05259 standard; protein; 204 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1598.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 204;
RESULT 1020
ID AAG10818 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9292.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 205;
RESULT 1021
ID AAG06864 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3796.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 205;
RESULT 1022
ID AAG59594 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77098.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 206;
RESULT 1023
ID AAG07268 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4357.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 206;
RESULT 1024
ID ABG03816 standard; protein; 209 AA.
DE Novel human diagnostic protein #3807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 209;
RESULT 1025
ID AAG59593 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77097.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 215;
RESULT 1026
ID AAG07267 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4356.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 215;
RESULT 1027
ID ABG12667 standard; protein; 225 AA.
DE Novel human diagnostic protein #12658.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 225;
RESULT 1028
ID AAY74526 standard; protein; 243 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO:526.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR ) CHIRON CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 243;
RESULT 1029
ID ABU24490 standard; protein; 265 AA.
DE Protein encoded by Prokaryotic essential gene #10017.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 265;
RESULT 1030
ID AAB96515 standard; protein; 271 AA.
DE Putative P. abyssi Fe-S oxidoreductase #7.
PN FR2792651-A1.
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PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 39.8%; Score 37; DB 4; Length 271;
Best Local Similarity 53.8%; Pred. No. 1e+03;
RESULT 1031
ID AAM17915 standard; protein; 276 AA.
DE Peptide #4349 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1032
ID ABB36945 standard; peptide; 276 AA.
DE Peptide #4451 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1033
ID AAM30426 standard; protein; 276 AA.
DE Peptide #4463 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1034
ID ABB31724 standard; peptide; 276 AA.
DE Peptide #4375 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1035
ID AAM70088 standard; protein; 276 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30394.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1036
ID ABG51785 standard; peptide; 276 AA.
DE Human liver peptide, SEQ ID No 30433.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1037
ID AAM05567 standard; protein; 276 AA.
DE Peptide #4249 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1038
ID ABG39722 standard; peptide; 276 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29387.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 276;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1039
ID ADA36649 standard; protein; 277 AA.
DE Acinetobacter baumannii protein #3810.
PN US6562958-B1.

PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 6; Length 277;
Best Local Similarity 44.4%; Pred. No. 1e+03;
RESULT 1040
ID AAY74527 standard; protein; 278 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO:528.
PN WO957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 39.8%; Score 37; DB 3; Length 278;
Best Local Similarity 60.0%; Pred. No. 1e+03;
RESULT 1041
ID ADD30040 standard; protein; 292 AA.
DE Plant yield-related protein from clone G1453.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 39.8%; Score 37; DB 7; Length 292;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1042
ID ADI44161 standard; protein; 292 AA.
DE Plant transcription factor related polypeptide #1669.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 39.8%; Score 37; DB 8; Length 292;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1043
ID AAU20366 standard; protein; 301 AA.
DE Human secreted protein, Seq ID No 358.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 301;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
RESULT 1044
ID ADX92357 standard; protein; 306 AA.
DE Plant full length insert polypeptide seqid 55021.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 306;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
RESULT 1045
ID ABB51278 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1235.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 307;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1046

ID ABB51275 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1232.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 307;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1047
ID ADX94522 standard; protein; 314 AA.
DE Plant full length insert polypeptide seqid 57186.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 314;
Best Local Similarity 58.8%; Pred. No. 1.2e+03;
RESULT 1048
ID AAW48792 standard; protein; 315 AA.
DE Homo sapiens sprouty 2 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 39.8%; Score 37; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1049
ID ABO07185 standard; protein; 315 AA.
DE Human p53 modifying protein, SEQ ID 145.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 39.8%; Score 37; DB 6; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1050
ID ADE61338 standard; protein; 315 AA.
DE Human Protein O43597, SEQ ID NO 7256.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1051
ID ADG14302 standard; protein; 315 AA.
DE Human Sprouty 2 (SPRY2), SEQ ID 4.
PN WO2003074007-A2.
PD 12-SEP-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1052
ID ADG47834 standard; protein; 315 AA.
DE Human sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1053
ID ADG47837 standard; protein; 315 AA.
DE Mouse sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1054
ID ADJ95401 standard; protein; 315 AA.
DE Human sprouty-2 polypeptide.
PN US6706871-B1.

PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1055
ID ADJ95404 standard; protein; 315 AA.
DE Mouse sprouty-2 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1056
ID ADN11324 standard; protein; 315 AA.
DE Human Sprouty2, marker for breast cancer.
PN WO2004029295-A1.
PD 08-APR-2004.
PA (SCTE-) AGENCY SCI TECHNOLOGY & RES.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1057
ID ADQ21111 standard; protein; 315 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3931.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1058
ID ADP23634 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO:812.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1059
ID ADS15841 standard; protein; 315 AA.
DE Human sprouty-2 SEQ ID 4.
PN WO2004082704-A1.
PD 30-SEP-2004.
PA (DNAV-) DनावेC RES INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1060
ID ADY19896 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 5702.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1061
ID ADY15230 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 1036.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1062
ID ADM25514 standard; protein; 316 AA.
DE Hyperthermophile Methanopyrus kandleri protein #120.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 39.8%; Score 37; DB 7; Length 316;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
RESULT 1063
ID ABB51277 standard; protein; 321 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1234.
PN WO200162891-A2.

PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 321;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1064
ID ABU29258 standard; protein; 324 AA.
DE Protein encoded by Prokaryotic essential gene #14785.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 324;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
RESULT 1065
ID AAB19393 standard; protein; 325 AA.
DE Amino acid sequence of a human secreted protein.
PN WO200061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Query Match 39.8%; Score 37; DB 3; Length 325;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1066
ID AAB23045 standard; protein; 326 AA.
DE Human peroxisome associated protein splice variant, SECX 3884846-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 3; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1067
ID ADA23352 standard; protein; 326 AA.
DE Human SECX polypeptide, SEC7 #2.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 39.8%; Score 37; DB 6; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1068
ID ADH87324 standard; protein; 339 AA.
DE Enterococcus faecalis polypeptide #1804.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 39.8%; Score 37; DB 7; Length 339;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
RESULT 1069
ID AAR22463 standard; protein; 343 AA.
DE Acetylpolylamine amidohydrolase.
PN JP04071489-A.
PD 06-MAR-1992.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 39.8%; Score 37; DB 2; Length 343;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1070
ID ADO57333 standard; protein; 351 AA.
DE Kidney development associated protein seqid 100.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
RESULT 1071
ID ADP29942 standard; protein; 351 AA.
DE Human secreted protein SEQ ID #709.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 38.5%; Pred. No. 1.3e+03;

RESULT 1072
ID ADA57263 standard; protein; 362 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1073
ID ADA57577 standard; protein; 362 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1074
ID ADA41146 standard; protein; 362 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1075
ID ADA41471 standard; protein; 362 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1076
ID ADC74585 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 1218.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1077
ID ADC74351 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 984.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1078
ID ADD38093 standard; protein; 362 AA.
DE Human secreted protein #276.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1079
ID ADD37992 standard; protein; 362 AA.
DE Human secreted protein #175.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1080
ID AAW88563 standard; protein; 363 AA.
DE Secreted protein encoded by gene 30 clone HTPBW79.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1081

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ID AAY36333 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 110.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 2; Length 363;
Pred. No. 1.4e+03;
RESULT 1082
ID ABB50330 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:278.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 363;
Pred. No. 1.4e+03;
RESULT 1083
ID ABB51276 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1233.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 363;
Pred. No. 1.4e+03;
RESULT 1084
ID ABO44587 standard; protein; 363 AA.
DE Novel human secreted protein #30.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 363;
Pred. No. 1.4e+03;
RESULT 1085
ID ABO26067 standard; protein; 363 AA.
DE Human protein from novel secreted protein gene 30.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 7; Length 363;
Pred. No. 1.4e+03;
RESULT 1086
ID ABB53913 standard; protein; 365 AA.
DE Lactococcus lactis protein serC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 39.8%; Score 37; DB 5; Length 365;
Pred. No. 1.4e+03;
RESULT 1087
ID ADS29312 standard; protein; 365 AA.
DE Bacterial polypeptide #18345.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 365;
Pred. No. 1.4e+03;
RESULT 1088
ID AAW88777 standard; protein; 370 AA.
DE Polypeptide fragment encoded by gene 30.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 2; Length 370;
Pred. No. 1.4e+03;
RESULT 1089
ID ABB50610 standard; protein; 370 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:558.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 370;
Pred. No. 1.4e+03;
RESULT 1090
ID ABO44867 standard; protein; 370 AA.
DE Novel human secreted protein #30 fragment #1.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 370;
Pred. No. 1.4e+03;
RESULT 1091
ID ABO26347 standard; protein; 370 AA.
DE Protein associated with novel secreted protein gene 30 #1.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 7; Length 370;
Pred. No. 1.4e+03;
RESULT 1092
ID AAY36194 standard; protein; 393 AA.
DE Human secreted protein #66.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 39.8%; Score 37; DB 2; Length 393;
Pred. No. 1.5e+03;
RESULT 1093
ID AAY94883 standard; protein; 393 AA.
DE Human protein clone HP10530.
PN WO20005367-A2.
PD 03-FEB-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 393;
Pred. No. 1.5e+03;
RESULT 1094
ID AAB61136 standard; protein; 393 AA.
DE Human NOV6 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 393;
Pred. No. 1.5e+03;
RESULT 1095
ID AAM79115 standard; protein; 393 AA.
DE Human protein SEQ ID NO 1777.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 393;
Pred. No. 1.5e+03;
RESULT 1096
ID AAB93277 standard; protein; 393 AA.
DE Human protein sequence SEQ ID NO:12320.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 393;
Pred. No. 1.5e+03;
RESULT 1097
ID ABO23238 standard; protein; 393 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV6.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 393;
Pred. No. 1.5e+03;
RESULT 1098
ID ADJ46046 standard; protein; 393 AA.
DE Novel human secreted protein-related protein sequence SeqId199.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA) EDWARDS J D M.
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PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1099
ID ADM56375 standard; protein; 393 AA.
DE Human cell adhesion molecule NOV6.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1100
ID ADF66739 standard; protein; 393 AA.
DE Novel human protein NOV6.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1101
ID ADI19776 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1102
ID ADO58690 standard; protein; 393 AA.
DE Human regulatory molecule HRM-11.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1103
ID ADO60249 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1104
ID ADP19455 standard; protein; 393 AA.
DE Human secreted polypeptide #306.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1105
ID ADQ65337 standard; protein; 393 AA.
DE Novel human protein sequence #310.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1106
ID ADA57578 standard; protein; 415 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1107
ID ADA41472 standard; protein; 415 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1108
ID ADC74586 standard; protein; 415 AA.
DE Human secreted protein - SEQ ID 1219.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1109
ID ADD38094 standard; protein; 415 AA.
DE Human secreted protein #277.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1110
ID AAW88745 standard; protein; 416 AA.
DE Secreted protein encoded by gene 30 clone HTSEV09.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1111
ID ABB50513 standard; protein; 416 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:461.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1112
ID AAM25861 standard; protein; 416 AA.
DE Human protein sequence SEQ ID NO:1376.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1113
ID ABO44770 standard; protein; 416 AA.
DE Novel human secreted protein #213.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1114
ID ABO26250 standard; protein; 416 AA.
DE Human protein from novel secreted protein gene 30 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1115
ID ABB11390 standard; peptide; 435 AA.
DE Human secreted protein homologue, SEQ ID NO:1760.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1116
ID AAM80099 standard; protein; 435 AA.
DE Human protein SEQ ID NO 3745.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 435;
RESULT 1117
ID ADS28270 standard; protein; 445 AA.
DE Bacterial polypeptide #17303.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 445;
RESULT 1118
ID ADF60384 standard; protein; 469 AA.
DE Human contig polypeptide sequence SEQ ID NO:2751.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 7; Length 469;
RESULT 1119
ID AAB69271 standard; protein; 494 AA.
DE HIV-1 non-subtype B clone 92RW009-6 gag protein.
PN WO200026416-A1.
PD 11-MAY-2000.
PA (UABR-) UAB RES FOUND.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 494;
RESULT 1120
ID ADX39491 standard; protein; 494 AA.
DE HIV Gag protein #67.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 9; Length 494;
RESULT 1121
ID ADT57574 standard; protein; 496 AA.
DE Plant polypeptide, SEQ ID 7651.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 496;
RESULT 1122
ID ADN17531 standard; protein; 497 AA.
DE Bacterial polypeptide #184.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 497;
RESULT 1123
ID ADY09236 standard; protein; 508 AA.
DE Plant full length insert polypeptide seqid 65051.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 508;
RESULT 1124
ID ADX80031 standard; protein; 533 AA.

DE Plant full length insert polypeptide seqid 49397.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 533;
RESULT 1125
ID ABU29646 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #15173.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 547;
RESULT 1126
ID ADC97213 standard; protein; 549 AA.
DE E. faecium protein sequence SEQ ID 6840.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 7; Length 549;
RESULT 1127
ID ADP29943 standard; protein; 561 AA.
DE Human secreted protein SEQ ID #710.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 561;
RESULT 1128
ID ABP73959 standard; protein; 569 AA.
DE Candida albicans essential protein SEQ ID NO 7796.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 5; Length 569;
RESULT 1129
ID ABG12666 standard; protein; 570 AA.
DE Novel human diagnostic protein #12657.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 570;
RESULT 1130
ID AAW83428 standard; protein; 611 AA.
DE Munc13-1-interacting domain of Doc2-alpha.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match
Best Local Similarity 39.8%; Score 37; DB 2; Length 611;
RESULT 1131
ID ADY23680 standard; protein; 616 AA.
DE Plant full length insert polypeptide seqid 71464.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 616;
RESULT 1132

ID ADK64436 standard; protein; 647 AA.
DE Disease treating protein complex-derived protein #1157.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 39.8%; Score 37; DB 7; Length 647;
Best Local Similarity 46.2%; Pred. No. 2.7e+03;
RESULT 1133
ID ADA55125 standard; protein; 707 AA.
DE Human protein, SEQ ID 2693.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 6; Length 707;
Best Local Similarity 38.5%; Pred. No. 3e+03;
RESULT 1134
ID ABP54927 standard; protein; 731 AA.
DE Mouse gelsolin.
PN WO200274982-A1.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 39.8%; Score 37; DB 5; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1135
ID ABM04819 standard; protein; 731 AA.
DE Murine gelsolin.
PN EP1284298-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 39.8%; Score 37; DB 6; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1136
ID ADF72344 standard; protein; 731 AA.
DE Mouse gelsolin protein SEQ ID NO:40.
PN WO2003103595-A2.
PD 18-DEC-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 39.8%; Score 37; DB 8; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1137
ID AAM933424 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3048.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1138
ID AAM93852 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3939.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1139
ID AAE29757 standard; protein; 733 AA.
DE Human nucleic acid-associated protein (NAAP-4).
PN WO200277231-A2.
PD 03-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 6; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1140
ID ADL31015 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3048.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1141

ID ADL31906 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3939.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1142
ID ABJ25779 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #437.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
RESULT 1143
ID ABJ26379 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #1037.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
RESULT 1144
ID ABB65490 standard; protein; 799 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23262.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.8%; Score 37; DB 4; Length 799;
Best Local Similarity 46.2%; Pred. No. 3.4e+03;
RESULT 1145
ID ABB07508 standard; protein; 802 AA.
DE Human aminoacyl tRNA synthetase (ATRS) polypeptide (ID: 7474756CD1).
PN WO200204611-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 802;
Best Local Similarity 38.5%; Pred. No. 3.4e+03;
RESULT 1146
ID ADR08945 standard; protein; 922 AA.
DE Human protein useful for treating neurological disease Seq 2451.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 922;
Best Local Similarity 53.8%; Pred. No. 4e+03;
RESULT 1147
ID ABB90849 standard; protein; 1055 AA.
DE Herbicidally active polypeptide SEQ ID NO 60.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 5; Length 1055;
Best Local Similarity 63.6%; Pred. No. 4.7e+03;
RESULT 1148
ID ABP57716 standard; protein; 1073 AA.
DE Novel human protein #3.
PN WO200277257-A1.
PD 03-OCT-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 6; Length 1073;
Best Local Similarity 53.8%; Pred. No. 4.8e+03;
RESULT 1149
ID ABU43426 standard; protein; 1096 AA.
DE Protein encoded by Prokaryotic essential gene #28953.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 1096;
Best Local Similarity 41.2%; Pred. No. 4.9e+03;
RESULT 1150
ID ADB70293 standard; protein; 1116 AA.

DE C. neoformans amino acid sequence SEQ ID NO:3337.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 1116;
Best Local Similarity 50.0%; Pred. No. 5e+03;
RESULT 1151
ID AAR13309 standard; protein; 1180 AA.
DE Modified thermostable protoxin.
PN EP440581-A.
PD 07-AUG-1991.
PA (CIBA) CIBA GEIGY AG.
Query Match 39.8%; Score 37; DB 2; Length 1180;
Best Local Similarity 46.2%; Pred. No. 5.3e+03;
RESULT 1152
ID ABUS4638 standard; protein; 1713 AA.
DE Human NOVX polypeptide #97.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 6; Length 1713;
Best Local Similarity 53.8%; Pred. No. 8.1e+03;
RESULT 1153
ID AAE14920 standard; protein; 1735 AA.
DE Rat Munc13-1 protein mutant (W464R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.2e+03;
RESULT 1154
ID AAE14910 standard; protein; 1735 AA.
DE Rat Munc13-1 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.2e+03;
RESULT 1155
ID AA83431 standard; protein; 1763 AA.
DE Rat Munc13-1.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 39.8%; Score 37; DB 2; Length 1763;
Best Local Similarity 53.8%; Pred. No. 8.4e+03;
RESULT 1156
ID ADN24058 standard; protein; 238 AA.
DE Bacterial polypeptide #6711.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.2%; Score 36.5; DB 8; Length 238;
Best Local Similarity 53.3%; Pred. No. 1e+03;
RESULT 1157
ID ABP41601 standard; protein; 261 AA.
DE Human ovarian antigen HOCPO73, SEQ ID NO:2733.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.2%; Score 36.5; DB 5; Length 261;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1158
ID ABO61655 standard; protein; 291 AA.
DE Klebsiella pneumoniae polypeptide seqid 8172.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.2%; Score 36.5; DB 7; Length 291;

Best Local Similarity 35.3%; Pred. No. 1.3e+03;
RESULT 1159
ID ABB70793 standard; protein; 308 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39171.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.2%; Score 36.5; DB 4; Length 308;
Best Local Similarity 52.9%; Pred. No. 1.4e+03;
RESULT 1160
ID AAY72889 standard; protein; 644 AA.
DE Human PCMVN5 mutant with deleted alpha helix 4 region.
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 644;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
RESULT 1161
ID AAY72887 standard; protein; 657 AA.
DE Human PCMVN5-PP mutant (L617P/W620P).
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1162
ID AAY72888 standard; protein; 657 AA.
DE Human PCMVN5-R mutant (W620R).
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1163
ID AAY72883 standard; protein; 657 AA.
DE Human p84N5 protein involved in cancer therapy.
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1164
ID ABP70646 standard; protein; 657 AA.
DE Amino acid sequence of p84N5, an expression product of the N5 gene.
PN WO2003002067-A2.
PD 09-JAN-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1165
ID ABO52983 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #12.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1166
ID ABO53063 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #40.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1167
ID ABG06945 standard; protein; 673 AA.
DE Novel human diagnostic protein #6936.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 39.2%; Score 36.5; DB 4; Length 673;
Best Local Similarity 46.2%; Pred. No. 3.4e+03;
RESULT 1168
ID AAU38327 standard; protein; 804 AA.
DE Salmonella typhi cellular proliferation protein #218.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.2%; Score 36.5; DB 4; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.2e+03;
RESULT 1169
ID ABU48260 standard; protein; 804 AA.
DE Protein encoded by Prokaryotic essential gene #33787.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.2%; Score 36.5; DB 6; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.2e+03;
RESULT 1170
ID AAW40059 standard; protein; 813 AA.
DE Mouse P300/CBP-associated transcriptional cofactor P/CAF.
PN WO9803652-A2.
PD 29-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 39.2%; Score 36.5; DB 2; Length 813;
Best Local Similarity 53.3%; Pred. No. 4.2e+03;
RESULT 1171
ID AAW40052 standard; protein; 832 AA.
DE Human P300/CBP-associated transcriptional cofactor P/CAF.
PN WO9803652-A2.
PD 29-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 39.2%; Score 36.5; DB 2; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1172
ID ADN06247 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) protein.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1173
ID ADN06310 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1174
ID ADN06311 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1175
ID ADN06309 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.

PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1176
ID ADN06312 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1177
ID ADO40043 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1178
ID ADO40046 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1179
ID ADO40045 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1180
ID ADO40044 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1181
ID ADO39984 standard; protein; 832 AA.
DE Human P300/CBP-associated factor (P/CAF) protein.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1182
ID ADZ70677 standard; protein; 832 AA.

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DE Human protein from lung cancer marker gene PCAF.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB ) BAYER PHARM CORP.
Query Match 39.2%; Score 36.5; DB 9; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1183
ID ADE14747 standard; peptide; 14 AA.
DE Fruit fly allostatin #4.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1184
ID ADE14700 standard; peptide; 14 AA.
DE DmPCR binding ligand #148.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1185
ID ADE14701 standard; peptide; 14 AA.
DE DmPCR binding ligand #149.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1186
ID ADL83600 standard; peptide; 14 AA.
DE Drosophila allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1187
ID ADE14703 standard; peptide; 15 AA.
DE DmPCR binding ligand #151.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 1188
ID ADL83599 standard; peptide; 15 AA.
DE Manducta sexta drostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 1189
ID ADH52754 standard; peptide; 29 AA.
DE Porphyromonas gulae B43 OprF peptide 2.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 7; Length 29;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
RESULT 1190
ID ADX88003 standard; protein; 61 AA.
DE Plant full length insert polypeptide seqid 50667.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 61;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
RESULT 1191
ID AAG02548 standard; protein; 70 AA.
DE Human secreted protein, SEQ ID NO: 6629.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Query Match 38.7%; Score 36; DB 3; Length 70;
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
RESULT 1192
ID ABP06392 standard; protein; 79 AA.
DE Human ORFX protein sequence SEQ ID NO:12766.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 79;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
RESULT 1193
ID ABU70954 standard; protein; 85 AA.
DE Human adipocyte Selected Interacting domain, SID, #585.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 38.7%; Score 36; DB 6; Length 85;
Best Local Similarity 50.0%; Pred. No. 4e+02;
RESULT 1194
ID AAU79594 standard; protein; 88 AA.
DE Human TRAIL splice variant 1, TRA-3-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 88;
Best Local Similarity 41.7%; Pred. No. 4.1e+02;
RESULT 1195
ID AAG12285 standard; protein; 89 AA.
DE Zea mays protein fragment SEQ ID NO: 11339.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 89;
Best Local Similarity 54.5%; Pred. No. 4.2e+02;
RESULT 1196
ID AAY75956 standard; protein; 90 AA.
DE Rat skin cell protein, SEQ ID 134.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 3; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1197
ID AAB55895 standard; protein; 90 AA.
DE Skin cell protein, SEQ ID NO: 134.
PN WO200069884-A2.
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PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 4; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1198
ID ABB72095 standard; protein; 90 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 134.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1199
ID AAU79595 standard; protein; 98 AA.
DE Human TRAIL splice variant 2, TRA-31-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
RESULT 1200
ID ABO84414 standard; protein; 98 AA.
DE Human cancer-associated protein HP7-053.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
RESULT 1201
ID AAU43074 standard; protein; 100 AA.
DE Propionibacterium acnes immunogenic protein #3970.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 1202
ID AAB93388 standard; protein; 100 AA.
DE Human protein sequence SEQ ID NO:12562.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
RESULT 1203
ID ABM39593 standard; protein; 100 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4269.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 100;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 1204
ID AAW19790 standard; protein; 101 AA.
DE Human apoptosis inducer cytokine TRAIL deletion variant.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1205
ID AAW56761 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv) clone protein sequence.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1206
ID AAY79163 standard; protein; 101 AA.
DE Human endothelial PAS domain protein-1 C-terminal polypeptide.

PN WO200009657-A2.
PD 24-FEB-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 38.7%; Score 36; DB 3; Length 101;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
RESULT 1207
ID AAE11032 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv).
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1208
ID ABU08559 standard; protein; 101 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL, deletion variant.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 6; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1209
ID ADK15500 standard; protein; 101 AA.
DE Human TRAIL protein (deletion variant).
PN US2004052788-A1.
PD 18-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1210
ID AEB92346 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv), SEQ ID 4.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1211
ID AAB43222 standard; protein; 104 AA.
DE Human ORFX ORF2986 polypeptide sequence SEQ ID NO:5972.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1212
ID AAG22301 standard; protein; 104 AA.
DE Zea mays protein fragment SEQ ID NO: 25176.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1213
ID AAG21375 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 23910.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1214
ID AAG33020 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 39947.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1215
ID ADT87801 standard; protein; 105 AA.
DE Plant homologue of yeast SRP YLR275W #2.
PN WO2004092398-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 38.7%; Score 36; DB 8; Length 105;

Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1216
ID AAU79600 standard; protein; 113 AA.
DE Human TRAIL splice variant 7, TRA-54-f1, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match
Best Local Similarity 38.7%; Score 36; DB 5; Length 113;
RESULT 1217
ID ADL98267 standard; protein; 120 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #4.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 120;
RESULT 1218
ID ADW00623 standard; protein; 120 AA.
DE Human protein encoded by gene splice variant #6.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 120;
RESULT 1219
ID AAG03752 standard; protein; 121 AA.
DE Human secreted protein, SEQ ID NO: 7833.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match
Best Local Similarity 38.7%; Score 36; DB 3; Length 121;
RESULT 1220
ID ABB69940 standard; protein; 122 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 122;
RESULT 1221
ID ADL98266 standard; protein; 122 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #3.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 122;
RESULT 1222
ID ADW00622 standard; protein; 122 AA.
DE Human protein encoded by gene splice variant #5.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 122;
RESULT 1223
ID AAY35754 standard; protein; 125 AA.
DE Chlamydia pneumoniae protein not found in C. trachomatis.
PN WO927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 38.7%; Score 36; DB 2; Length 125;
RESULT 1224
ID ADY30583 standard; protein; 127 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_010.aa.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.

Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 127;
RESULT 1225
ID AAU54614 standard; protein; 130 AA.
DE Propionibacterium acnes immunogenic protein #15510.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 130;
RESULT 1226
ID ABM51133 standard; protein; 130 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15809.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 130;
RESULT 1227
ID ABP72618 standard; protein; 131 AA.
DE Snowdrop agglutinin-Manduca sexta allatostatin protein fusion.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 131;
RESULT 1228
ID AAB67715 standard; protein; 133 AA.
DE Protein encoded by cDNA clone with similarity to murine GL50 cDNA.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 133;
RESULT 1229
ID ABB70442 standard; protein; 137 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38118.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 137;
RESULT 1230
ID AAU67799 standard; protein; 137 AA.
DE Propionibacterium acnes immunogenic protein #28695.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 137;
RESULT 1231
ID ABM64318 standard; protein; 137 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28994.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 137;
RESULT 1232
ID AAG20539 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22770.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 38.7%; Score 36; DB 3; Length 144;
RESULT 1233
ID AAG47787 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60268.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 38.7%; Score 36; DB 3; Length 144;
RESULT 1234
ID ADY30583 standard; protein; 127 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_010.aa.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.

RESULT 1234
ID ADR09299 standard; protein; 151 AA.
DE Human protein useful for treating neurological disease Seq 2805.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 46.2%; Pred. No. 7.6e+02;
RESULT 1235
ID ADY12886 standard; protein; 151 AA.
DE Plant full length insert polypeptide seqid 68701.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
RESULT 1236
ID AAB58333 standard; protein; 157 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 671.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 38.7%; Score 36; DB 3; Length 157;
Best Local Similarity 54.5%; Pred. No. 8e+02;
RESULT 1237
ID AAG33019 standard; protein; 163 AA.
DE Zea mays protein fragment SEQ ID NO: 39946.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 163;
Best Local Similarity 54.5%; Pred. No. 8.3e+02;
RESULT 1238
ID ADL98264 standard; protein; 169 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #1.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 169;
Best Local Similarity 41.7%; Pred. No. 8.7e+02;
RESULT 1239
ID ADW00620 standard; protein; 169 AA.
DE Human protein encoded by gene splice variant #3.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 169;
Best Local Similarity 41.7%; Pred. No. 8.7e+02;
RESULT 1240
ID AAG21373 standard; protein; 172 AA.
DE Zea mays protein fragment SEQ ID NO: 23908.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 172;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
RESULT 1241
ID AAG60079 standard; protein; 174 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77779.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 174;
Best Local Similarity 38.5%; Pred. No. 9e+02;
RESULT 1242
ID AAG60078 standard; protein; 176 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77778.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 176;

Best Local Similarity 38.5%; Pred. No. 9.1e+02;
RESULT 1243
ID AAG60077 standard; protein; 179 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77777.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 179;
Best Local Similarity 38.5%; Pred. No. 9.2e+02;
RESULT 1244
ID ADF55456 standard; protein; 179 AA.
DE Human novel polypeptide #20.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 38.7%; Score 36; DB 7; Length 179;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
RESULT 1245
ID ADB63818 standard; protein; 185 AA.
DE Human protein encoded by clone ADRGL20021910.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 185;
Best Local Similarity 42.9%; Pred. No. 9.6e+02;
RESULT 1246
ID AAU79599 standard; protein; 188 AA.
DE Human TRAIL splice variant 6, TRA-33-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 188;
Best Local Similarity 41.7%; Pred. No. 9.8e+02;
RESULT 1247
ID ADY11445 standard; protein; 188 AA.
DE Plant full length insert polypeptide seqid 67260.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 188;
Best Local Similarity 54.5%; Pred. No. 9.8e+02;
RESULT 1248
ID ABG21529 standard; protein; 190 AA.
DE Novel human diagnostic protein #21520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 190;
Best Local Similarity 50.0%; Pred. No. 9.9e+02;
RESULT 1249
ID ABG00247 standard; protein; 192 AA.
DE Novel human diagnostic protein #238.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 192;
Best Local Similarity 50.0%; Pred. No. 1e+03;
RESULT 1250
ID ABB72279 standard; protein; 193 AA.
DE Human protein isolated from skin cells SEQ ID NO: 491.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 193;
Best Local Similarity 66.7%; Pred. No. 1e+03;
RESULT 1251

ID ADU00112 standard; protein; 203 AA.
DE Amino acid sequence of G-protein coupled receptor GCREC-4.
PN WO2004092350-A2.
PD 28-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 38.7%; Score 36; DB 8; Length 203;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1252
ID AAY09197 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) alternative sequence.
PN WO9919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1253
ID AAY09196 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) polypeptide.
PN WO9919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1254
ID ADT90843 standard; protein; 208 AA.
DE Human DNAX IL-40.
PN US2004192891-A1.
PD 30-SEP-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1255
ID ADT61031 standard; protein; 208 AA.
DE Human cytokine DNAX IL-40 (DIL-40).
PN US6800460-B1.
PD 05-OCT-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1256
ID ADY57156 standard; protein; 208 AA.
DE Human DNAX IL-40 protein.
PN US2005048625-A1.
PD 03-MAR-2005.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 9; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1257
ID AAU99301 standard; protein; 212 AA.
DE Human TRAIL splice variant 8, rpl-6-6, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 212;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
RESULT 1258
ID AEB40635 standard; protein; 212 AA.
DE L. pneumophila protein SEQ ID NO 4967.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 212;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1259
ID AEB37312 standard; protein; 216 AA.
DE L. pneumophila protein SEQ ID NO 1644.
PN WO2005049642-A2.
PD 02-JUN-2005.

PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 216;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1260
ID AAB94978 standard; protein; 226 AA.
DE Human protein sequence SEQ ID NO:16560.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 226;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1261
ID AAG20538 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22769.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1262
ID AAG47786 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60267.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1263
ID ABB92117 standard; protein; 227 AA.
DE Herbicidally active polypeptide SEQ ID NO 1328.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1264
ID ABP79680 standard; protein; 233 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 5890.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 38.7%; Score 36; DB 6; Length 233;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1265
ID ADD12586 standard; protein; 233 AA.
DE Human ENZM-46 protein SEQ ID NO:46.
PN WO2003072729-A2.
PD 04-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 38.7%; Score 36; DB 7; Length 233;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1266
ID ADH71888 standard; protein; 235 AA.
DE Human protein of the invention NOV31h SEQ ID NO:784.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 235;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
RESULT 1267
ID ADM05434 standard; protein; 242 AA.
DE Human protein of the invention SEQ ID NO:4119.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1268
ID ADF59116 standard; protein; 244 AA.
DE Human polypeptide sequence SEQ ID NO:1524.
PN WO2003080795-A2.
PD 02-OCT-2003.

PA (HYSE-) HYSEQ INC. 38.7%; Score 36; DB 7; Length 244;
Query Match 50.0%; Pred. No. 1.3e+03;
RESULT 1269
ID ABB5303 standard; protein; 245 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22701.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 245;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1270
ID ABB50023 standard; protein; 246 AA.
DE Listeria monocytogenes protein #2727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 38.7%; Score 36; DB 5; Length 246;
Best Local Similarity 30.8%; Pred. No. 1.3e+03;
RESULT 1271
ID AAU79598 standard; protein; 246 AA.
DE Human TRAIL splice variant 5, TRA-20-SP6, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (KHOS/) KHOSRAVI R.
PA (YELI/) YELIN R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 246;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
RESULT 1272
ID ADI17038 standard; protein; 247 AA.
DE Human NOVX protein homologue SeqID 574.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 247;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1273
ID ADX72396 standard; protein; 250 AA.
DE Plant full length insert polypeptide seqid 41762.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 250;
Best Local Similarity 35.7%; Pred. No. 1.4e+03;
RESULT 1274
ID ABM94614 standard; protein; 250 AA.
DE M. xanthus protein sequence, seq id 13813.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 38.7%; Score 36; DB 9; Length 250;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
RESULT 1275
ID AAW84141 standard; peptide; 252 AA.
DE Desaturase enzyme peptide sequence.
PN WO9846763-A1.
PD 22-OCT-1998.
PA (CALJ) CALGENE LLC.
PA (ABBO) ABBOTT LAB.
Query Match 38.7%; Score 36; DB 2; Length 252;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
RESULT 1276
ID ADY26629 standard; protein; 262 AA.
DE Streptomyces vinaceus VioH protein.
PN US2005042726-A1.
PD 24-FEB-2005.
PA (THOM/) THOMAS M G.

PA (CHAN/) CHAN Y A.
PA (OZAN/) OZANICK S G. 38.7%; Score 36; DB 9; Length 262;
Query Match 50.0%; Pred. No. 1.4e+03;
RESULT 1277
ID AAY72935 standard; protein; 266 AA.
DE OmpA signal peptide-human TRAIL fusion protein.
PN WO200125397-A2.
PD 12-APR-2001.
PA (VION-) VION PHARM INC.
Query Match 38.7%; Score 36; DB 4; Length 266;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
RESULT 1278
ID ABU09032 standard; protein; 267 AA.
DE Human tumour wilting extract protein, Apo-2L I_100.
PN CN1367248-A.
PD 04-SEP-2002.
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
Query Match 38.7%; Score 36; DB 6; Length 267;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1279
ID ABR82204 standard; protein; 270 AA.
DE Chimeric hTNFalpha/hTRAIL protein.
PN WO2003050254-A2.
PD 19-JUN-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 38.7%; Score 36; DB 6; Length 270;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1280
ID ADL98265 standard; protein; 271 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #2.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 271;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1281
ID ADW00621 standard; protein; 271 AA.
DE Human protein encoded by gene splice variant #4.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 271;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1282
ID ADF58901 standard; protein; 274 AA.
DE Human polypeptide sequence SEQ ID NO:1309.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 7; Length 274;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1283
ID ADT59020 standard; protein; 278 AA.
DE Plant polypeptide, SEQ ID 9097.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 38.7%; Score 36; DB 8; Length 278;
Best Local Similarity 45.5%; Pred. No. 1.5e+03;
RESULT 1284
ID AAW76332 standard; protein; 279 AA.
DE Human TL2 (TRAIL), ligand for TR5.
PN EP867509-A2.
PD 30-SEP-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 279;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1285
ID AAW95032 standard; protein; 279 AA.
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
PN EP897114-A2.
PD 17-FEB-1999.

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PA (SMIK ) SMITHKLINE BEECHAM CORP.
  Query Match      38.7%; Score 36; DB 2; Length 279;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1286
ID ADX71478 standard; protein; 279 AA.
DE Plant full length insert polypeptide seqid 40844.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
  Query Match      38.7%; Score 36; DB 8; Length 279;
  Best Local Similarity 25.0%; Pred. No. 1.5e+03;
RESULT 1287
ID ADN95444 standard; protein; 280 AA.
DE Human BEC/LEC-related protein sequence SeqID367.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN ) LICENTIA LTD.
  Query Match      38.7%; Score 36; DB 7; Length 280;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1288
ID AAW19777 standard; protein; 281 AA.
DE Novel cytokine Apo-2 ligand.
PN WO9725428-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1289
ID AAW27134 standard; protein; 281 AA.
DE Human Apoptosis inducing molecule-I (AIM-I).
PN WO9733899-A1.
PD 18-SEP-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1290
ID AAW19787 standard; protein; 281 AA.
DE Human apoptosis inducer cytokine TRAIL.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMV ) IMMUNEX CORP.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1291
ID AAW76829 standard; protein; 281 AA.
DE Human TL2 protein.
PN EP870827-A2.
PD 14-OCT-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1292
ID AAW56760 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMV ) IMMUNEX CORP.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1293
ID AAW44354 standard; protein; 281 AA.
DE Human AGP-1.
PN WO9746686-A2.
PD 11-DEC-1997.
PA (AMGB-) AMGEN INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1294
ID AAY01517 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR ) BIO MERIEUX.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1295
ID AAY01516 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR ) BIO MERIEUX.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1296
ID AAY27018 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D269A.
PN WO936535-A1.
PD 22-JUL-1999.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1297
ID AAY27019 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
PN WO936535-A1.
PD 22-JUL-1999.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1298
ID AAY27016 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A.
PN WO936535-A1.
PD 22-JUL-1999.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1299
ID AAY27017 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D218A.
PN WO936535-A1.
PD 22-JUL-1999.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1300
ID AAY27012 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) polypeptide.
PN WO936535-A1.
PD 22-JUL-1999.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 2; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1301
ID AAY81956 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence.
PN US6046048-A.
PD 04-APR-2000.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 3; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1302
ID AAB24038 standard; protein; 281 AA.
DE Human PRO1096 protein sequence SEQ ID NO:51.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
  Query Match      38.7%; Score 36; DB 3; Length 281;
  Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1303
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ID AAB08545 standard; protein; 281 AA.
DE Amino acid sequence of a human TRAIL polypeptide.
PN WO200048619-A1.
PD 24-AUG-2000.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1304
ID AAB28691 standard; protein; 281 AA.
DE Human AGP-1.
PN WO200063253-A1.
PD 26-OCT-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1305
ID AAB50977 standard; protein; 281 AA.
DE Human PRO1096 protein.
PN WO200073348-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1306
ID AAB67243 standard; protein; 281 AA.
DE Human Apo2 ligand.
PN WO200100832-A1.
PD 04-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1307
ID AAE11031 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1308
ID AAB48350 standard; protein; 281 AA.
DE Human TL2 polypeptide.
PN WO200077191-A1.
PD 21-DEC-2000.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1309
ID ABB08133 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN WO200236141-A2.
PD 10-MAY-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1310
ID ABG31630 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO200266044-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1311
ID AAU75062 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6329148-B1.
PD 11-DEC-2001.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1312
ID ABG72257 standard; protein; 281 AA.

DE Human tumour related apoptosis inducing ligand (TRAIL).
PN CN1354183-A.
PD 19-JUN-2002.
PA (TWO-) NO 2 MILITARY MEDICAL COLLEGE PLA.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1313
ID AAM51077 standard; protein; 281 AA.
DE Human Apo-2 ligand (TRAIL).
PN WO200209755-A2.
PD 07-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1314
ID ABP51954 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence SEQ ID NO:4.
PN WO200248376-A2.
PD 20-JUN-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1315
ID AAO19095 standard; protein; 281 AA.
DE C neoformans antigen expressing dendritic cell related protein #4.
PN WO200266053-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1316
ID AAU79593 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1317
ID ABG73861 standard; protein; 281 AA.
DE Human Apo-2 ligand protein.
PN US6462176-B1.
PD 08-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1318
ID ABU10205 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN US2003004313-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1319
ID ABU71443 standard; protein; 281 AA.
DE Human neoplasia inhibiting PRO polypeptide PRO1096.
PN US2002192209-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1320
ID ABG72738 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN WO200283946-A1.
PD 24-OCT-2002.
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;

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RESULT 1321
ID AAO29543 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003042367-A2.
PD 22-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1322
ID ABU08558 standard; protein; 281 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMMV ) IMMUNEX CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1323
ID ABR42313 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003040307-A2.
PD 15-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1324
ID ABG71905 standard; protein; 281 AA.
DE Human TRAIL receptor-associated protein.
PN WO200279377-A2.
PD 10-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1325
ID ABP60546 standard; protein; 281 AA.
DE Human tumour necrosis factor TRAIL.
PN WO200294192-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1326
ID AAE36258 standard; protein; 281 AA.
DE Human TR4 ligand, TRAIL protein.
PN WO200297033-A2.
PD 05-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1327
ID AAO31151 standard; protein; 281 AA.
DE Human TNF-related apoptosis-inducing ligand (TRAIL).
PN WO2003054216-A2.
PD 03-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1328
ID ABO25125 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
PN US2003013099-A1.
PD 16-JAN-2003.
PA (LASE/) LASEK A K W.
PA (JONE/) JONES D A.
PA (KARP/) KARP A R.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1329
ID ADB61480 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R115C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1330
ID ADB61482 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N134C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1331
ID ADB61484 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant B144C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1332
ID ADB61495 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant H264C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1333
ID ADB61478 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S111C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1334
ID ADB61494 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E263C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1335
ID ADB61481 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant B116C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1336
ID ADB61487 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1337
ID ADB61485 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N152C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1338
ID ADB61490 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant K179C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
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Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1357
ID ADK72313 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #7.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1358
ID ADK72305 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1359
ID ADK72309 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #5.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1360
ID ADK72303 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1361
ID ADK72304 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #2.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1362
ID ADK72308 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #4.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1363
ID ADK72312 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #6.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1364
ID ADK72307 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1365
ID ADK72296 standard; protein; 281 AA.
DE Human wild-type Apo-2 ligand, seq id 1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1366
ID ADK72310 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1367
ID ADJ63976 standard; protein; 281 AA.
DE Human apoptosis inducing molecule 1, AIM-1.
PN US2004038347-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1368
ID ADL71816 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-1 (AIM-I) protein.
PN US2004047864-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1369
ID ADK15498 standard; protein; 281 AA.
DE Human TRAIL protein.
PN US2004052788-A1.
PD 18-MAR-2004.
PA (IMMV ) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1370
ID ADN07587 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-1 protein.
PN US2004048340-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1371
ID ADR14209 standard; protein; 281 AA.
DE Human NF-kappaB pathway-associated protein SeqID210.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1372
ID ADK82215 standard; protein; 281 AA.
DE Human TRAIL amino acid sequence SEQ ID NO:66.
PN WO2004016753-A2.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1373
ID ADS88000 standard; protein; 281 AA.
DE Tumour treatment-related human protein sequence SeqID36.
PN WO2004034995-A2.
PD 29-APR-2004.
PA (UYPI-) UNIV PITTSBURGH.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1374
ID ABO84415 standard; protein; 281 AA.
DE Human cancer-associated protein HP7-053.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1375
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ID ADP23388 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO:566.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1376
ID ADT55244 standard; protein; 281 AA.
DE Amino acid sequence of human TRAIL protein.
PN WO2004087930-A2.
PD 14-OCT-2004.
PA (UYSL-) UNIV SAINT LOUIS.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1377
ID ADU22883 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (Apo2L) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1378
ID ADU22881 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (TRAIL) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1379
ID ADU77157 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN WO2004101608-A2.
PD 25-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1380
ID ADW02206 standard; protein; 281 AA.
DE Human membrane bound TRAIL protein.
PN WO200500220-A2.
PD 06-JAN-2005.
PA (CELL-) CELL GENESYS INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1381
ID ADY34239 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2005016236-A2.
PD 24-FEB-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1382
ID ADY14868 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 674.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1383
ID ADY14870 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 676.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1384
ID ADY19766 standard; protein; 281 AA.

ID PRO polypeptide SEQ ID NO 5572.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1385
ID ADZ72350 standard; protein; 281 AA.
DE Human Apo-2 ligand protein, SEQ ID NO: 1.
PN US2005089958-A1.
PD 28-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1386
ID AEA21853 standard; protein; 281 AA.
DE Human kininogen D5-TRAIL related protein SEQ ID NO 4.
PN CN1546528-A.
PD 17-NOV-2004.
PA (UYPL-) UNIV PLA SECOND MILITARY MEDICAL.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1387
ID AEA23811 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 353.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1388
ID AEA23728 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 270.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1389
ID AEA27598 standard; protein; 281 AA.
DE Human TRAIL protein SEQ ID NO:66.
PN US2005129616-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1390
ID AEA55214 standard; protein; 281 AA.
DE Human TRAIL protein, SEQ ID NO:66.
PN US2005129699-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1391
ID AEB16293 standard; protein; 281 AA.
DE Trail cytokine.
PN WO2005056596-A1.
PD 23-JUN-2005.
PA (UYGR-) RIJKSUNIV GRONINGEN.
PA (EUMO-) EURO MOLECULAR BIOLOGY LAB.
PA (UYNA-) UNIV NAT IRELAND.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1392
ID AEA81246 standard; protein; 281 AA.
DE Human tumor necrosis factor superfamily-10 protein.
PN US2005136465-A1.
PD 23-JUN-2005.
PA (CLER/) CLERC R G.
PA (DUCH/) DUCHATEAU-NGUYEN G.
PA (GARD/) GARDES C.
PA (MIZR/) MIZRAHI J.

PA (OSTE/) OSTENSON C. 38.7%; Score 36; DB 9; Length 281;
Query Match 41.7%; Pred. No. 1.5e+03;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1393
ID AEB92344 standard; protein; 281 AA.
DE Human TRAIL, SEQ ID 2.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1394
ID ABM67549 standard; protein; 283 AA.
DE Phototachidus luminescens protein sequence #646.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 6; Length 283;
Best Local Similarity 47.1%; Pred. No. 1.6e+03;
RESULT 1395
ID ADH71894 standard; protein; 284 AA.
DE Human protein of the invention NOV31k SEQ ID NO:790.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 284;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1396
ID AAB08727 standard; protein; 288 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1397
ID AAU99785 standard; protein; 288 AA.
DE Human B7 related protein-1 (B7RP1) #1.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1398
ID ADH71880 standard; protein; 290 AA.
DE Human protein of the invention NOV31d SEQ ID NO:776.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 290;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1399
ID AAB08729 standard; protein; 302 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1400
ID AAB87395 standard; protein; 302 AA.
DE Human gene 2 encoded secreted protein HMWDB84, SEQ ID NO:136.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1401
ID AAG67292 standard; protein; 302 AA.
DE Amino acid sequence of a human hB7-H2 polypeptide.
PN WO200164704-A1.

PD 07-SEP-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1402
ID ABG65402 standard; protein; 302 AA.
DE Human albumin fusion protein #2077.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1403
ID AAU99789 standard; protein; 302 AA.
DE Human B7 related protein-1 (B7RP1) #2.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1404
ID ADH47719 standard; protein; 302 AA.
DE NOV3a protein, SEQ ID 16.
PN WO200268647-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1405
ID ADA41234 standard; protein; 302 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1406
ID ADC74429 standard; protein; 302 AA.
DE Human secreted protein - SEQ ID 1062.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1407
ID ADD25558 standard; protein; 302 AA.
DE , Binding domain-immunoglobulin fusion protein-associated protein #56.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1408
ID ADP68255 standard; protein; 302 AA.
DE Human NOV3a protein, a B7-H2 like protein SeqID 16.
PN WO200281510-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1409
ID ADH71892 standard; protein; 302 AA.
DE Human protein of the invention NOV31j SEQ ID NO:788.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1410
ID ADH71886 standard; protein; 302 AA.
DE Human protein of the invention NOV31g SEQ ID NO:782.
PN WO2003102155-A2.

PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1411
ID ADH71884 standard; protein; 302 AA.
DE Human protein of the invention NOV31f SEQ ID NO:780.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1412
ID ADH71896 standard; protein; 302 AA.
DE Human protein of the invention NOV31l SEQ ID NO:792.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1413
ID ADH73010 standard; protein; 302 AA.
DE Human B7-related protein-1, B7RP-1.
PN US2004001831-A1.
PD 01-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
PA (KOCH-) KOCH INST ROBERT.
Query Match
Best Local Similarity 42.9%; Score 36; DB 8; Length 302;
RESULT 1414
ID ADL78669 standard; protein; 302 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 2151.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1415
ID ADL25602 standard; protein; 302 AA.
DE Human diagnostic protein, NOV3a.
PN US2004005557-A1.
PD 08-JAN-2004.
PA (PADI/) PADIGARU M.
PA (ALSO/) ALSOBROOK J P.
PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BOLD/) BOLDOG F L.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASM/) CASMAN S J.
PA (GUOX/) GUO X.
PA (EDIN/) EDINGER S R.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (PENA/) PENNA C E A.
PA (TCHE/) TCHERNEV V T.
PA (ZERH/) ZERHUSEN B D.
PA (MILL/) MILLET I.
PA (MILL/) MILLER C E.
PA (LEPL/) LEPPLEY D M.
PA (SMIT/) SMITHSON G.
PA (BAUM/) BAUMGARTNER J C.
PA (HERR/) HERRMANN J L.
PA (PEYM/) PEYMAN J A.
PA (GORM/) GORMAN L.
PA (MEZE/) MEZES P D.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (GERL/) GERLACH V.

PA (GROS/) GROSSE W M.
PA (LIUX/) LIU X.
PA (ELLE/) ELLERMAN K.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D J.
PA (BURG/) BURGESS C E. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1416
ID ADN59025 standard; protein; 302 AA.
DE Human B7H protein #3.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1417
ID ADN59021 standard; protein; 302 AA.
DE Human B7H protein #1.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1418
ID ADR89355 standard; protein; 302 AA.
DE Human ICOS Ligand protein for immunotherapy method.
PN WO2004073732-A1.
PD 02-SEP-2004.
PA (LORA-) LORANTIS LTD. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1419
ID AEA18914 standard; protein; 302 AA.
DE Amino acid sequence of the human B7-like protein.
PN WO2005044999-A2.
PD 19-MAY-2005.
PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC. 38.7%; Score 36; DB 9; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1420
ID ADX76510 standard; protein; 303 AA.
DE Plant full length insert polypeptide seqid 45876.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y. 38.7%; Score 36; DB 8; Length 303;
Query Match
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1421
ID ABG30730 standard; protein; 304 AA.
DE Human B7-H2 transcript 1 (B7-H2 V1) polypeptide.
PN WO200253733-A2.
PD 11-JUL-2002.
PA (FARB) BAYER AG. 38.7%; Score 36; DB 5; Length 304;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1422
ID AAB67713 standard; protein; 309 AA.
DE Amino acid sequence of a human GL50 polypeptide.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GEMY) GENETICS INST INC. 38.7%; Score 36; DB 4; Length 309;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1423
ID AAO15802 standard; protein; 309 AA.
DE Human B7RP-1 protein.
PN US2002106730-A1.

PD 08-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 38.7%; Score 36; DB 5; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1424
ID ADH71882 standard; protein; 309 AA.
DE Human protein of the invention NOV31e SEQ ID NO:778.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1425
ID ADN59023 standard; protein; 309 AA.
DE Human B7H protein #2.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1426
ID ADQ76299 standard; protein; 309 AA.
DE Human B7RP-1 protein.
PN US2004137577-A1.
PD 15-JUL-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1427
ID ADN42318 standard; protein; 310 AA.
DE Human novel proteinNOV 54b.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 38.7%; Score 36; DB 8; Length 310;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1428
ID AAB93542 standard; protein; 314 AA.
DE Human protein sequence SEQ ID NO:12910.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1429
ID AAB94208 standard; protein; 314 AA.
DE Human protein sequence SEQ ID NO:14557.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 314;

Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1430
ID AAB36628 standard; protein; 314 AA.
DE Human FLEXHT-50 protein sequence SEQ ID NO:50.
PN WO200070047-A2.
PD 23-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 38.7%; Score 36; DB 4; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1431
ID AAE14787 standard; protein; 314 AA.
DE Human purple acid phosphatase.
PN WO200240684-A2.
PD 23-MAY-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1432
ID ADW07261 standard; protein; 314 AA.
DE Human hepatotoxicity biomarker protein BMS-PTX-062 SeqID13.
PN US2004265889-A1.
PD 30-DEC-2004.
PA (DURH/) DURHAM S K.
PA (DAMB/) DAMBACH D.
PA (HEFT/) HEFTA S.
PA (MOUL/) MOULIN F.
PA (GAOJ/) GAO J.
PA (OPIT/) OPITECK G.
PA (STOR/) STORM S M.
PA (GARU/) GARULACAN L A.
PA (LINJ/) LIN J.
Query Match 38.7%; Score 36; DB 9; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1433
ID ADY17085 standard; protein; 321 AA.
DE PRO polypeptide SEQ ID NO 2891.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 321;
Best Local Similarity 41.7%; Pred. No. 1.8e+03;
RESULT 1434
ID AAY74886 standard; protein; 327 AA.
DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1246.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
RESULT 1435
ID AAY74884 standard; protein; 327 AA.
DE Neisseria gonorrhoea ORF 298 protein sequence SEQ ID NO:1242.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
RESULT 1436
ID AAY74885 standard; protein; 327 AA.
DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1244.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
RESULT 1437
ID ADW17396 standard; protein; 328 AA.
DE Eucalyptus grandis transcription factor protein MYB family Seq 1152.
PN WO2005001050-A2.
PD 06-JAN-2005.

PA (ARBO-) ARBORGEN LLC. 38.7%; Score 36; DB 9; Length 328;
Query Match
Best Local Similarity 58.3%; Pred. No. 1.8e+03;
RESULT 1438
ID ADQ94415 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A.
PN WO2004065552-A2.
PD 05-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
RESULT 1439
ID ADR89010 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A (LDH-A) polypeptide.
PN WO2004071405-A2.
PD 26-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
RESULT 1440
ID ABP78644 standard; protein; 335 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 3818.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
RESULT 1441
ID ADB08318 standard; protein; 336 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:2258.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP-) WYETH HOLDINGS CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 336;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
RESULT 1442
ID ABB10322 standard; protein; 343 AA.
DE Human CDNA SEQ ID NO: 630.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 343;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1443
ID ABP66909 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 630.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 38.7%; Score 36; DB 5; Length 343;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1444
ID AAU18067 standard; protein; 344 AA.
DE Human immunoglobulin polypeptide SEQ ID No 212.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1445
ID ABB10504 standard; protein; 344 AA.
DE Human CDNA SEQ ID NO: 812.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1446
ID ABP67091 standard; protein; 344 AA.

DE Human polypeptide SEQ ID NO 812.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 38.7%; Score 36; DB 5; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1447
ID ADB31691 standard; protein; 344 AA.
DE Human novel protein SEQ ID NO 212.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1448
ID AAU18065 standard; protein; 345 AA.
DE Human immunoglobulin polypeptide SEQ ID No 210.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1449
ID ABB10502 standard; protein; 345 AA.
DE Human CDNA SEQ ID NO: 810.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1450
ID ABP67089 standard; protein; 345 AA.
DE Human polypeptide SEQ ID NO 810.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 38.7%; Score 36; DB 5; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1451
ID ADB31689 standard; protein; 345 AA.
DE Human novel protein SEQ ID NO 210.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 7; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1452
ID AAU15973 standard; protein; 351 AA.
DE Human novel secreted protein, Seq ID 926.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 351;
Best Local Similarity 38.9%; Pred. No. 2e+03;
RESULT 1453
ID ABU55042 standard; protein; 351 AA.
DE Human novel polypeptide #129.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 351;
Best Local Similarity 38.9%; Pred. No. 2e+03;
RESULT 1454
ID AAG81561 standard; protein; 352 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:216.
PN WO200134809-A2.
PD 17-MAY-2001.

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PA (GLAX ) GLAXO GROUP LTD.
Query Match      38.7%; Score 36; DB 4; Length 352;
Best Local Similarity 61.5%; Pred. No. 2e+03;
RESULT 1455
ID ADB80938 standard; protein; 359 AA.
DE RING-SH complex related protein, SEQ ID NO 12.
PN WO2003033646-A2.
PD 24-APR-2003.
PA (PROT-) PROTEOLOGICS INC.
Query Match      38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2e+03;
RESULT 1456
ID ADE54266 standard; protein; 359 AA.
DE Human Protein O00623, SEQ ID NO 69.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match      38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2e+03;
RESULT 1457
ID AAU36115 standard; protein; 361 AA.
DE Klebsiella pneumoniae cellular proliferation protein #103.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match      38.7%; Score 36; DB 4; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1458
ID ABU28113 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #13640.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1459
ID ABU31873 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #17400.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1460
ID ADQ94417 standard; protein; 361 AA.
DE Rat mitochondrial lactate dehydrogenase A.
PN WO2004065552-A2.
PD 05-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match      38.7%; Score 36; DB 8; Length 361;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1461
ID ADR89012 standard; protein; 361 AA.
DE Rat mitochondrial form of LDH-A polypeptide.
PN WO2004071405-A2.
PD 26-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match      38.7%; Score 36; DB 8; Length 361;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1462
ID ABG22417 standard; protein; 362 AA.
DE Novel human diagnostic protein #22408.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match      38.7%; Score 36; DB 4; Length 362;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
RESULT 1463
ID AAU18005 standard; protein; 370 AA.
DE Human immunoglobulin polypeptide SEQ ID No 150.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      38.7%; Score 36; DB 4; Length 370;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1464
ID ADB31629 standard; protein; 370 AA.
DE Human novel protein SEQ ID NO 150.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      38.7%; Score 36; DB 7; Length 370;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1465
ID ADC31206 standard; protein; 374 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1288.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match      38.7%; Score 36; DB 7; Length 374;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
RESULT 1466
ID ADH52744 standard; protein; 375 AA.
DE Porphyromonas gulae B69 OprF protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ ) PFIZER PROD INC.
Query Match      38.7%; Score 36; DB 7; Length 375;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1467
ID ADH52741 standard; protein; 375 AA.
DE Porphyromonas gulae B43 OprF protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ ) PFIZER PROD INC.
Query Match      38.7%; Score 36; DB 7; Length 375;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1468
ID ABO66029 standard; protein; 377 AA.
DE Klebsiella pneumoniae polypeptide seqid 12546.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      38.7%; Score 36; DB 7; Length 377;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
RESULT 1469
ID ADI16664 standard; protein; 382 AA.
DE Human NOVX protein to treat human pathological conditions SeqID200.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match      38.7%; Score 36; DB 5; Length 382;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
RESULT 1470
ID AAU23676 standard; protein; 387 AA.
DE Novel human enzyme polypeptide #762.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      38.7%; Score 36; DB 4; Length 387;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
RESULT 1471
ID ABR53859 standard; protein; 387 AA.
DE Protein sequence #SEQ ID 2583.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match      38.7%; Score 36; DB 6; Length 387;
Best Local Similarity 77.8%; Pred. No. 2.2e+03;
RESULT 1472
ID ADK64914 standard; protein; 387 AA.
DE Disease treating protein complex-derived protein #1559.
PN EP1338608-A2.
```


PD 27-AUG-2003.
PA (CELL-) CELLZOME AG. 38.7%; Score 36; DB 7; Length 387;
Query Match 77.8%; Pred. No. 2.2e+03;
RESULT 1473
ID AAO19905 standard; protein; 388 AA.
DE Human TA4 receptor associated protein swissnew/070528/5H4_CAVPO.
PN WO2002101043-A2.
PD 19-DEC-2002.
PA (FARB) BAYER AG. 38.7%; Score 36; DB 6; Length 388;
Query Match 41.2%; Pred. No. 2.2e+03;
RESULT 1474
ID AAU09397 standard; protein; 390 AA.
DE Soluble Porphyromonas gingivalis polypeptide from PG32.
PN WO200183530-A1.
PD 08-NOV-2001.
PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 5; Length 390;
Query Match 42.9%; Pred. No. 2.2e+03;
RESULT 1475
ID AAY34490 standard; protein; 391 AA.
DE Porphyromonas gingivalis protein PG32.
PN WO9929870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 2; Length 391;
Query Match 42.9%; Pred. No. 2.2e+03;
RESULT 1476
ID AAY34365 standard; protein; 395 AA.
DE Porphyromonas gingivalis protein PG32.
PN WO9929870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 2; Length 395;
Query Match 42.9%; Pred. No. 2.3e+03;
RESULT 1477
ID ABG12815 standard; protein; 400 AA.
DE Novel human diagnostic protein #12806.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 38.7%; Score 36; DB 4; Length 400;
Query Match 50.0%; Pred. No. 2.3e+03;
RESULT 1478
ID ABU65118 standard; protein; 403 AA.
DE Human NOV51a protein.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 5; Length 403;
Query Match 66.7%; Pred. No. 2.3e+03;
RESULT 1479
ID ADL04887 standard; protein; 403 AA.
DE M. catarrhalis protein #653.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP. 38.7%; Score 36; DB 8; Length 403;
Query Match 71.4%; Pred. No. 2.3e+03;
RESULT 1480
ID ADN61887 standard; protein; 404 AA.
DE Human novel protein NOV51a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M. 38.7%; Score 36; DB 8; Length 409;
PA (SPYT/) SPYTEK K A. 38.7%; Score 36; DB 8; Length 409;
PA (SHEN/) SHENOY S G. 38.7%; Score 36; DB 8; Length 409;
PA (TAUP/) TAUPIER R J. 38.7%; Score 36; DB 8; Length 409;
PA (PENA/) PENA C E A. 38.7%; Score 36; DB 8; Length 409;
PA (LILL/) LI L. 38.7%; Score 36; DB 8; Length 409;
PA (ZERH/) ZERHUSEN B D. 38.7%; Score 36; DB 8; Length 409;
PA (GUSE/) GUSEV V Y. 38.7%; Score 36; DB 8; Length 409;

PA (JIWW/) JI W. 38.7%; Score 36; DB 8; Length 404;
PA (GORM/) GORMAN L. 38.7%; Score 36; DB 8; Length 404;
PA (MILL/) MILLER C E. 38.7%; Score 36; DB 8; Length 404;
PA (KEKU/) KEKUDA R. 38.7%; Score 36; DB 8; Length 404;
PA (PATT/) PATTURAJAN M. 38.7%; Score 36; DB 8; Length 404;
PA (GANG/) GANGOLLI E A. 38.7%; Score 36; DB 8; Length 404;
PA (VERN/) VERNET C A M. 38.7%; Score 36; DB 8; Length 404;
PA (GUOX/) GUO X S. 38.7%; Score 36; DB 8; Length 404;
PA (TCHE/) TCHERNEV V T. 38.7%; Score 36; DB 8; Length 404;
PA (FERN/) FERNANDES E R. 38.7%; Score 36; DB 8; Length 404;
PA (CASM/) CASMAN S J. 38.7%; Score 36; DB 8; Length 404;
PA (MALY/) MALYANKAR U M. 38.7%; Score 36; DB 8; Length 404;
PA (GERL/) GERLACH V. 38.7%; Score 36; DB 8; Length 404;
PA (LIUY/) LIU Y. 38.7%; Score 36; DB 8; Length 404;
PA (ANDE/) ANDERSON D W. 38.7%; Score 36; DB 8; Length 404;
PA (SPAD/) SPADERNA S K. 38.7%; Score 36; DB 8; Length 404;
PA (CATT/) CATTERTON E. 38.7%; Score 36; DB 8; Length 404;
PA (LEIT/) LEITE M W. 38.7%; Score 36; DB 8; Length 404;
PA (ZHON/) ZHONG H. 38.7%; Score 36; DB 8; Length 404;
PA (ALSO/) ALSOBROOK J P. 38.7%; Score 36; DB 8; Length 404;
PA (LEPL/) LEPLEY D M. 38.7%; Score 36; DB 8; Length 404;
PA (RIEG/) RIEGER D K. 38.7%; Score 36; DB 8; Length 404;
PA (BURG/) BURGESS C E. 38.7%; Score 36; DB 8; Length 404;
Query Match 66.7%; Pred. No. 2.3e+03;
RESULT 1481
ID AAY96727 standard; protein; 409 AA.
DE Casein kinase II interacting protein 1 (CKIP-1).
PN WO200036100-A1.
PD 22-JUN-2000.
PA (UYWO-) UNIV WESTERN ONTARIO. 38.7%; Score 36; DB 3; Length 409;
PA (UYMA-) UNIV MANITOBA. 38.7%; Score 36; DB 3; Length 409;
PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND. 38.7%; Score 36; DB 3; Length 409;
Query Match 50.0%; Pred. No. 2.4e+03;
RESULT 1482
ID AAM51211 standard; protein; 409 AA.
DE Human osteoclast expressed polypeptide SEQ ID NO 8.
PN JP2001231573-A. 38.7%; Score 36; DB 3; Length 409;
PD 28-AUG-2001.
PA (SHIO) SHIONOGI & CO LTD. 38.7%; Score 36; DB 4; Length 409;
Query Match 50.0%; Pred. No. 2.4e+03;
RESULT 1483
ID ADQ19480 standard; protein; 409 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2299.
PN WO2004048938-A2. 38.7%; Score 36; DB 4; Length 409;
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC. 38.7%; Score 36; DB 8; Length 409;
Query Match 50.0%; Pred. No. 2.4e+03;
RESULT 1484
ID ADRI4341 standard; protein; 409 AA.
DE Human NF-kappaB pathway-associated protein SeqID342.
PN WO2004065577-A2. 38.7%; Score 36; DB 8; Length 409;
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO. 38.7%; Score 36; DB 8; Length 409;
Query Match 50.0%; Pred. No. 2.4e+03;
RESULT 1485
ID ADP55230 standard; protein; 409 AA.
DE Human PRO protein sequence SEQ ID NO:1206.
PN WO2004039956-A2. 38.7%; Score 36; DB 8; Length 409;
PD 13-MAY-2004.
PA (GETH) GENENTECH INC. 38.7%; Score 36; DB 8; Length 409;
Query Match 50.0%; Pred. No. 2.4e+03;
RESULT 1486
ID AAY76047 standard; protein; 411 AA.
DE Rat skin cell protein, SEQ ID NO:302.
PN WO9955865-A1. 38.7%; Score 36; DB 8; Length 409;
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD. 38.7%; Score 36; DB 8; Length 409;

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Query Match
Best Local Similarity 38.7%; Score 36; DB 3; Length 411;
RESULT 1487
ID AAB55986 standard; protein; 411 AA.
DE Skin cell protein, SEQ ID NO: 302.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 411;
RESULT 1488
ID ABB72186 standard; protein; 411 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 302.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 38.7%; Score 36; DB 5; Length 411;
RESULT 1489
ID ABG00248 standard; protein; 418 AA.
DE Novel human diagnostic protein #239.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 418;
RESULT 1490
ID AAM39789 standard; protein; 419 AA.
DE Human polypeptide SEQ ID NO 2934.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 419;
RESULT 1491
ID AAB93457 standard; protein; 419 AA.
DE Human protein sequence SEQ ID NO:12716.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 38.7%; Score 36; DB 4; Length 419;
RESULT 1492
ID ABM80981 standard; protein; 419 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81664, SEQ:2528.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 419;
RESULT 1493
ID ADU60360 standard; protein; 419 AA.
DE Housekeeping gene protein, SEQ ID 321.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA ) NGK INSULATORS LTD.
Query Match
Best Local Similarity 38.7%; Score 36; DB 8; Length 419;
RESULT 1494
ID AAR88131 standard; protein; 422 AA.
DE Aureobasidin sensitivity gene spaur1S product.
PN EP692534-A2.
PD 17-JAN-1996.
PA (TAKI ) TAKARA SHUZO CO LTD.
Query Match
Best Local Similarity 38.7%; Score 36; DB 2; Length 422;
RESULT 1495
ID AAR88130 standard; protein; 422 AA.
DE Aureobasidin resistance gene spaur1R product.
PN EP692534-A2.
PD 17-JAN-1996.
PA (TAKI ) TAKARA SHUZO CO LTD.
Query Match
Best Local Similarity 38.7%; Score 36; DB 2; Length 422;
RESULT 1496
ID ABU20958 standard; protein; 431 AA.
DE Protein encoded by Prokaryotic essential gene #6485.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 38.7%; Score 36; DB 6; Length 431;
RESULT 1497
ID ADZ68028 standard; protein; 440 AA.
DE Escherichia coli HipA7 protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 440;
RESULT 1498
ID ADZ68026 standard; protein; 440 AA.
DE Escherichia coli HipA protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 440;
RESULT 1499
ID ADZ68032 standard; protein; 440 AA.
DE Escherichia coli HipAD291A protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 440;
RESULT 1500
ID ADZ68030 standard; protein; 440 AA.
DE Escherichia coli HipAD88N protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match
Best Local Similarity 38.7%; Score 36; DB 9; Length 440;
RESULT 1501
ID ADZ68030 standard; protein; 440 AA.
DE Escherichia coli HipAD88N protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:54:14 ; Search time 8.81633 Seconds
(without alignments)
196.443 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	47.3	1249	2 F86909	probable DNA gyrase
2	44	47.3	1273	2 T10006	DNA topoisomerase
3	43	46.2	221	2 T29509	hypothetical prote
4	43	46.2	518	2 E84536	hypothetical prote
5	43	46.2	601	2 S38171	peptide transport
6	42	45.2	316	2 I38754	transcription fact
7	42	45.2	420	2 T45592	hypothetical prote
8	42	45.2	478	2 A49228	trypsin-like prote
9	42	45.2	681	2 I38755	transcription fact
10	42	45.2	1097	2 A56138	transcription fact
11	42	45.2	1356	2 T16754	hypothetical prote
12	42	45.2	1464	2 S47555	N-methyl-D-asparta
13	41.5	44.6	353	2 S37138	protoporphyrin IX
14	41.5	44.6	355	2 A89858	hypothetical prote
15	41.5	44.6	632	2 T16128	hypothetical prote
16	41	44.1	449	2 H84870	probable glucosylt
17	41	44.1	502	2 T29729	hypothetical prote
18	41	44.1	766	1 WZBEC5	infected cell prot
19	41	44.1	925	2 T37831	hypothetical prote
20	40.5	43.5	792	2 G86564	phenylalanyl tRNA
21	40.5	43.5	792	2 H72058	phenylalanine-tRNA
22	40.5	43.5	792	2 D81608	phenylalanine-tRNA
23	40	43.0	235	2 S73609	MG381 homolog H03
24	40	43.0	317	2 A47336	R-phycocerythrin ga
25	40	43.0	574	2 T29615	hypothetical prote
26	40	43.0	1491	1 S43793	copper-transportin
27	40	43.0	1500	2 S36149	copper-transportin
28	40	43.0	1985	2 I61776	Munc13-2 - rat
29	39.5	42.5	778	2 T40570	probable nuclear p

30	39.5	42.5	1137	2 G84581	copla-like retroel
31	39	41.9	70	2 T32770	hypothetical prote
32	39	41.9	71	2 T17765	hypothetical prote
33	39	41.9	165	2 C95036	PTS system, IIA co
34	39	41.9	214	2 A81697	hypothetical prote
35	39	41.9	277	2 F65014	xanthosine phospho
36	39	41.9	324	2 S73000	hypothetical prote
37	39	41.9	428	2 AD3593	dihydroorotase (EC
38	39	41.9	450	2 JC7266	3',5'-cyclic-nucle
39	39	41.9	505	2 T51403	hypothetical prote
40	39	41.9	659	2 G97906	transcription anti
41	39	41.9	929	2 T17392	vrl1 protein - Dic
42	39	41.9	1411	2 S40525	copper-transportin
43	39	41.9	1451	1 I58124	copper-transportin
44	39	41.9	1465	1 S78555	copper-transportin
45	39	41.9	1743	2 T26859	hypothetical prote
46	38	40.9	100	2 G71950	hypothetical prote
47	38	40.9	225	2 C86563	CT465 hypothetical
48	38	40.9	225	2 C72062	conserved hypothet
49	38	40.9	287	2 H90314	conserved hypothet
50	38	40.9	288	2 H81309	hypothetical prote
51	38	40.9	339	2 I58295	RAD51 protein homo
52	38	40.9	339	2 A48221	RAD51 protein homo
53	38	40.9	345	2 S64151	hypothetical prote
54	38	40.9	361	2 A95089	conserved hypothet
55	38	40.9	385	2 T22666	hypothetical prote
56	38	40.9	395	2 S44454	transcription fact
57	38	40.9	414	2 S62462	protein phosphatas
58	38	40.9	430	2 T44851	molybdopterin co-f
59	38	40.9	436	2 T39837	MAD box transcript
60	38	40.9	446	2 C86459	probable serine ca
61	38	40.9	448	2 I50730	yes-associated pro
62	38	40.9	498	2 A47286	3',5'-cyclic-AMP p
63	38	40.9	503	2 G85432	transcription init
64	38	40.9	551	2 T05667	probable growth re
65	38	40.9	558	2 T10672	aspartate-tRNA lig
66	38	40.9	653	2 A39922	potassium channel
67	38	40.9	654	2 S11049	potassium channel
68	38	40.9	660	2 S24125	potassium channel
69	38	40.9	757	1 S64742	dynammin-related pr
70	38	40.9	772	2 S22660	excision repair pr
71	38	40.9	844	2 T38730	probable helicase
72	38	40.9	913	2 T15474	hypothetical prote
73	38	40.9	997	2 JC6067	CCAAT-binding fact
74	38	40.9	998	2 A36368	transcription fact
75	38	40.9	1068	1 A43322	1-phosphatidylinos
76	38	40.9	1068	1 I38110	1-phosphatidylinos
77	38	40.9	1276	2 S69048	probable membrane
78	38	40.9	1364	2 T40839	hypothetical prote
79	38	40.9	2201	2 AH0095	probable sideropho
80	37.5	40.3	372	2 B84262	hypothetical prote
81	37.5	40.3	838	2 A96557	probable receptor
82	37	39.8	193	2 H86404	probable lipid tra
83	37	39.8	194	2 C82244	hypothetical prote
84	37	39.8	249	2 A97227	polyferredoxin lim
85	37	39.8	256	2 T30932	hypothetical prote
86	37	39.8	265	2 T31245	transglycosylase h
87	37	39.8	271	2 C75060	hydrogenase (EC 1.
88	37	39.8	341	2 T48858	acetylpolylamine an
89	37	39.8	365	2 C86700	phosphoserine tran
90	37	39.8	377	2 AC3426	mannosyltransferas
91	37	39.8	386	2 T18890	hypothetical prote
92	37	39.8	404	2 G87757	protein D1007.8 li
93	37	39.8	420	2 S62541	hypothetical prote
94	37	39.8	425	2 T33111	hypothetical prote
95	37	39.8	445	2 D83932	aminotransferase (
96	37	39.8	447	2 I49126	protein-tyrosine-p
97	37	39.8	463	2 S43787	glutamate-1-semial
98	37	39.8	465	2 T02698	Nicotiana tabacum
99	37	39.8	505	2 T41303	hypothetical prote
100	37	39.8	509	2 E86273	hypothetical prote
101	37	39.8	510	1 FOLJTM	gag polyprotein -
102	37	39.8	529	2 B49993	glycylpeptide N-te

103	37	39.8	608	1	ABXL68	68K serum albumin	176	36	38.7	1072	2	AD1280
104	37	39.8	647	2	S48471	probable membrane	177	36	38.7	1072	2	AD1643
105	37	39.8	652	2	T16582	hypothetical prote	178	36	38.7	1144	2	T13749
106	37	39.8	731	1	A32621	gelsolin, cytosoli	179	36	38.7	1181	2	A41052
107	37	39.8	870	2	T25338	hypothetical prote	180	36	38.7	1204	2	A96676
108	37	39.8	930	2	T20817	hypothetical prote	181	36	38.7	1210	2	A53183
109	37	39.8	989	2	T46659	period clock prote	182	36	38.7	1320	2	G81961
110	37	39.8	1047	2	B71402	hypothetical prote	183	36	38.7	1645	2	AG1897
111	37	39.8	1064	2	F86182	hypothetical prote	184	36	38.7	1722	2	E89753
112	37	39.8	1082	2	T15269	hypothetical prote	185	36	38.7	2156	1	RRVUNE
113	37	39.8	1170	2	I45914	hypothetical prote	186	36	38.7	2195	2	S61103
114	37	39.8	1735	2	A57607	integrin alpha 2 s	187	36	38.7	4753	1	A47437
115	37	39.8	13055	2	T16580	Munc13-1 - rat	188	35.5	38.2	278	2	B82388
116	36.5	39.2	78	2	F97852	hypothetical prote	189	35.5	38.2	349	2	T00526
117	36.5	39.2	238	2	T15817	hypothetical prote	190	35.5	38.2	356	2	S73315
118	36.5	39.2	657	2	A53545	hypothetical prote	191	35.5	38.2	401	2	F86754
119	36.5	39.2	804	2	AD0958	protein p84 - huma	192	35.5	38.2	591	2	E81687
120	36.5	39.2	832	1	S71788	P/CAP protein - hu	193	35.5	38.2	591	2	B71531
121	36.5	39.2	1756	2	T07566	hypothetical prote	194	35.5	38.2	742	1	S47018
122	36.5	39.2	1889	2	T50069	dynein heavy chain	195	35.5	38.2	742	2	C84319
123	36.5	39.2	4196	2	T43274	dynein heavy chain	196	35.5	38.2	1258	2	F96753
124	36	38.7	15	2	A61612	allatostatin - tob	197	35	37.6	42	2	I48240
125	36	38.7	68	2	A81968	hypothetical prote	198	35	37.6	89	2	S78744
126	36	38.7	108	2	C64516	hypothetical prote	199	35	37.6	130	2	H72642
127	36	38.7	121	2	JC7630	C-type allatostati	200	35	37.6	144	2	S66493
128	36	38.7	166	2	F59091	hypothetical prote	201	35	37.6	147	2	D27733
129	36	38.7	168	2	AG2198	hypothetical prote	202	35	37.6	157	2	H64965
130	36	38.7	176	2	T48292	hypothetical prote	203	35	37.6	157	2	C90980
131	36	38.7	218	2	D71693	hypothetical prote	204	35	37.6	157	2	H85825
132	36	38.7	227	2	T00671	probable methyl ch	205	35	37.6	161	2	T22222
133	36	38.7	246	2	AB1345	hypothetical prote	206	35	37.6	161	2	T41833
134	36	38.7	268	2	T40101	hypothetical prote	207	35	37.6	219	2	T08083
135	36	38.7	271	2	AG0757	hypothetical prote	208	35	37.6	223	2	I59173
136	36	38.7	282	2	S39972	probable cobalt tr	209	35	37.6	245	2	T28148
137	36	38.7	297	2	S66102	leucine-rich prote	210	35	37.6	245	2	S09666
138	36	38.7	327	2	A81839	protein secretion	211	35	37.6	254	2	C70682
139	36	38.7	327	2	D81103	probable periplasm	212	35	37.6	259	2	T28147
140	36	38.7	332	2	A23083	hypothetical prote	213	35	37.6	266	2	C71531
141	36	38.7	361	2	T49337	L-lactate dehydrog	214	35	37.6	267	1	JQ1324
142	36	38.7	363	2	T22594	hypothetical prote	215	35	37.6	267	2	JG0191
143	36	38.7	387	2	S12773	hypothetical prote	216	35	37.6	267	2	JG0191
144	36	38.7	393	2	A49008	mitochondrial impo	217	35	37.6	278	2	E81426
145	36	38.7	403	2	T38078	paired box transcr	218	35	37.6	281	2	JC4295
146	36	38.7	440	2	F64904	hypothetical prote	219	35	37.6	284	2	G82234
147	36	38.7	449	2	B84871	hipA protein - Esc	220	35	37.6	296	2	G90063
148	36	38.7	483	2	AB0072	probable glucosylt	221	35	37.6	297	2	G88035
149	36	38.7	506	1	FOLJG3	tagaturonate reduc	222	35	37.6	309	2	T41494
150	36	38.7	543	2	T37570	gag polyprotein -	223	35	37.6	313	2	T48439
151	36	38.7	562	2	E81069	WD repeat protei	224	35	37.6	324	2	T05273
152	36	38.7	562	2	T27807	glutaminyl-tRNA sy	225	35	37.6	342	2	T18474
153	36	38.7	573	2	D81799	hypothetical prote	226	35	37.6	344	2	F69272
154	36	38.7	579	2	A84227	glutamine-tRNA lig	227	35	37.6	344	2	C70208
155	36	38.7	581	2	T41210	hypothetical prote	228	35	37.6	349	2	T50895
156	36	38.7	593	2	S48135	hypothetical prote	229	35	37.6	351	2	D64134
157	36	38.7	593	2	S51776	hypothetical prote	230	35	37.6	351	2	A86045
158	36	38.7	594	1	A46758	glutamate decarbox	231	35	37.6	362	2	E91198
159	36	38.7	594	2	S51775	glutamate decarbox	232	35	37.6	362	2	A39714
160	36	38.7	594	2	JC4065	glutamate decarbox	233	35	37.6	364	2	A30341
161	36	38.7	622	2	E97126	glutamate decarbox	234	35	37.6	364	2	G69377
162	36	38.7	644	2	A36325	DNA mismatch repai	235	35	37.6	365	2	AD2669
163	36	38.7	644	2	C86747	epidermal growth f	236	35	37.6	368	2	B97451
164	36	38.7	646	2	S47929	topoisomerase IV s	237	35	37.6	376	2	T16147
165	36	38.7	654	2	B75587	signal recognition	238	35	37.6	380	2	E81302
166	36	38.7	695	2	T39242	probable N-glycosi	239	35	37.6	391	2	T23227
167	36	38.7	725	2	T19994	hypothetical prote	240	35	37.6	405	1	F69611
168	36	38.7	741	2	A45771	hypothetical prote	241	35	37.6	408	2	T42650
169	36	38.7	792	2	AB0038	2-5A-dependent RNA	242	35	37.6	411	2	B91220
170	36	38.7	817	2	T24063	probable outer mem	243	35	37.6	411	2	D86066
171	36	38.7	852	2	S57984	hypothetical prote	244	35	37.6	411	2	A65184
172	36	38.7	912	2	T02892	probable membrane	245	35	37.6	411	2	D88037
173	36	38.7	967	2	D72308	hypothetical prote	246	35	37.6	411	2	T03897
174	36	38.7	1003	2	T24545	conserved hypothet	247	35	37.6	414	2	B89024
175	36	38.7	1012	2	T13712	hypothetical prote	248	35	37.6	414	2	T34000
						dof protein - frui						G82174

SNF2-type helicase
SNF2-type helicase
dof protein - frui
parasporal crystal
hypothetical prote
epidermal growth f
phosphoribosylform
two-component hybr
protein F11C7.4 [i
genome polyprotein
SEC16 protein - ye
LDL-receptor-relat
probable maltose O
probable GDGL-moti
protoporphyrin IX
prophage pi2 prote
ATP synthase, chai
probable ATP synth
cdcH protein - Hal
cell division cycl
Similar to downy m
LDH-A - mouse (fira
protein YDR363w-a
hypothetical prote
serotonin receptor
hypothetical prote
DNA gyrase inhibit
SbmC protein [impo
SbmC protein [impo
hypothetical prote
ACMPV orf93 - Bom
H+-transporting tw
glutamate decarbox
class II histocomp
psbG protein - whe
probable cySH - My
class II histocomp
hypothetical prote
DNA excision repai
XPA protein - Afri
parB family protei
heat-shock protein
conserved hypothet
hypothetical prote
protein M01D1.8 [i
zinc finger, ADP-r
probable RNA-bindi
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypothet
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peptide transport
sepl [imported] -
type III secretion
G protein-coupled
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bacteriochlorophyl
chorismate synthas
chorismate synthas
hypothetical prote
probable type I re
hypothetical prote
cytochrome P450 cy
hypothetical prote
probable arylsulfa
probable arylsulfa
arylsulfatase acti
protein K02E7.2 [i
hypothetical prote
protein R02D1.1 [i
hypothetical prote
hypothetical prote

249 35 37.6 421 2 T35205 citrate synthase-1
250 35 37.6 426 2 F70343 enolase - Aquifex
251 35 37.6 431 2 G81179 oxidoreductase, pr
252 35 37.6 440 2 T01115 probable protein d
253 35 37.6 440 2 I49624 gap junction prote
254 35 37.6 441 2 T20840 hypothetical prote
255 35 37.6 443 1 A46248 dihydroorotate oxi
256 35 37.6 444 2 S57989 probable membrane
257 35 37.6 451 2 S44446 GDP dissociation i
258 35 37.6 454 2 H85293 hypothetical prote
259 35 37.6 454 2 A56954 yes-associated pro
260 35 37.6 455 2 T05804 hypothetical prote
261 35 37.6 458 2 T19941 hypothetical prote
262 35 37.6 461 1 DCHUO ornithine decarbox
263 35 37.6 472 2 I64098 glutamate-ammonia
264 35 37.6 505 2 S50567 hypothetical prote
265 35 37.6 506 2 S55786 DNA nucleotidylexo
266 35 37.6 511 2 E90083 t-complex protein1
267 35 37.6 514 2 B64055 periplasmic oligop
268 35 37.6 541 2 G90192 conserved hypothet
269 35 37.6 543 2 S73820 type I restriction
270 35 37.6 564 2 S44611 C02F5.9 protein -
271 35 37.6 569 2 A36187 interleukin-1 rece
272 35 37.6 580 2 T43310 glycerone kinase (
273 35 37.6 580 2 F84471 hypothetical prote
274 35 37.6 585 2 S61534 glutamate decarbox
275 35 37.6 593 1 A41367 glutamate decarbox
276 35 37.6 594 1 B41935 glutamate decarbox
277 35 37.6 599 2 S47928 signal recognition
278 35 37.6 611 1 WIWLEP E1 protein - Europ
279 35 37.6 613 1 WIWLEP E1 protein - deer
280 35 37.6 616 1 A40457 replication protei
281 35 37.6 618 2 T39985 probable arginyl-t
282 35 37.6 622 2 T37257 hypothetical prote
283 35 37.6 643 2 T19199 hypothetical prote
284 35 37.6 649 2 S74823 N-acetylmuramoyl-L
285 35 37.6 702 2 C86268 F13B4.2 protein -
286 35 37.6 711 2 T05148 protein kinase hom
287 35 37.6 716 2 G01627 androgen receptor
288 35 37.6 723 2 S70098 probable membrane
289 35 37.6 728 2 A86453 CDS protein F9L11.
290 35 37.6 749 2 B86606 primosomal protein
291 35 37.6 749 2 C72018 infected cell prot
292 35 37.6 773 2 T42575 ribonucleoside-dip
293 35 37.6 781 2 B64135 hypothetical prote
294 35 37.6 802 2 B84560 probable PTS syate
295 35 37.6 831 2 G91036 hypothetical prote
296 35 37.6 831 2 A85881 hypothetical prote
297 35 37.6 831 2 D65012 probable phosphoen
298 35 37.6 916 2 G81797 preprotein translo
299 35 37.6 916 2 D81072 preprotein translo
300 35 37.6 958 2 T51148 hypothetical prote
301 35 37.6 993 2 S21964 mating-type switch
302 35 37.6 1081 2 T31329 receptor tyrosine
303 35 37.6 1135 2 J50605 M polypeptide - Ha
304 35 37.6 1155 2 A26513 parasporal crystal
305 35 37.6 1181 2 C82500 IcmF-related prote
306 35 37.6 1190 2 F86677 pyruvate-flavodoxi
307 35 37.6 1217 2 D88996 protein Cl7B7.7 [i
308 35 37.6 1464 1 S29159 glutamate receptor
309 35 37.6 1464 2 A43274 N-methyl D-asparta
310 35 37.6 1704 2 T43141 vitellogenin 1 - m
311 35 37.6 1945 2 T13937 plexin A - fruit f
312 35 37.6 2368 2 S46005 ESR1 protein - yea
313 35 37.6 4767 2 T31345 hypothetical prote
314 34.5 37.1 58 2 S58628 hypothetical prote
315 34.5 37.1 145 2 D64202 DNA-directed RNA p
316 34.5 37.1 389 2 B82618 hypothetical prote
317 34.5 37.1 537 2 D89889 conserved hypothet
318 34.5 37.1 804 1 ISECTB DNA topoisomerase
319 34.5 37.1 804 2 B91208 DNA gyrase subunit
320 34.5 37.1 804 2 D86054 hypothetical prote
321 34.5 37.1 1297 2 S25714 son-of-sevenless-2

322 34 36.6 63 1 FEDV2V
323 34 36.6 96 2 T04223
324 34 36.6 101 2 B86645
325 34 36.6 107 2 A82815
326 34 36.6 114 2 AE1349
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328 34 36.6 145 2 S34574
329 34 36.6 176 2 A97808
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334 34 36.6 230 2 AF3113
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337 34 36.6 238 2 T30945
338 34 36.6 241 2 T33932
339 34 36.6 257 2 T28946
340 34 36.6 266 2 F81687
341 34 36.6 273 2 T51512
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348 34 36.6 309 2 A36064
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352 34 36.6 317 2 S77827
353 34 36.6 322 2 B81336
354 34 36.6 323 2 S43850
355 34 36.6 323 2 S36636
356 34 36.6 325 2 T40264
357 34 36.6 330 2 T51834
358 34 36.6 334 2 C69148
359 34 36.6 334 2 T19519
360 34 36.6 339 2 S35642
361 34 36.6 341 2 E83779
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363 34 36.6 348 2 T39358
364 34 36.6 351 2 AC2289
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366 34 36.6 367 2 JC6087
367 34 36.6 380 2 T19280
368 34 36.6 382 2 S74947
369 34 36.6 387 2 AI1567
370 34 36.6 388 2 D82023
371 34 36.6 388 2 E81244
372 34 36.6 411 1 OKRTL
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376 34 36.6 425 2 D64542
377 34 36.6 425 2 D71965
378 34 36.6 428 2 JQ1864
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384 34 36.6 467 2 D83055
385 34 36.6 472 2 A33312
386 34 36.6 474 2 T27566
387 34 36.6 479 2 E69613
388 34 36.6 480 2 S46153
389 34 36.6 481 2 A89102
390 34 36.6 498 2 T51430
391 34 36.6 503 2 A28415
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393 34 36.6 503 2 JX0071
394 34 36.6 503 2 S52085

ferredoxin [4Fe-4S
hypothetical prote
Glu-tRNA amidotran
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dTDP-glucose 4,6-d
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RAD51 protein homo
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heat-inducible tra
DNA-directed RNA p
hypothetical prote
angiotensin II rec
helix-loop-helix t
hypothetical prote
hypothetical prote
probable lipoprote
conserved hypothet
protein-lysine 6-o
aureobasidin a res
histidine-tRNA lig
probable exported
apolipoprotein N-a
apolipoprotein n-a
hypothetical 47.0K
hypothetical prote
pmBA-related prote
delta-8 sphingolip
probable dolichyl-
hypothetical prote
poly(A) polymerase
sarcoplasmic retic
hypothetical prote
ATP-dependent RNA
probable membrane
protein F25E5.4 [i
dolichyl-phosphate
steroid 11beta-mon
steroid 11beta-mon
steroid 11-beta-hy

395	34	36.6	516	2	G95406	probable ABC trans	468	34	36.6	1212	2	T13804	shs protein - frui
396	34	36.6	520	2	T20007	hypothetical prote	469	34	36.6	1214	2	T18549	DNA polymerase hom
397	34	36.6	530	2	D82412	chaperonin, 60 Kd	470	34	36.6	1214	2	T30941	DNA polymerase - C
398	34	36.6	543	2	A72292	hypothetical prote	471	34	36.6	1239	2	G71266	probable ATP-depen
399	34	36.6	544	2	S62527	probable amino-aci	472	34	36.6	1263	2	T13805	spalt-related prot
400	34	36.6	544	2	H86828	fructuronate reduc	473	34	36.6	1299	2	A86366	T26J12.6 protein -
401	34	36.6	554	2	T43211	cytoplasmic signal	474	34	36.6	1328	2	T23007	hypothetical prote
402	34	36.6	557	1	WZBYI	isocitrate lyase (475	34	36.6	1345	2	T44204	capsid protein U57
403	34	36.6	560	1	RGNVPM	trans-activating t	476	34	36.6	1345	2	T44017	major capsid prote
404	34	36.6	560	2	T10414	immediate early pr	477	34	36.6	1397	2	T10466	DNA topoisomerase
405	34	36.6	564	2	E64241	threonine-trNA lig	478	34	36.6	1536	1	RGYS3	regulatory protein
406	34	36.6	578	2	AF1958	L-aspartate oxidas	479	34	36.6	1557	2	T28811	hypothetical prote
407	34	36.6	584	2	T18908	hypothetical prote	480	34	36.6	1658	2	S55101	hypothetical prote
408	34	36.6	594	2	D64676	oligopeptide ABC t	481	34	36.6	1787	2	F84528	probable retroelem
409	34	36.6	607	2	H64041	probable long-chai	482	34	36.6	1919	2	T40032	hypothetical prote
410	34	36.6	608	2	A53195	afamin precursor -	483	34	36.6	2049	2	T43161	hypothetical prote
411	34	36.6	615	2	T15423	hypothetical prote	484	34	36.6	2180	2	A47651	sodium channel pro
412	34	36.6	616	2	T38717	probable GTP-bindi	485	34	36.6	2761	2	T29285	zinc-finger protei
413	34	36.6	623	2	D71435	hypothetical prote	486	34	36.6	2907	2	A57278	hypothetical prote
414	34	36.6	623	2	T28051	hypothetical prote	487	34	36.6	3507	2	T34513	fibrillin-2 precur
415	34	36.6	632	2	G88109	protein T24E12.10	488	34	36.6	3724	2	T18427	hypothetical prote
416	34	36.6	638	1	YSBST2	threonine-trNA lig	489	33.5	36.0	78	2	T17963	hypothetical prote
417	34	36.6	638	2	T21321	hypothetical prote	490	33.5	36.0	168	2	A28476	myosin heavy chain
418	34	36.6	640	1	UZADP7	terminal protein p	491	33.5	36.0	168	2	B25217	myosin heavy chain
419	34	36.6	658	2	A86231	hypothetical prote	492	33.5	36.0	169	2	A25217	myosin heavy chain
420	34	36.6	660	2	T38294	sec-7 cytohesin-li	493	33.5	36.0	258	2	T35147	glutamate uptake s
421	34	36.6	666	2	T43171	cytoplasmic signal	494	33.5	36.0	294	2	C75574	conserved hypothet
422	34	36.6	670	2	H96707	probable receptor	495	33.5	36.0	359	2	D81711	phospholipase D fa
423	34	36.6	672	2	T24507	hypothetical prote	496	33.5	36.0	374	2	AH1825	protoporphylin IX
424	34	36.6	715	2	JC4560	methylmalonyl-CoA	497	33.5	36.0	493	2	T05105	hypothetical prote
425	34	36.6	716	2	A86181	hypothetical prote	498	33.5	36.0	508	2	AG2206	serine/threonine k
426	34	36.6	739	2	T15215	hypothetical prote	499	33.5	36.0	523	2	H90529	potassium uptake p
427	34	36.6	755	2	G84791	probable ABC trans	500	33.5	36.0	838	2	S38156	hypothetical prote
428	34	36.6	757	2	C70034	conserved hypothet	501	33.5	36.0	953	2	F96498	hypothetical prote
429	34	36.6	764	2	I39934	protective antigen	502	33.5	36.0	1776	2	G86280	protein T5E21.13 [
430	34	36.6	764	2	S64951	hypothetical prote	503	33.5	36.0	1804	2	AF2250	serine/threonine k
431	34	36.6	804	2	T18014	hypothetical prote	504	33.5	36.0	1938	1	JX0178	myosin heavy chain
432	34	36.6	818	2	F97348	heavy-metal transp	505	33.5	36.0	1940	2	A29320	myosin heavy chain
433	34	36.6	857	2	S33821	median body protei	506	33	35.5	74	2	AF3436	myosin heavy chain
434	34	36.6	861	2	B84885	probable transcrip	507	33	35.5	75	2	C90601	hypothetical prote
435	34	36.6	876	2	T33176	hypothetical prote	508	33	35.5	76	2	AD1442	hypothetical prote
436	34	36.6	908	2	A33280	sarcalumenin precu	509	33	35.5	103	2	T13589	gp37-1 (Bacterioph
437	34	36.6	957	2	A49847	nitrite reductase	510	33	35.5	108	2	T00420	probable small nuc
438	34	36.6	962	2	D70661	probable membranep	511	33	35.5	110	2	H64512	hypothetical prote
439	34	36.6	967	2	G96637	hypothetical prote	512	33	35.5	113	2	AH3438	hypothetical prote
440	34	36.6	981	2	T51921	hypothetical prote	513	33	35.5	115	2	T38514	small nuclear ribo
441	34	36.6	997	2	S44457	period clock prote	514	33	35.5	118	2	I38861	small nuclear ribo
442	34	36.6	1010	2	S45389	probable membrane	515	33	35.5	128	2	AF2143	hypothetical prote
443	34	36.6	1014	2	H71602	protein with DnaJ	516	33	35.5	135	2	C69446	hypothetical prote
444	34	36.6	1036	2	S73601	protein P200 - Myc	517	33	35.5	137	2	AI1375	hypothetical prote
445	34	36.6	1058	2	AG2541	cation efflux syst	518	33	35.5	152	2	T07858	glycine-rich prote
446	34	36.6	1075	2	G59434	KIAA0411 protein [519	33	35.5	155	2	S75888	hypothetical prote
447	34	36.6	1075	2	C96682	protein FlE22.16 [520	33	35.5	161	2	T00729	hypothetical prote
448	34	36.6	1133	2	S54496	probable membrane	521	33	35.5	161	2	F72861	AcOrf-93 protein -
449	34	36.6	1135	1	GNVUH7	M polyprotein - Ha	522	33	35.5	162	2	D84959	small protein B [i
450	34	36.6	1135	1	GNVUH7	M polyprotein - Ha	523	33	35.5	164	2	S73814	probable 5-formyl
451	34	36.6	1155	2	S02134	parasporal crystal	524	33	35.5	167	2	T12580	GRP-binding protei
452	34	36.6	1155	2	I39838	parasporal crystal	525	33	35.5	177	2	A86610	frame-shift with C
453	34	36.6	1156	2	JD0002	parasporal crystal	526	33	35.5	188	2	F81808	hypothetical prote
454	34	36.6	1156	2	A29125	parasporal crystal	527	33	35.5	188	2	AC3613	probable s-adenosy
455	34	36.6	1156	2	A29838	parasporal crystal	528	33	35.5	195	2	I46272	trophoblast interf
456	34	36.6	1165	2	S11446	parasporal crystal	529	33	35.5	195	2	A96731	unknown protein F5
457	34	36.6	1166	2	S32645	parasporal crystal	530	33	35.5	200	2	S55609	hypothetical prote
458	34	36.6	1171	2	A37829	parasporal crystal	531	33	35.5	210	2	T05541	heat shock protein
459	34	36.6	1171	2	I40572	parasporal crystal	532	33	35.5	216	1	TLBPX2	tail fiber protein
460	34	36.6	1172	2	S32689	parasporal crystal	533	33	35.5	220	2	A41662	hypothetical prote
461	34	36.6	1174	2	A42459	parasporal crystal	534	33	35.5	223	2	S06576	finger protein (cl
462	34	36.6	1176	2	A48970	parasporal crystal	535	33	35.5	237	2	A45587	lectin - Dioclea l
463	34	36.6	1182	2	T30189	myelin transcripti	536	33	35.5	237	2	T27145	hypothetical prote
464	34	36.6	1187	2	T46637	transcription fact	537	33	35.5	243	2	C64124	molybdopterin bios
465	34	36.6	1188	2	T46608	zinc finger protei	538	33	35.5	247	1	D24706	modulation protein
466	34	36.6	1189	2	S00944	parasporal crystal	539	33	35.5	247	2	H95319	phosphoadenylyl-su
467	34	36.6	1190	2	T38636	tat binding homolo	540	33	35.5	249	2	C85592	molybdopterin bios

541	33	35.5	249	2	H90741	molybdopterin bio
542	33	35.5	257	2	D81086	FrpC operon protei
543	33	35.5	258	2	G96798	hypothetical prote
544	33	35.5	263	2	A2534	hypothetical prote
545	33	35.5	267	2	T00114	exodeoxyribonuclea
546	33	35.5	271	2	B81182	FrpC operon protei
547	33	35.5	275	2	A82257	oxidoreductase, sh
548	33	35.5	284	2	S52672	hypothetical prote
549	33	35.5	287	2	S25259	streptomycin resis
550	33	35.5	289	2	A84790	probable RNA-bind
551	33	35.5	294	2	T24776	hypothetical prote
552	33	35.5	298	2	C82073	signal peptidase I
553	33	35.5	299	2	T25596	hypothetical prote
554	33	35.5	301	2	B69815	CDP-glucose 4,6-de
555	33	35.5	304	2	T09357	hypothetical prote
556	33	35.5	305	2	C89915	hypothetical prote
557	33	35.5	305	2	A89721	protein T10B10.4 [
558	33	35.5	307	2	T16457	hypothetical prote
559	33	35.5	309	2	T48125	syndecan-1 - Chine
560	33	35.5	310	2	S43101	SEP5 protein - fru
561	33	35.5	314	2	B95034	dihydropteroate sy
562	33	35.5	314	2	B97905	dihydropteroate sy
563	33	35.5	316	1	A43661	dihydropteroate sy
564	33	35.5	326	2	A54497	surface membrane p
565	33	35.5	330	2	AD2854	conserved hypothet
566	33	35.5	336	2	H70328	hypothetical prote
567	33	35.5	338	2	E95251	hypothetical prote
568	33	35.5	338	2	B98116	ornithine carbamoy
569	33	35.5	349	2	T23931	hypothetical prote
570	33	35.5	356	2	AE2729	cytochrome oxidase
571	33	35.5	363	2	A85700	probable GTP-bind
572	33	35.5	363	2	AB0721	probable ATP/GTP-b
573	33	35.5	363	2	H64866	probable GTP-bind
574	33	35.5	363	2	D90842	probable GTP-bind
575	33	35.5	363	2	T64150	probable GTP-bind
576	33	35.5	363	2	AD0245	conserved hypothet
577	33	35.5	367	1	I69653	UDPgalactopyranose
578	33	35.5	371	2	G87644	hypothetical prote
579	33	35.5	372	2	F97510	BA483f11.2.1 (coxI
580	33	35.5	373	2	F81438	probable periplasm
581	33	35.5	383	1	C53309	prgY protein - Ent
582	33	35.5	386	2	A97631	hypothetical 37.4K
583	33	35.5	387	2	S77268	carboxymorspermid
584	33	35.5	391	2	T40029	hypothetical prote
585	33	35.5	396	2	D64022	hypothetical prote
586	33	35.5	401	2	H84828	hypothetical prote
587	33	35.5	408	2	T01006	hypothetical prote
588	33	35.5	410	1	IXBE10	alpha trans-induci
589	33	35.5	410	2	H69307	bacteriochlorophyl
590	33	35.5	413	2	A97173	flagellar switch p
591	33	35.5	417	2	F71238	hypothetical prote
592	33	35.5	418	2	S44646	hypothetical prote
593	33	35.5	419	2	S06784	hypothetical prote
594	33	35.5	420	2	A45166	protein-lysine 6-o
595	33	35.5	422	2	S37280	cyclin A - mouse
596	33	35.5	422	2	S38501	cyclin A2 - mouse
597	33	35.5	423	2	AC3553	4-aminobutyrate tr
598	33	35.5	426	2	S16416	gene E46 protein -
599	33	35.5	433	2	T19632	hypothetical prote
600	33	35.5	434	2	D71309	47K integral membr
601	33	35.5	436	2	T00908	hypothetical prote
602	33	35.5	443	2	AI3525	4-aminobutyrate tr
603	33	35.5	445	2	T28988	hypothetical prote
604	33	35.5	450	1	DCCHO	ornithine decarbox
605	33	35.5	453	2	JC5607	replication initia
606	33	35.5	455	1	DCHYOC	orn

614	33	35.5	469	2	A71369	probable sugar ABC
615	33	35.5	470	2	C70641	hypothetical prote
616	33	35.5	475	2	T20706	hypothetical prote
617	33	35.5	477	2	S74716	hypothetical prote
618	33	35.5	480	2	A86371	hypothetical prote
619	33	35.5	498	2	A97061	uncharacterized pr
620	33	35.5	505	2	AC2107	hypothetical prote
621	33	35.5	514	2	S72847	hypothetical prote
622	33	35.5	514	2	E84145	transposase (22) B
623	33	35.5	536	2	S06548	finger protein (cl
624	33	35.5	541	2	T13162	cytosolic phosphol
625	33	35.5	554	2	C70512	hypothetical prote
626	33	35.5	556	2	T49501	hypothetical prote
627	33	35.5	565	1	HMIVE5	hemagglutinin prec
628	33	35.5	565	2	A25226	RAD7 protein - yea
629	33	35.5	584	2	F75090	archaeosine trna-r
630	33	35.5	591	2	T43443	hypothetical prote
631	33	35.5	615	2	S06546	finger protein (cl
632	33	35.5	618	2	T44595	alcaligin synthesi
633	33	35.5	643	1	FOVZZW	major core protein
634	33	35.5	643	2	G89008	protein T27C4.2 [i
635	33	35.5	644	1	FOVZ5R	major core protein
636	33	35.5	644	2	T37390	A4L protein - vari
637	33	35.5	644	2	A72164	major core protein
638	33	35.5	644	2	D36848	major core protein
639	33	35.5	644	2	T28545	hypothetical prote
640	33	35.5	649	2	B75317	threonyl-tRNA synt
641	33	35.5	651	2	C86333	hypothetical prote
642	33	35.5	660	2	AB0794	probable lipopolys
643	33	35.5	660	2	F85865	probable transform
644	33	35.5	660	2	G91021	probable transform
645	33	35.5	660	2	E64996	hypothetical prote
646	33	35.5	661	2	B75084	ferrous iron trans
647	33	35.5	662	2	E83201	conserved hypothet
648	33	35.5	663	2	S54426	DNA topoisomerase
649	33	35.5	664	2	S60062	hevin precursor -
650	33	35.5	665	2	B89911	topoisomerase IV s
651	33	35.5	667	2	AD0295	probable formyltr
652	33	35.5	672	2	B84782	probable receptor-
653	33	35.5	677	2	T19281	hypothetical prote
654	33	35.5	681	2	JX0338	rabphilin-3A - mou
655	33	35.5	682	2	T10319	envelope protein E
656	33	35.5	684	2	I58166	rabphilin-3A - rat
657	33	35.5	686	2	E87624	phospholipase C [i
658	33	35.5	693	2	C84495	hypothetical prote
659	33	35.5	702	2	T01763	threonine-tRNA lig
660	33	35.5	704	2	A48097	rabphilin-3A - bov
661	33	35.5	709	2	T51624	threonine-tRNA lig
662	33	35.5	712	1	YSHUT	threonine-tRNA lig
663	33	35.5	734	1	YSBYTC	threonine-tRNA lig
664	33	35.5	745	1	S75354	probable copper-tr
665	33	35.5	746	1	QRECFC	ferrienterochelin
666	33	35.5	746	2	G90706	hypothetical prote
667	33	35.5	746	2	B85557	hypothetical prote
668	33	35.5	747	2	T23882	hypothetical prote
669	33	35.5	753	2	T19338	hypothetical prote
670	33	35.5	765	2	T29582	hypothetical prote
671	33	35.5	766	1	B43684	probable RNA-direc
672	33	35.5	776	2	T20896	hypothetical prote
673	33	35.5	787	2	E82323	organic solvent to
674	33	35.5	790	1	G69071	heavy-metal-transp
675	33	35.5	790	2	T15709	hypothetical prote
676	33	35.5	802	2	F90060	copper-transportin
677	33	35.5	803	1	E70041	probable copper-tr
678	33	35.5	812	2	E95029	formate acetyltran
679	33	35.5	815	2	H97900	formate C-acetyltr
680	33	35.5	815	2	G82861	conjugal transfer
681	33	35.5	821	2	T24728	hypothetical prote
682	33	35.5	825	2	I46078	endothelin convert
683	33	35.5	826	2	G97073	uncharacterized pr
684	33	35.5	863	2	F84504	probable retroelem
685	33	35.5	870	2	T30110	hypothetical prote
686	33	35.5	904	2	T40072	P Type Copper ATPa

687	33	35.5	910	2	G84648	probable disease r	760	32.5	34.9	443	2	AH2415	two-component hybr
688	33	35.5	915	2	B59433	chromosome 5 GAP-1	761	32.5	34.9	491	2	T01856	hypothetical prote
689	33	35.5	921	2	D82513	malt regulatory pr	762	32.5	34.9	499	2	T03213	probable ribosomal
690	33	35.5	944	2	T38130	probable helicase	763	32.5	34.9	532	2	AB1369	conserved hypothet
691	33	35.5	946	2	S48433	inositol-1,4,5-tri	764	32.5	34.9	538	2	T03232	probable ribosomal
692	33	35.5	987	2	A12011	peptide synthetase	765	32.5	34.9	590	2	A96656	unknown protein, 3
693	33	35.5	1011	2	T17430	tol protein - Neur	766	32.5	34.9	635	2	T23465	hypothetical prote
694	33	35.5	1015	2	T32186	hypothetical prote	767	32.5	34.9	681	2	AD3318	DNA primase (EC 2.
695	33	35.5	1040	2	T39936	probable helicase	768	32.5	34.9	695	1	VHIMV	nucleocapsid prote
696	33	35.5	1045	2	S60571	integrin alpha v c	769	32.5	34.9	695	2	S44049	nucleocapsid prote
697	33	35.5	1071	1	PXBIVA	H+-exporting ATPas	770	32.5	34.9	759	2	S62067	Ty1 enhancer activ
698	33	35.5	1081	2	T20698	hypothetical prote	771	32.5	34.9	770	2	B48910	desmocollin 1b pre
699	33	35.5	1081	2	S51899	probable protein k	772	32.5	34.9	781	2	T26080	hypothetical prote
700	33	35.5	1083	2	T26844	hypothetical prote	773	32.5	34.9	824	2	A48910	desmocollin 1a pre
701	33	35.5	1088	2	A46080	H+-exporting ATPas	774	32.5	34.9	840	2	I37281	Dscla precursor -
702	33	35.5	1093	2	B86748	hypothetical prote	775	32.5	34.9	893	2	F86476	protein F1504.39 l
703	33	35.5	1093	2	T50652	AP-3 complex beta3	776	32.5	34.9	894	2	I37282	Dsclb precursor -
704	33	35.5	1094	2	T50651	AP3-complex beta-3	777	32.5	34.9	932	2	S65214	probable alpha/gam
705	33	35.5	1099	2	A59311	myosin VIII, ZMM3	778	32.5	34.9	1356	2	JC1402	protein-tyrosine k
706	33	35.5	1099	2	AB1065	conserved hypothet	779	32.5	34.9	1367	2	A41228	protein-tyrosine k
707	33	35.5	1116	2	B88612	protein Y76A2A.2 l	780	32.5	34.9	1417	2	T18418	hypothetical prote
708	33	35.5	1135	2	T42723	probable DNA-direc	781	32.5	34.9	1946	2	AC2141	serine/threonine k
709	33	35.5	1135	2	T42368	DNA-directed RNA p	782	32.5	34.9	3020	2	A43932	mucin 2 precursor,
710	33	35.5	1152	2	T27531	hypothetical prote	783	32	34.4	50	2	H82588	hypothetical prote
711	33	35.5	1168	2	T37496	probable pre-mRNA	784	32	34.4	73	2	T25926	hypothetical prote
712	33	35.5	1176	2	A22617	parasporal crystal	785	32	34.4	98	2	T26046	probable membrane
713	33	35.5	1176	2	JC2219	parasporal crystal	786	32	34.4	104	2	S50936	hypothetical prote
714	33	35.5	1176	2	JT0241	parasporal crystal	787	32	34.4	109	2	T00234	hypothetical prote
715	33	35.5	1176	2	S02215	parasporal crystal	788	32	34.4	110	2	S41557	hypothetical prote
716	33	35.5	1177	2	A49785	parasporal crystal	789	32	34.4	115	2	A55827	blue copper protei
717	33	35.5	1178	1	USBSXH	parasporal crystal	790	32	34.4	125	2	T49512	hypothetical prote
718	33	35.5	1189	2	A12493	WD-repeat protein	791	32	34.4	136	1	B64956	flagellar protein
719	33	35.5	1191	2	T31091	hypothetical prote	792	32	34.4	136	2	H90961	flagellar protein
720	33	35.5	1195	2	S38174	probable purine nu	793	32	34.4	136	2	H85809	hypothetical prote
721	33	35.5	1220	2	S17179	Ca2+-transporting	794	32	34.4	145	2	H82498	hypothetical prote
722	33	35.5	1238	1	JC5573	copper-transportin	795	32	34.4	154	2	E83634	hypothetical prote
723	33	35.5	1287	2	A41685	SIL protein - huma	796	32	34.4	158	2	T09295	probable heat shoc
724	33	35.5	1320	2	G81017	phosphoribosylform	797	32	34.4	159	2	E75151	molybdenum cofacto
725	33	35.5	1332	2	S41552	probable transcrip	798	32	34.4	165	2	H71649	hypothetical prote
726	33	35.5	1341	2	S50366	probable membrane	799	32	34.4	166	2	AH2568	hypothetical prote
727	33	35.5	1345	1	VCBEH6	major capsid prote	800	32	34.4	168	2	E69198	Ni,Fe-Hydrogenase
728	33	35.5	1480	2	T05566	hypothetical prote	801	32	34.4	174	2	T50419	hypothetical prote
729	33	35.5	1523	2	T13953	MEGF5 protein - ra	802	32	34.4	175	2	AC2876	conserved hypothet
730	33	35.5	1529	2	T16779	hypothetical prote	803	32	34.4	177	2	E97652	hypothetical prote
731	33	35.5	1531	2	T42218	slit-1 protein hom	804	32	34.4	180	1	A39167	placental protein
732	33	35.5	1549	2	T13940	ankyrin - fruit fl	805	32	34.4	185	2	AE0736	probable bacteriop
733	33	35.5	1619	2	S67083	hypothetical prote	806	32	34.4	186	2	T39759	hypothetical prote
734	33	35.5	1715	2	T30559	resistance protein	807	32	34.4	191	2	S78155	ribosomal protein
735	33	35.5	1744	2	JH0720	tanabin - African	808	32	34.4	192	2	D69061	precorrin-8W decar
736	33	35.5	1761	2	T13675	hypothetical prote	809	32	34.4	196	2	G89950	conserved hypothet
737	33	35.5	1792	2	T20363	hypothetical prote	810	32	34.4	200	2	T25406	hypothetical prote
738	33	35.5	1838	2	H86337	protein F5M15.26 l	811	32	34.4	203	2	T48718	mitochondrial ribo
739	33	35.5	2123	2	F86348	hypothetical prote	812	32	34.4	204	2	T01447	hypothetical prote
740	33	35.5	2185	1	S60200	acetyl-CoA carboxy	813	32	34.4	204	2	T28939	hypothetical prote
741	33	35.5	2324	1	A29924	acetyl-CoA carboxy	814	32	34.4	205	2	A71567	probable GMP kinas
742	33	35.5	2364	2	A56577	microtubule-associ	815	32	34.4	212	2	F72752	hypothetical prote
743	33	35.5	2427	2	T16613	hypothetical prote	816	32	34.4	213	2	D82849	cell division prot
744	33	35.5	2464	1	QRMSPI	microtubule-associ	817	32	34.4	213	2	D70211	lipoprotein homolo
745	33	35.5	2717	2	A34203	DNA-binding protei	818	32	34.4	215	2	E70350	probable thiamin p
746	33	35.5	2918	2	A54105	fibrillin-2 precur	819	32	34.4	219	1	TLBPT2	tail fiber protein
747	33	35.5	4687	1	A39638	plectin - rat	820	32	34.4	221	1	TLBP64	tail fiber protein
748	32.5	34.9	136	2	T45080	hypothetical prote	821	32	34.4	226	2	AC0176	probable exported
749	32.5	34.9	207	2	A12505	hypothetical prote	822	32	34.4	230	1	TLBPK3	tail fiber protein
750	32.5	34.9	238	2	H82084	aerobic respiratio	823	32	34.4	231	2	T45566	hypothetical prote
751	32.5	34.9	241	2	F97202	hypothetical prote	824	32	34.4	237	2	E81298	hypothetical prote
752	32.5	34.9	247	2	E86723	transcription regu	825	32	34.4	242	2	E89813	hypothetical prote
753	32.5	34.9	332	2	T51269	hypothetical prote	826	32	34.4	246	2	T19850	hypothetical prote
754	32.5	34.9	352	2	T05106	hypothetical prote	827	32	34.4	247	2	T49991	probable protein p
755	32.5	34.9	371	2	C97355	uncharacterized pr	828	32	34.4	254	2	H89772	hypothetical prote
756	32.5	34.9	411	2	T29475	hypothetical prote	829	32	34.4	255	2	H83700	transcription acti
757	32.5	34.9	412	2	T09313	immediate-early pr	830	32	34.4	255	2	AC3292	glucose-1-phosphat
758	32.5	34.9	413	1	S16426	tyrosine-tRNA liga	831	32	34.4	257	2	C81206	FrpC operon protei
759	32.5	34.9	441	2	F88930	protein R11G11.12	832	32	34.4	259	2	T36172	hypothetical prote

833	32	34.4	259	2	H88969	protein F15E11.5 [906	32	34.4	402	2	B82982	DNA/pantothenate m
834	32	34.4	261	2	T51243	Sc11 protein [impo	907	32	34.4	403	2	S53477	IMP dehydrogenase
835	32	34.4	264	2	AB2326	hypothetical prote	908	32	34.4	404	2	D86321	hypothetical prote
836	32	34.4	265	2	G37271	metalloproteinase	909	32	34.4	405	2	T37022	probable lycopene
837	32	34.4	268	2	F37271	metalloproteinase	910	32	34.4	410	2	T36610	hypothetical prote
838	32	34.4	268	2	T32775	hypothetical prote	911	32	34.4	412	1	B70125	hemolysin homolog
839	32	34.4	271	2	S35026	hypothetical prote	912	32	34.4	412	2	JC4921	double C2 protein
840	32	34.4	278	2	C69854	conserved hypotHet	913	32	34.4	415	2	T48171	hypothetical prote
841	32	34.4	278	2	AD2325	hypothetical prote	914	32	34.4	416	2	D69251	hypothetical prote
842	32	34.4	278	2	T22640	hypothetical prote	915	32	34.4	421	2	T43534	transcription fact
843	32	34.4	278	2	AH2981	hypothetical prote	916	32	34.4	421	2	T05032	protein kinase hom
844	32	34.4	278	2	H98301	dipeptide transpor	917	32	34.4	424	2	B95201	3-hydroxy-3-methyl
845	32	34.4	281	2	A10126	conserved hypotHet	918	32	34.4	424	2	H98067	hydroxymethylgluta
846	32	34.4	281	2	D82554	tRNA/rRNA methyltr	919	32	34.4	424	2	S27783	hypothetical prote
847	32	34.4	281	2	C82547	hypothetical prote	920	32	34.4	426	2	H87462	enolase [imported]
848	32	34.4	285	2	B82459	hypothetical prote	921	32	34.4	427	2	T46265	hypothetical prote
849	32	34.4	287	2	T40403	hypothetical prote	922	32	34.4	428	2	A81841	phosphopyruvate hy
850	32	34.4	288	2	D82781	conserved hypotHet	923	32	34.4	428	2	D81100	enolase NMB1285 [i
851	32	34.4	289	2	E69207	conserved hypotHet	924	32	34.4	431	2	C95023	competence-induced
852	32	34.4	290	2	E37271	metalloproteinase	925	32	34.4	435	2	T24074	hypothetical prote
853	32	34.4	291	2	S48252	serine-rich protei	926	32	34.4	437	2	B71953	hypothetical prote
854	32	34.4	294	2	T20338	hypothetical prote	927	32	34.4	440	2	S37303	sox-4 protein - mo
855	32	34.4	297	2	C96524	FlilA17.4 [imported	928	32	34.4	443	2	A70438	flagellar export p
856	32	34.4	300	2	AB0762	conserved hypotHet	929	32	34.4	444	2	E70201	pantothenate perme
857	32	34.4	304	2	S12975	coat protein - pot	930	32	34.4	447	2	G86940	probable enolase [
858	32	34.4	304	2	AG0926	hypothetical prote	931	32	34.4	451	2	C49898	cellobiose phospho
859	32	34.4	304	2	T48281	hypothetical prote	932	32	34.4	453	2	F82702	conserved hypotHet
860	32	34.4	306	2	S19997	hypothetical prote	933	32	34.4	455	2	AH0794	o-succinylbenzoate
861	32	34.4	307	2	G69211	conserved hypotHet	934	32	34.4	456	2	AE3341	cobG protein (EC 1
862	32	34.4	308	2	A86246	hypothetical prote	935	32	34.4	460	2	T27770	hypothetical prote
863	32	34.4	308	2	T46294	hypothetical prote	936	32	34.4	461	2	F82700	enolase XF1291 [im
864	32	34.4	308	2	H89839	hypothetical prote	937	32	34.4	461	2	T51458	hypothetical prote
865	32	34.4	310	1	S37695	calcium-binding pr	938	32	34.4	461	2	A46394	suppressor protein
866	32	34.4	311	2	E96714	probable DNA-bindi	939	32	34.4	465	2	T26146	hypothetical prote
867	32	34.4	313	2	F71285	hypothetical prote	940	32	34.4	466	2	T44350	hypothetical prote
868	32	34.4	323	2	T28951	hypothetical prote	941	32	34.4	466	2	AI1707	transcription regu
869	32	34.4	328	2	AB0301	conserved hypotHet	942	32	34.4	468	1	B64896	hypothetical prote
870	32	34.4	330	2	T39698	protein tyrosine p	943	32	34.4	468	2	D85734	hypothetical prote
871	32	34.4	330	2	AG2129	iron(III) dicitrat	944	32	34.4	468	2	C90884	probable transcrip
872	32	34.4	331	2	A83678	hypothetical prote	945	32	34.4	469	1	P2WL35	L2 protein - human
873	32	34.4	332	1	DEMSLM	L-lactate dehydrog	946	32	34.4	469	2	S36525	L2 protein - human
874	32	34.4	335	2	T49145	ornithine carbanoy	947	32	34.4	470	2	B86165	hypothetical prote
875	32	34.4	337	2	T46742	hypothetical prote	948	32	34.4	471	1	S62590	peptidyl-prolyl ci
876	32	34.4	340	2	F85724	hypothetical prote	949	32	34.4	472	1	B53236	transcription fact
877	32	34.4	341	2	T47338	hypothetical prote	950	32	34.4	472	2	S36519	L2 protein - human
878	32	34.4	341	2	H90797	probable tellurium	951	32	34.4	474	2	AF0669	probable regulator
879	32	34.4	344	2	B83605	probable acetylpol	952	32	34.4	474	2	I38240	transcription fact
880	32	34.4	345	2	H90515	lipocate-protein li	953	32	34.4	475	1	JN0327	sulfate adenylyltr
881	32	34.4	346	2	T30463	hypothetical prote	954	32	34.4	475	2	E91079	hypothetical prote
882	32	34.4	348	2	AI3626	inositol 2-dehydro	955	32	34.4	475	2	F85924	hypothetical prote
883	32	34.4	354	2	JC4212	nitrilase (EC 3.5.	956	32	34.4	478	1	FOVWVL	gag polyprotein -
884	32	34.4	358	2	AC0740	probable integrase	957	32	34.4	481	2	S56299	hypothetical prote
885	32	34.4	359	2	JC2134	angiotensin II rec	958	32	34.4	481	2	AD1337	transcription regu
886	32	34.4	361	2	AG0335	chorismate synthas	959	32	34.4	498	2	D83994	xylose kinase xylB
887	32	34.4	361	2	D97956	conserved hypotHet	960	32	34.4	498	2	T09436	gag polyprotein -
888	32	34.4	363	2	D81037	GTP-binding protei	961	32	34.4	500	1	FOVWLV	gag polyprotein -
889	32	34.4	366	2	A83061	conserved hypotHet	962	32	34.4	500	1	A44001	gag polyprotein -
890	32	34.4	367	2	T10207	oleoyl-lacetyl-carri	963	32	34.4	500	2	G71836	anthranilate synth
891	32	34.4	367	2	B56598	endothelial kinase	964	32	34.4	500	2	B64680	gag polyprotein -
892	32	34.4	370	2	I40085	gtcs protein - Bac	965	32	34.4	500	2	S33979	gag polyprotein -
893	32	34.4	372	2	T08273	conserved hypotHet	966	32	34.4	502	1	FOVWA2	zinc transporter 2
894	32	34.4	373	2	JC7289	G-protein coupled	967	32	34.4	503	2	S54302	gag polyprotein -
895	32	34.4	379	2	C86821	hypothetical prote	968	32	34.4	506	1	A38068	gag protein - simi
896	32	34.4	383	2	S53379	probable membrane	969	32	34.4	507	2	T11559	gag polyprotein -
897	32	34.4	385	2	A85607	hypothetical prote	970	32	34.4	507	2	S04237	gag polyprotein -
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899	32	34.4	387	2	E71711	probable o-sialogl	972	32	34.4	511	2	AI3112	oligopeptide ABC t
900	32	34.4	390	2	G01936	Abl binding protei	973	32	34.4	511	2	D98174	gag polyprotein -
901	32	34.4	391	2	D64366	hypothetical prote	974	32	34.4	512	1	FOVWH3	gag polyprotein -
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903	32	34.4	401	2	A57226	mei-S332 protein -	976	32	34.4	512	2	B71474	probable hsp60 cha
904	32	34.4	402	2	S55465	chalcone synthase	977	32	34.4	512	2	H85878	multidrug resistan
905	32	34.4					978	32	34.4	512	2	F91034	multidrug resistan

979 32 34.4 512 2 D65010 multidrug resistanc
980 32 34.4 515 2 B89648 protein lin-14 [im
981 32 34.4 518 2 G70174 hypothetical prote
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983 32 34.4 521 1 FOLJCA gag polyprotein -
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990 32 34.4 522 2 B71807 DNA repair protein
991 32 34.4 523 1 S48997 IMP dehydrogenase
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1005 32 34.4 559 2 T29693 hypothetical prote
1006 32 34.4 565 2 H72253 DNA primase - Ther
1007 32 34.4 577 1 VGBEG1 glycoprotein E - S
1008 32 34.4 579 2 E96496 unknown protein, 5
1009 32 34.4 582 2 H70588 probable pros prot
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1011 32 34.4 585 2 S38155 hypothetical prote
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1013 32 34.4 591 1 S22664 virulence-associat
1014 32 34.4 593 2 S15215 virulence-associat
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1023 32 34.4 622 2 D71078 aldehyde-ferredoxi
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1025 32 34.4 623 2 T52128 ABC1 protein homol
1026 32 34.4 624 2 S50650 hypothetical prote
1027 32 34.4 631 2 T40189 probable biotin-pr
1028 32 34.4 633 2 D82527 proteinase IV XF26
1029 32 34.4 635 2 A81656 threonyl-tRNA synt
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1036 32 34.4 650 2 T00081 hypothetical prote
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1041 32 34.4 692 2 A36143 phospholipase C (E
1042 32 34.4 692 2 E83230 non-hemolytic phos
1043 32 34.4 694 2 F82511 vgrG protein VCA00
1044 32 34.4 694 2 F90609 exodeoxyribonuclea
1045 32 34.4 700 2 T10566 probable serine/th
1046 32 34.4 703 2 T39997 Thslp - fission ye
1047 32 34.4 711 2 S68443 double-stranded RN
1048 32 34.4 711 2 G86526 hypothetical prote
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1051 32 34.4 718 2 G70978 probable copper-tr

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1099 32 34.4 1076 2 T24887
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1109 32 34.4 1135 2 JQ2163
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1119 32 34.4 1220 2 A30802
1120 32 34.4 1220 2 I55491
1121 32 34.4 1220 2 S13057
1122 32 34.4 1224 2 H96615
1123 32 34.4 1231 2 T18532
1124 32 34.4 1233 2 T14157

hypothetical prote
TonB-dependent out
probable membrane
glycerol-3-phospha
cell division prot
probable Athlia re
semaphorin E - mou
hypothetical prote
glycoprotein iib -
chloride channel p
hypothetical prote
probable membrane
probable transcrip
hydrogenase matura
hypothetical prote
hypothetical prote
beta-catenin - Hyd
hypothetical prote
conjugal transfer
exocyst complex pr
monocyte surface a
vacuolar membrane
hypothetical prote
cation-transportin
RNA12 protein - ye
ATP-dependent RNA
hypothetical prote
pre-mRNA splicing
insulinase-type zi
rep-1 protein, for
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
adenosine triphosp
probable mmpL2 pro
probable villin [i
DNA-directed RNA p
cis-Golgi matrix p
probable glng - My
probable kinesin h
hypothetical prote
hypothetical prote
hydroxymethylgluta
type I restriction
hypothetical prote
probable (Xeroderm
hypothetical prote
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hypothetical prote
surface-located me
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DNA mismatch repai
ATP-dependent nucl
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two-component sens
hypothetical 126.5
DNA-directed DNA p
DNA-directed DNA p
hypothetical prote
hypothetical prote
vgrG protein VCI41
hypothetical prote
Ca2+-transporting
hypothetical prote
protein kinase SK2
Ca2+-transporting
adenosine triphosp
Ca2+-transporting
hypothetical prote
serine/threonine pr
serine/threonine p

1125	32	34.4	1257	2	A88536	protein B0523.5 [i	1198	31.5	33.9	827	2	S75622	hypothetical prote
1126	32	34.4	1263	2	F44466	DNA-directed RNA p	1199	31.5	33.9	840	2	I48968	major fibrous shea
1127	32	34.4	1283	2	T13799	neurexin IV - frui	1200	31.5	33.9	849	2	I49060	major 80,000 Mr fi
1128	32	34.4	1300	2	S73679	probable lipoprote	1201	31.5	33.9	861	2	T41945	primase - human he
1129	32	34.4	1379	2	JC4954	vascular endotheli	1202	31.5	33.9	1024	2	G72041	exodeoxyribonuclea
1130	32	34.4	1384	2	T26656	hypothetical prote	1203	31.5	33.9	1024	2	F86582	exodeoxyribonuclea
1131	32	34.4	1405	2	T04426	hypothetical prote	1204	31.5	33.9	1024	2	D81624	exodeoxyribonuclea
1132	32	34.4	1416	2	E88550	protein ZC84.1 [im	1205	31.5	33.9	1025	2	I59331	thyrotropin-releas
1133	32	34.4	1466	2	G84516	probable retroelem	1206	31.5	33.9	1150	2	H96501	probable retroelem
1134	32	34.4	1499	2	B59431	Rho GTPase activat	1207	31.5	33.9	1175	2	S52417	E-selectin ligand-
1135	32	34.4	1501	2	T42724	p190-B protein - m	1208	31.5	33.9	1226	2	S69078	hypothetical prote
1136	32	34.4	1509	2	T19486	hypothetical prote	1209	31.5	33.9	1381	2	S55619	capsid protein 25
1137	32	34.4	1513	1	RNRZC2	DNA-directed RNA p	1210	31.5	33.9	1484	2	T42632	breast cancer tumo
1138	32	34.4	1520	2	B82274	conserved hypothet	1211	31.5	33.9	1672	2	C81675	polymorphic membra
1139	32	34.4	1547	2	S69842	TyB protein - yeas	1212	31.5	33.9	1787	2	AC2009	serine/threonine k
1140	32	34.4	1560	2	T02885	peroxisome prolife	1213	31.5	33.9	1796	2	AC1895	serine/threonine k
1141	32	34.4	1571	2	T14155	zinc finger protei	1214	31.5	33.9	4588	2	T28667	dynein beta heavy
1142	32	34.4	1616	2	G64242	cytadherence-acces	1215	31	33.3	66	2	AG1908	hypothetical prote
1143	32	34.4	1727	2	T50073	myosin-like coiled	1216	31	33.3	82	2	AG0714	hypothetical prote
1144	32	34.4	1735	1	S22812	DNA-directed RNA p	1217	31	33.3	98	2	S06671	cinnamomin - Phyto
1145	32	34.4	1759	2	T18868	myoblast city prot	1218	31	33.3	101	2	T21657	hypothetical prote
1146	32	34.4	1825	2	T42725	actin binding prot	1219	31	33.3	103	2	A72713	hypothetical prote
1147	32	34.4	1872	2	JC4976	plexin 3 precursor	1220	31	33.3	110	2	B41323	ribulose-bisphosph
1148	32	34.4	1885	2	T30847	actin binding prot	1221	31	33.3	111	2	B71115	hypothetical prote
1149	32	34.4	1927	2	A59236	embryonic muscle m	1222	31	33.3	111	2	S10222	hypothetical prote
1150	32	34.4	2033	2	T30849	actin binding prot	1223	31	33.3	111	2	S12179	transcription fact
1151	32	34.4	2042	2	T18399	variant-specific s	1224	31	33.3	113	2	S12184	transcription fact
1152	32	34.4	2090	2	S26058	probable transform	1225	31	33.3	114	2	S40340	Ig kappa chain V-J
1153	32	34.4	2207	2	T42759	Munc13-3 protein -	1226	31	33.3	114	2	S12185	transcription fact
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1155	32	34.4	2297	2	AB2494	hypothetical prote	1228	31	33.3	115	2	S12187	transcription fact
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1157	32	34.4	2824	2	T22759	hypothetical prote	1230	31	33.3	118	2	AH0986	phage-like lysozym
1158	32	34.4	2844	2	S28291	hypothetical prote	1231	31	33.3	118	2	S26611	transcription fact
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1161	32	34.4	3744	2	S46715	peptide synthetase	1234	31	33.3	123	2	S26610	transcription fact
1162	32	34.4	6486	2	T31076	hypothetical prote	1235	31	33.3	124	2	S76185	hypothetical prote
1163	31.5	33.9	60	2	S35180	tyrocidine synthet	1236	31	33.3	127	2	H82181	hypothetical prote
1164	31.5	33.9	91	2	S17627	cytochrome P450 (c	1237	31	33.3	135	2	T40281	gtp-binding protei
1165	31.5	33.9	143	2	T36669	Ig kappa chain V r	1238	31	33.3	136	2	JU0266	envelope polyprote
1166	31.5	33.9	168	2	AB1238	probable anti-sigm	1239	31	33.3	136	2	TU0954	envelope polyprote
1167	31.5	33.9	168	2	AI1600	E. coli YbdM prote	1240	31	33.3	139	2	S06550	finger protein (cl
1168	31.5	33.9	200	2	AG2261	E. coli YbdM prote	1241	31	33.3	142	2	S25093	phospholipase A2 (
1169	31.5	33.9	220	2	T20059	transcription regu	1242	31	33.3	142	2	G75109	hypothetical prote
1170	31.5	33.9	274	2	AH2462	hypothetical prote	1243	31	33.3	145	2	S30247	Hin-1 protein - hu
1171	31.5	33.9	277	2	T20065	biotin acetyl-CoA	1244	31	33.3	152	2	T32784	hypothetical prote
1172	31.5	33.9	296	2	S75601	hypothetical prote	1245	31	33.3	153	2	A26092	myosin I1 regulato
1173	31.5	33.9	302	2	T32234	hypothetical prote	1246	31	33.3	153	2	S77187	hypothetical prote
1174	31.5	33.9	320	2	C83628	hypothetical prote	1247	31	33.3	154	2	B84973	aspartate carbamoy
1175	31.5	33.9	330	2	T22411	probable oxidoredu	1248	31	33.3	154	2	S28181	transcription fact
1176	31.5	33.9	331	2	G02431	hypothetical prote	1249	31	33.3	160	2	C69355	hypothetical prote
1177	31.5	33.9	340	1	C64360	geranylgeranyl tra	1250	31	33.3	165	2	AH3295	acetyltransferase
1178	31.5	33.9	357	2	T46868	conserved hypothet	1251	31	33.3	169	2	JC6013	hypothetical k pro
1179	31.5	33.9	357	2	S75252	protoporphyrin IX	1252	31	33.3	171	2	E97074	probable acetyltra
1180	31.5	33.9	370	2	AB3334	protoporphyrin IX	1253	31	33.3	171	2	T48393	hypothetical prote
1181	31.5	33.9	374	2	JC2123	daunorubicin resis	1254	31	33.3	173	2	S10548	lectin - barnacle
1182	31.5	33.9	380	2	G69893	major allergen Cry	1255	31	33.3	178	2	S74564	hypothetical prote
1183	31.5	33.9	380	2	T44811	butyryl-CoA dehydr	1256	31	33.3	184	2	A83316	hypothetical prote
1184	31.5	33.9	380	2	A83458	acyl-CoA dehydroge	1257	31	33.3	184	2	G85955	hypothetical prote
1185	31.5	33.9	392	2	T35487	hypothetical prote	1258	31	33.3	192	2	D64481	hypothetical prote
1186	31.5	33.9	401	2	A81335	hypothetical prote	1259	31	33.3	194	2	A72167	hypothetical prote
1187	31.5	33.9	438	2	D72404	tyrosine-tRNA liga	1260	31	33.3	199	2	E86081	A28L protein - var
1188	31.5	33.9	559	1	R3ZMS3	flagellum-specific	1261	31	33.3	199	2	S40863	hypothetical prote
1189	31.5	33.9	559	2	T20709	ribosomal protein	1262	31	33.3	199	2	E91234	hypothetical prote
1190	31.5	33.9	591	2	B72121	hypothetical prote	1263	31	33.3	203	2	AD1369	hypothetical prote
1191	31.5	33.9	591	2	H86501	ATP synthase, chai	1264	31	33.3	207	2	S59142	hypothetical prote
1192	31.5	33.9	595	2	JC8012	G protein-coupled	1265	31	33.3	208	2	C81160	uracil phosphoribo
1193	31.5	33.9	607	2	E84827	hypothetical prote	1266	31	33.3	209	2	F82483	hypothetical prote
1194	31.5	33.9	673	2	T06294	hypothetical prote	1267	31	33.3	212	2	S03070	gag protein - huma
1195	31.5	33.9	673	2	H69828	ABC transporter (A	1268	31	33.3	212	2	D82383	conserved hypothet
1196	31.5	33.9	693	2	T00256	hypothetical prote	1269	31	33.3	213	2	T06333	probable glutathio
1197	31.5	33.9	696	2	JC7361	folitropin recept	1270	31	33.3	217	2	H64956	yedG protein - Esc

1271	31	33.3	218	2	JC7147	trichothecene bios
1272	31	33.3	219	2	G86620	dethiobiotin synth
1273	31	33.3	219	2	F72004	dethiobiotin synth
1274	31	33.3	220	2	A81311	probable periplasm
1275	31	33.3	221	2	T43159	ubiquitin-protein
1276	31	33.3	221	2	AF2316	endonuclease V [im
1277	31	33.3	222	2	F90962	hypothetical prote
1278	31	33.3	222	2	F85810	hypothetical prote
1279	31	33.3	226	2	A35968	tox regulon transc
1280	31	33.3	227	2	T37499	probable ubiquitin
1281	31	33.3	228	2	T15236	hypothetical prote
1282	31	33.3	230	2	B83325	probable transport
1284	31	33.3	231	2	B64249	tRNA (guanine-N1-)
1285	31	33.3	231	2	S73286	phycobilisome rod-
1286	31	33.3	231	2	S33552	hypothetical prote
1287	31	33.3	232	1	JH0597	transcription fact
1288	31	33.3	234	2	A41178	heparin-binding gr
1289	31	33.3	236	2	E84307	glucose 1-dehydrog
1290	31	33.3	237	2	S46685	hypothetical prote
1291	31	33.3	238	2	S78571	transcription fact
1292	31	33.3	239	2	AF0750	RNA polymerase sig
1293	31	33.3	239	2	E90961	RNA polymerase sig
1294	31	33.3	239	2	JC4346	RNA polymerase sig
1295	31	33.3	239	2	B85809	RNA polymerase sig
1296	31	33.3	239	2	S11895	transcription init
1297	31	33.3	241	1	JQ1641	phosphoprotein P -
1298	31	33.3	241	2	T23428	hypothetical prote
1299	31	33.3	241	2	A87551	glutathione S-tran
1300	31	33.3	241	2	T16802	hypothetical prote
1301	31	33.3	242	2	A96794	unknown protein F1
1302	31	33.3	245	2	S10658	hypothetical prote
1303	31	33.3	245	2	H86151	hypothetical prote
1304	31	33.3	246	2	C64054	tRNA (guanine-N1-)
1305	31	33.3	247	2	C82307	tRNA (guanine-N1-)
1306	31	33.3	249	2	C81180	tRNA (guanine-N1-)
1307	31	33.3	249	2	A81924	probable tRNA (gua
1308	31	33.3	249	2	T32566	hypothetical prote
1309	31	33.3	251	2	H82864	conserved hypoteth
1310	31	33.3	252	2	C83178	tRNA (guanine-N1-)
1311	31	33.3	252	2	F65084	hypothetical prote
1312	31	33.3	252	2	S30292	mating-type switch
1313	31	33.3	255	2	T24406	hypothetical prote
1314	31	33.3	256	2	A11119	transcription regu
1315	31	33.3	256	2	AD1480	transcription regu
1316	31	33.3	257	2	C97109	specialized DNA-de
1317	31	33.3	257	2	I40621	probable transcrip
1318	31	33.3	257	2	T40880	hypothetical prote
1319	31	33.3	258	2	T34422	hypothetical prote
1320	31	33.3	261	2	T41508	hypothetical prote
1321	31	33.3	261	2	D90562	hypothetical prote
1322	31	33.3	262	2	B83126	probable transcrip
1323	31	33.3	263	2	G81272	hypothetical prote
1324	31	33.3	263	4	I67792	probable glucosylc
1325	31	33.3	266	1	WQECMP	phosphotransferase
1326	31	33.3	266	2	H90944	mannose-specific P
1327	31	33.3	266	2	C85793	PTS enzyme IIC, ma
1328	31	33.3	268	2	AB1087	PTS system mannose
1329	31	33.3	268	2	AT1450	PTS system mannose
1330	31	33.3	268	2	H83320	probable transcrip
1331	31	33.3	272	2	T33515	hypothetical prote
1332	31	33.3	272	2	F70979	hypothetical prote
1333	31	33.3	273	2	T50938	Ditr protein [impo
1334	31	33.3	274	2	T37877	O9 mannan biosynth
1335	31	33.3	276	2	T38825	hypothetical prote
1336	31	33.3	278	2	A56570	homeobox protein D
1337	31	33.3	280	2	I55577	Fc gamma (IgG) rec
1338	31	33.3	281	1	T15613	probable phosphoes
1339	31	33.3	281	2	T50351	probable methyltra
1340	31	33.3	282	2	B84984	geranyltransf
1341	31	33.3	283	2	S42634	homeoprotein, IDX-
1342	31	33.3	284	2	D81075	conserved hypoteth
1343	31	33.3	284	2	S39581	IPP1 protein - mou

1344	31	33.3	287	2	T27056	hypothetical prote
1345	31	33.3	290	2	T50432	hypothetical prote
1346	31	33.3	291	2	AI3092	hypothetical prote
1347	31	33.3	296	2	AB0557	cytochrome o ubiqu
1348	31	33.3	296	2	E42226	heme O synthase -
1349	31	33.3	296	2	F85539	Protoheme IX farne
1350	31	33.3	296	2	B90689	Protoheme IX farne
1351	31	33.3	297	2	F64206	lipopolysaccharide
1352	31	33.3	297	2	F90287	antibiotic ABC tra
1353	31	33.3	303	2	JS0379	hypothetical 35.5K
1354	31	33.3	304	2	A89905	hypothetical prote
1355	31	33.3	305	2	A71324	conserved hypoteth
1356	31	33.3	310	2	T31799	hypothetical prote
1357	31	33.3	312	2	H97297	probable transcrip
1358	31	33.3	314	2	AG3410	chlorAMphenicol-se
1359	31	33.3	314	2	F90569	conserved hypoteth
1360	31	33.3	318	2	A99510	hypothetical prote
1361	31	33.3	318	2	A85066	hypothetical prote
1362	31	33.3	320	1	C71071	hypothetical prote
1363	31	33.3	323	2	AI2024	hypothetical prote
1364	31	33.3	326	1	S17954	alkanal monooxygen
1365	31	33.3	326	2	JC4196	36K hydrophobic nu
1366	31	33.3	326	2	A96608	hypothetical prote
1367	31	33.3	327	2	JC4195	36k hydrophobic nu
1368	31	33.3	328	2	F72260	hypothetical prote
1369	31	33.3	330	2	S49471	transcription init
1370	31	33.3	330	2	AG0855	RNA polymerase sig
1371	31	33.3	330	2	S47534	transcription init
1372	31	33.3	331	2	JQ2018	hypothetical 36.5K
1373	31	33.3	331	2	A86278	hypothetical prote
1374	31	33.3	331	2	A99179	conserved hypoteth
1375	31	33.3	332	1	DEHULM	L-lactate dehydrog
1376	31	33.3	332	2	T00847	probable membrane
1377	31	33.3	334	2	F89008	protein W08A12.4 [
1378	31	33.3	335	2	A40267	interleukin-5 rece
1379	31	33.3	336	2	G95051	ketol-acid reducto
1380	31	33.3	336	2	AD1566	hypothetical prote
1381	31	33.3	337	2	AI2723	naphthalene 1,2-di
1382	31	33.3	337	2	B97505	phenol hydroxylase
1383	31	33.3	337	2	D70132	hypothetical prote
1384	31	33.3	338	2	A82890	hypothetical prote
1385	31	33.3	340	2	B86778	ketol-acid reducto
1386	31	33.3	340	2	C97922	ketol-acid reducto
1387	31	33.3	343	2	G71499	probable D-Ala-D-A
1388	31	33.3	343	2	T19082	hypothetical prote
1389	31	33.3	343	2	T22053	hypothetical prote
1390	31	33.3	344	1	S35140	probable ketol-aci
1391	31	33.3	347	2	T40599	hypothetical prote
1392	31	33.3	347	2	AD3513	channel protein vi
1393	31	33.3	348	1	B46216	transcription fact
1394	31	33.3	349	2	A25952	glycerol-3-phospha
1395	31	33.3	349	2	D69856	conserved hypoteth
1396	31	33.3	351	2	D48552	orf U51053 - infec
1397	31	33.3	351	2	S52708	hypothetical prote
1398	31	33.3	354	2	B55733	G protein-coupled
1399	31	33.3	354	2	AG3315	lipopolysaccharide
1400	31	33.3	355	2	G88216	protein B0495.1 [l
1401	31	33.3	355	2	F96940	beta-mannanase lim
1402	31	33.3	357	2	S63142	hypothetical prote
1403	31	33.3	357	2	A96194	hypothetical prote
1404	31	33.3	358	2	S45911	hypothetical prote
1405	31	33.3	359	2	T02608	hypothetical prote
1406	31	33.3	360	2	AB0172	probable outer mem
1407	31	33.3	361	2	A53860	chondroadherin pre
1408	31	33.3	363	2	G70145	glycerol-3-phospha
1409	31	33.3	363	2	C70462	DNA polymerase III
1410	31	33.3	363	2	S66114	creatine kinase ho
1411	31	33.3	364	1	JT0741	GTP-binding protei
1412	31	33.3	364	1	A55014	GTP-binding protei
1413	31	33.3	366	2	AH2237	septum site-determ
1414	31	33.3	368	1	S64487	GTP-binding protei
1415	31	33.3	370	2	A27098	larvicidal toxin 4
1416	31	33.3	370	2	S07712	larvicidal toxin 4

1417 31 33.3 370 2 D28211 larvicidal toxin 4
1418 31 33.3 370 2 G90122 hypothetical prote
1419 31 33.3 370 2 T52141 hypothetical prote
1420 31 33.3 372 2 T06745 hypothetical prote
1421 31 33.3 374 1 LQBPRA RNA ligase (ATP) (
1422 31 33.3 374 1 A39878 Fc gamma (IgG) rec
1423 31 33.3 375 2 AH1685 hypothetical prote
1424 31 33.3 376 2 T28935 hypothetical prote
1425 31 33.3 380 2 A86401 protein T22C5.1 [i
1426 31 33.3 381 2 T10707 adenosylmethionine
1427 31 33.3 381 2 T49544 hypothetical prote
1428 31 33.3 382 2 C83337 hypothetical prote
1429 31 33.3 383 2 JC2472 brain and reproduc
1430 31 33.3 384 2 S58446 sigma S - Salmonel
1431 31 33.3 384 2 A86324 protein Fl4D16.19
1432 31 33.3 385 2 S66292 actin-crosslinking
1433 31 33.3 386 2 D59237 probable citrate s
1434 31 33.3 387 2 S55550 5-HT4S receptor -
1435 31 33.3 387 2 G64489 hypothetical prote
1436 31 33.3 388 2 T31306 hypothetical prote
1437 31 33.3 390 2 B84727 molybdopterin synt
1438 31 33.3 390 2 T41199 dom34 protein homo
1439 31 33.3 391 2 H97491 alanine racemase (
1440 31 33.3 391 2 AG2709 alanine racemase [
1441 31 33.3 392 2 T01617 probable protein k
1442 31 33.3 393 2 A80216 phosphoribosylglyc
1443 31 33.3 396 2 H72224 hypothetical prote
1444 31 33.3 397 2 JE0082 GPI-linked recepto
1445 31 33.3 397 2 AC2006 hypothetical prote
1446 31 33.3 398 2 S56699 naringenin-chalcon
1447 31 33.3 399 2 AD2917 conserved hypothet
1448 31 33.3 399 2 G97691 hypothetical prote
1449 31 33.3 400 1 S22539 transcription fact
1450 31 33.3 402 2 D75592 hypothetical prote
1451 31 33.3 403 1 S35541 transcription fact
1452 31 33.3 404 2 T21251 hypothetical prote
1453 31 33.3 406 2 S55549 serotonin 4 recept
1454 31 33.3 410 2 S68515 probable arginine
1455 31 33.3 410 2 A41465 arginine deiminase
1456 31 33.3 411 1 OXMSL protein-lysine 6-o
1457 31 33.3 412 2 T41552 hypothetical prote
1458 31 33.3 412 2 B81356 ankyrin repeat-con
1459 31 33.3 413 2 E86400 protein T17H3.4 [i
1460 31 33.3 413 2 AC3614 dtdp-4-dehydroram
1461 31 33.3 414 2 T38742 hypothetical prote
1462 31 33.3 417 1 OXHUL protein-lysine 6-o
1463 31 33.3 417 2 A96610 probable pectinase
1464 31 33.3 418 2 E86395 hypothetical prote
1465 31 33.3 420 2 S21052 interleukin-5 rece
1466 31 33.3 421 2 C82253 folypolyglutamate
1467 31 33.3 423 2 E72004 adenosylmethionine
1468 31 33.3 423 2 F86620 hypothetical prote
1469 31 33.3 423 2 T09338 DnaJ-like protein
1470 31 33.3 424 2 F82503 proton/glutamate s
1471 31 33.3 425 2 I64250 hypothetical prote
1472 31 33.3 425 2 F83990 lactose transport
1473 31 33.3 426 2 T41682 hypothetical prote
1474 31 33.3 429 2 B90576 hemolysin c [impor
1475 31 33.3 429 2 T45040 hypothetical prote
1476 31 33.3 430 1 A46216 transcription fact
1477 31 33.3 431 1 JC2002 transcription fact
1478 31 33.3 432 2 T34154 hypothetical prote
1479 31 33.3 432 2 AI2379 hypothetical prote
1480 31 33.3 435 2 T23364 hypothetical prote
1481 31 33.3 436 2 S72701 adenosylmethionine
1482 31 33.3 437 2 B70540 probable adenosylm
1483 31 33.3 438 2 T45602 glucosyltransferas
1484 31 33.3 438 2 I38946 melanoma ubiquitou
1485 31 33.3 438 2 F81659 D-alanyl-D-alanine
1486 31 33.3 440 2 T32151 hypothetical prote
1487 31 33.3 440 2 S69728 hypothetical prote
1488 31 33.3 441 2 T48960 vacuolar H(+)-ATPa
1489 31 33.3 443 2 H84414 hypothetical prote

1490 31 33.3 444 2 H83624 probable porin PA0
1491 31 33.3 445 2 S27492 hypothetical prote
1492 31 33.3 445 2 T26762 hypothetical prote
1493 31 33.3 446 2 D71418 hypothetical prote
1494 31 33.3 447 2 T12978 hypothetical prote
1495 31 33.3 447 2 T39170 probable cis-mucon
1496 31 33.3 447 2 AH0536 conserved hypothet
1497 31 33.3 448 2 F95036 PTS system, IIC co
1498 31 33.3 448 2 B97907 phosphotransferase
1499 31 33.3 449 2 G89841 hypothetical prote
1500 31 33.3 450 2 H84448 probable MYB famil

ALIGNMENTS

RESULT 1
F86909
probable DNA gyrase subunit A [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F86909
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1249 <STO>
A;Cross-references: UNIPARC:UPI0000165F27; GB:AL450380; NID:gi13092418; PIDN:CAC29514.1;
C;Genetics:
A;Gene: gyrA

Query Match 47.3%; Score 44; DB 2; Length 1249;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VEEDQFSQNPISCFE 18
|||||:|:|:|:
Db 469 VEEDSFNQHNVDVCVQ 483

RESULT 2
T10006
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) A - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10006
R;Cole, S.T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16916
A;Accession: T10006
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1273 <COL>
A;Cross-references: UNIPROT:Q57532; UNIPARC:UPI000016FAEB; EMBL:Z70722; NID:e1059634; PII
C;Genetics:
A;Gene: gyrA
C;Keywords: isomerase

Query Match 47.3%; Score 44; DB 2; Length 1273;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VEEDQFSQNPISCFE 18
|||||:|:|:|:
Db 469 VEEDSFNQHNVDVCVQ 483

RESULT 3
T29509
hypothetical protein W05H7.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C/Accession: T29509
R/Wohldmann, P.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A/Description: The sequence of C. elegans cosmid W05H7.
A/Reference number: Z20630
A/Accession: T29509
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-221 <WOH>
A/Cross-references: UNIPARC:UPI000017935A; EMBL:U97552; PIDN:AAB52865.1; GSPDB:GN00028;
A/Experimental source: strain Bristol N2; clone W05H7
C/Genetics:
A/Gene: CESP:W05H7.5
A/Map position: X
A/Introns: 30/1; 61/1; 172/3; 183/1
C/Superfamily: Caenorhabditis elegans hypothetical protein W05H7.5

Query Match 46.2%; Score 43; DB 2; Length 221;
Best Local Similarity 53.3%; Pred. No. 8.4;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLVEEDQFSQNPISC 16
|:| ||:| |||
Db 152 SIVNPHFSDSPISC 166

RESULT 4
E84536
hypothetical protein At2g16090 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: E84536
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: E84536
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-518 <STO>
A/Cross-references: UNIPROT:Q9XII0; UNIPARC:UPI000009CCB6; GB:AE002093; NID:g4678205; PT
C/Genetics:
A/Gene: At2g16090
A/Map position: 2

Query Match 46.2%; Score 43; DB 2; Length 518;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VEEDQFSQNPISC 16
||:|:|:|
Db 216 VEDDELSHSPCSC 228

RESULT 5
S38171
peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae)
N/Alternate names: peptide permease PTR2; protein YKR093w; protein YKR413
C/Species: Saccharomyces cerevisiae
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: S38171; S40646; S37700
R/Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo,
submitted to the Protein Sequence Database, March 1994
A/Reference number: S38158
A/Accession: S38171
A/Molecule type: DNA

A/Residues: 1-601 <BAL>
A/Cross-references: UNIPROT:P32901; UNIPARC:UPI00001329B5; EMBL:Z28318; NID:g486582; PID
A/Experimental source: strain S288C
R/Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Jin
Yeast 9, 1349-1354, 1993
A/Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo
A/Reference number: S40644; MUID:94205265; PMID:8154186
A/Accession: S40646
A/Molecule type: DNA
A/Residues: 1-601 <BOU>
A/Cross-references: UNIPARC:UPI00001329B5; EMBL:X73541; NID:g450550; PIDN:CAA51947.1; PII
A/Experimental source: strain S288C
A/Note: the authors did not translate the codon for residue 200
R/Becker, J.M.; Perry, J.R.; Basrai, M.A.; Naider, F.R.
submitted to the EMBL Data Library, March 1993
A/Description: Isolation and characterization of a Saccharomyces cerevisiae peptide trans
A/Reference number: S37700
A/Accession: S37700
A/Molecule type: DNA
A/Residues: 1-38,'T',40-466,'LLANTRICLDFFFRDLCLYHWVG',470,'RLFQS',471,'SPHEIVY',473-474,'
A/Cross-references: UNIPARC:UPI000017B2F9; EMBL:L11994
C/Genetics:
A/Gene: SGD:PTR2
A/Cross-references: SGD:S0001801; MIPS:YKR093w
A/Map position: 11R
C/Keywords: membrane protein

Query Match 46.2%; Score 43; DB 2; Length 601;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 EEDQFSQNPIS 15
|||:| |||
Db 569 EEDDFDLNPIS 579

RESULT 6
I38754
transcription factor REST (version 1) - human (fragment)
N/Alternate names: neural-restrictive silencer factor; RE1-silencing transcription factor
C/Species: Homo sapiens (man)
C/Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C/Accession: I38754
R/Schoenherr, C.J.; Anderson, D.J.
Science 267, 1360-1363, 1995
A/Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multip
A/Reference number: I38754; MUID:95176234; PMID:7871435
A/Accession: I38754
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-316 <RES>
A/Cross-references: UNIPROT:Q12956; UNIPARC:UPI0000070017; EMBL:U13877; NID:g606943; PID
C/Genetics:
A/Gene: GDB:REST; NRSF
A/Cross-references: GDB:702138
A/Map position: 4q12-4q12
C/Keywords: transcription regulation

Query Match 45.2%; Score 42; DB 2; Length 316;
Best Local Similarity 53.3%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLVEEDQFSQNPISC 16
| || ||:| |||
Db 207 STAEEDFSKGPISC 221

RESULT 7
T45592
hypothetical protein F12A12.70 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C/Accession: T45592

R;Foldes, R.L.; Adams, S.L.; Fantaske, R.P.; Kamboj, R.K.
Biochim. Biophys. Acta 1223, 155-159, 1994
A;Title: Human N-methyl-D-aspartate receptor modulatory subunit hNR2A: cloning and sequence
A;Reference number: S47555; MUID:94339179; PMID:8061049
A;Accession: S47555
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1464 <POL>
A/Cross-references: UNIPROT:Q12879; UNIPARC:UPI000000D7AB; GB:U09002; NID:g558748; PIDN:
C;Superfamily: N-methyl-D-aspartate receptor 2A; glutamate receptor homology
F;428-854/Domain: glutamate receptor homology <GRH>

Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPIIS 15
| : : | | | : |
Db 1018 VDSIRQDSLQNPFVS 1032

RESULT 13
S37138
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) - Cryptomonas sp.
C;Species: Cryptomonas sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37138
R;Douglas, S.E.; Reith, M.
submitted to the EMBL Data Library, March 1993
A;Description: A bchi homolog, encoding a subunit of Mg chelatase, is located on the pl
A;Reference number: S37138
A;Accession: S37138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <DOU>
A/Cross-references: UNIPROT:Q39516; UNIPARC:UPI0000127871; EMBL:Z21976; NID:g398949; PID
C;Genetics:
A;Start codon: GTG
C;Superfamily: magnesium chelatase, subunit ChlI
C;Keywords: lyase

Query Match 44.6%; Score 41.5; DB 2; Length 353;
Best Local Similarity 42.1%; Pred. No. 26;
Matches 8; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 VSLVEE-DQFSQNPIISCFE 18
| : : | : : | : : |
Db 225 VKIVEQRSEFDKNPSACLE 243

RESULT 14
A89858
hypothetical protein SA0781 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89858
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <KUR>
A/Cross-references: UNIPROT:Q99VP6; UNIPARC:UPI000000C7F68; GB:BA000018; PID:g13700723; F
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0781

Query Match 44.6%; Score 41.5; DB 2; Length 355;
Best Local Similarity 34.6%; Pred. No. 26;

Matches 9; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

Qy 1 VSLVEEDQF-----SQNPISCF 17
| : : | | | | : : |
Db 106 VKIIEQQFKCHIDTIKKQVPVCCF 131

RESULT 15
T16128
hypothetical protein F21H12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16128
R;Pavello, T.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F21H12.
A;Reference number: Z18464
A;Accession: T16128
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-632 <FAV>
A/Cross-references: UNIPROT:Q09312; UNIPARC:UPI000012A562; EMBL:U23176; NID:g726404; PID
C;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F21H12.5
A;Introns: 14/3; 92/3; 151/2; 235/3; 440/2; 483/2; 551/2

Query Match 44.6%; Score 41.5; DB 2; Length 632;
Best Local Similarity 56.2%; Pred. No. 50;
Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 SLVEEDQFSQNPIISCF 17
| : : | | | | : : |
Db 115 SRLSDDFSQN-VRCF 129

Search completed: December 22, 2005, 03:05:58
Job time : 47.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:42:57 ; Search time 54 Seconds
(without alignments)
235.176 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	93	100.0	229	2	Q9H5X9_HUMAN	Q9h5x9 homo sapien
2	93	100.0	229	2	Q53R12_HUMAN	Q53r12 homo sapien
3	93	100.0	229	2	Q6UWS1_HUMAN	Q6uws1 homo sapien
4	93	100.0	229	2	Q5U609_HUMAN	Q5u609 homo sapien
5	70	75.3	226	2	Q9CQY8_MOUSE	Q9cqy8 m mus muscu
6	70	75.3	226	2	Q9D3R0_MOUSE	Q9d3r0 mus musculu
7	70	75.3	226	2	Q9D3Q0_MOUSE	Q9d3q0 mus musculu
8	47	50.5	126	2	Q9C252_NEUCR	Q9c252 neurospora
9	46	49.5	601	2	Q7V7K2_PROMM	Q7v7k2 prochloroco
10	45	48.4	143	2	Q4N5J1_THEPA	Q4n5j1 theileria p
11	45	48.4	238	2	Q7T301_BRARE	Q7t301 brachydanio
12	45	48.4	410	2	Q9VDK6_DROME	Q9vdk6 drosophila
13	45	48.4	575	2	Q61CF7_CAEBR	Q61cf7 caenorhabdi
14	45	48.4	805	2	Q55DX2_DICDI	Q55dx2 dictyosteli
15	44	47.3	1273	1	GYRA_MYCLE	Q57532 mycobacteri
16	44	47.3	1710	2	Q4RM05_TETNG	Q4rm05 tetraodon n
17	43.5	46.8	1144	2	Q612X4_CAEBR	Q612x4 caenorhabdi
18	43	46.2	124	2	Q8ILR4_PLAF7	Q8ilr4 plasmodium
19	43	46.2	216	2	Q58AT8_CAEEL	Q58at8 caenorhabdi
20	43	46.2	435	2	Q54F45_DICDI	Q54f45 dictyosteli
21	43	46.2	491	2	Q90D04_9HIV1	Q90d04 human immun
22	43	46.2	518	2	Q9XII0_ARATH	Q9xii0 arabidopsis
23	43	46.2	601	1	PTR2_YEAST	P32901 saccharomyc
24	43	46.2	890	2	Q87GP6_VIBPA	Q87gp6 vibrio para
25	43	46.2	1112	2	Q4N6M1_THEPA	Q4n6m1 theileria p
26	43	46.2	1418	2	Q86HT4_DICDI	Q86ht4 dictyosteli
27	43	46.2	1466	2	Q554X7_DICDI	Q554x7 dictyosteli
28	43	46.2	1679	2	Q7PHR1_ANOGA	Q7phr1 anopheles g
29	43	46.2	1749	2	Q7RGH9_PLAYO	Q7rgh9 plasmodium
30	43	46.2	3005	2	Q50LG3_ALTAL	Q50lg3 alternaria
31	42.5	45.7	209	2	Q8W1X7_ALLCE	Q8w1x7 allium cepa

32	42	45.2	87	2	Q57L77_SALCH	Q57l77 salmonella
33	42	45.2	182	2	Q582P7_STRYP	Q582p7 trypanosoma
34	42	45.2	226	2	Q5M469_STRT2	Q5m469 streptococc
35	42	45.2	226	2	Q5LZL6_STRT1	Q5lzl6 streptococc
36	42	45.2	316	2	Q12956_HUMAN	Q12956 homo sapien
37	42	45.2	388	2	Q8KLJ8_STRTO	Q8klj8 streptomyce
38	42	45.2	420	2	Q9SNC3_ARATH	Q9snc3 arabidopsis
39	42	45.2	454	2	Q8IWI3_HUMAN	Q8iwi3 homo sapien
40	42	45.2	472	2	Q50VT4_ENTHI	Q50vt4 entamoeba h
41	42	45.2	522	2	Q60694_MOUSE	Q60694 mus musculu
42	42	45.2	525	2	Q4VAD6_MOUSE	Q4vad6 mus musculu
43	42	45.2	549	2	Q8JTM8_LSDV	Q8jtm8 lumpy skin
44	42	45.2	550	2	Q91ML3_LSDV	Q91ml3 lumpy skin
45	42	45.2	551	2	Q8JTY6_LSDV	Q8jty6 lumpy skin
46	42	45.2	681	2	Q12957_HUMAN	Q12957 homo sapien
47	42	45.2	762	2	Q6AMC0_DESPS	Q6amc0 desulfotale
48	42	45.2	852	2	Q9CW43_MOUSE	Q9cw43 mus musculu
49	42	45.2	900	2	Q6EQM5_ORYSA	Q6eqm5 oryza sativ
50	42	45.2	948	2	Q8S7M6_ORYSA	Q8s7m6 oryza sativ
51	42	45.2	982	2	Q7XBZ3_ORYSA	Q7xbz3 oryza sativ
52	42	45.2	1065	2	Q21992_CABEL	Q21992 caenorhabdi
53	42	45.2	1082	2	Q8VIG1_MOUSE	Q8vig1 mus musculu
54	42	45.2	1097	2	Q13127_HUMAN	Q13127 homo sapien
55	42	45.2	1126	2	Q59ER1_HUMAN	Q59er1 homo sapien
56	42	45.2	1464	1	NMDE1_HUMAN	Q12879 homo sapien
57	42	45.2	1464	1	NMDE1_PANTR	Q5is45 pan troglod
58	42	45.2	1464	2	Q547U9_HUMAN	Q547u9 homo sapien
59	42	45.2	1491	2	Q59EW6_HUMAN	Q59ew6 homo sapien
60	42	45.2	1587	2	Q53P23_ORYSA	Q53p23 oryza sativ
61	42	45.2	2418	2	Q8I1R9_PLAF7	Q8i1r9 plasmodium
62	42	45.2	4337	2	Q54B24_DICDI	Q54b24 dictyosteli
63	41.5	44.6	353	1	CHLI_GUIITH	Q39516 guillardia
64	41.5	44.6	355	2	Q99VF6_STAAN	Q99vf6 staphylococ
65	41.5	44.6	355	2	Q931V4_STAAM	Q931v4 staphylococ
66	41.5	44.6	632	1	FBF2_CABEL	Q09312 caenorhabdi
67	41	44.1	160	2	Q4XX10_PLACH	Q4xx10 plasmodium
68	41	44.1	187	2	Q5TF17_HUMAN	Q5tf17 homo sapien
69	41	44.1	239	1	GRPE_PROMP	Q7v3q4 prochloroco
70	41	44.1	254	2	Q76930_9HIV2	Q76930 human immun
71	41	44.1	260	2	Q8LFC3_ARATH	Q8lfc3 arabidopsis
72	41	44.1	302	2	Q54964_RAT	Q54964 rattus norv
73	41	44.1	316	2	Q6PNE0_HUMAN	Q6pne0 homo sapien
74	41	44.1	319	1	SPY1_HUMAN	Q43609 homo sapien
75	41	44.1	326	1	239A_HUMAN	O15442 homo sapien
76	41	44.1	326	1	239A_MOUSE	Q912g2 mus musculu
77	41	44.1	334	2	Q50S99_ENTHI	Q50sv9 entamoeba h
78	41	44.1	339	2	Q6FEN2_ACTIAD	Q6fen2 acinetobact
79	41	44.1	362	2	Q54EV8_DICDI	Q54ev8 dictyosteli
80	41	44.1	388	2	Q4SXK3_TETNG	Q4sxx3 tetraodon n
81	41	44.1	400	2	Q5RGZ5_BRARE	Q5rgz5 brachydanio
82	41	44.1	402	2	Q9SRU1_ARATH	Q9srul arabidopsis
83	41	44.1	421	2	Q5E9M2_BOVIN	Q5e9m2 bos taurus
84	41	44.1	421	2	Q5E9P4_BOVIN	Q5e9p4 bos taurus
85	41	44.1	421	2	Q5EAB8_BOVIN	Q5eab8 bos taurus
86	41	44.1	449	2	Q22822_ARATH	Q22822 arabidopsis
87	41	44.1	496	1	CBLC_MOUSE	Q80xl1 mus musculu
88	41	44.1	510	2	Q4RUC1_TETNG	Q4ruc1 tetraodon n
89	41	44.1	512	2	Q93ZR8_ARATH	Q93zr8 arabidopsis
90	41	44.1	526	2	Q4S3S8_TETNG	Q4s3s8 tetraodon n
91	41	44.1	545	2	Q9HEK1_NEUCR	Q9hek1 neurospora
92	41	44.1	559	2	Q53PG5_ORYSA	Q53pg5 oryza sativ
93	41	44.1	564	2	Q7RVW0_NEUCR	Q7rvw0 neurospora
94	41	44.1	606	2	Q6Y9B1_BORHE	Q6y9b1 borrelia he
95	41	44.1	606	2	Q8BI29_MOUSE	Q8bi29 mus musculu
96	41	44.1	609	2	Q7R0R9_GIALA	Q7r0r9 giardia lam
97	41	44.1	739	2	Q4T141_TETNG	Q4t141 tetraodon n
98	41	44.1	766	1	P RTP_EHV1	P68351 equine herp
99	41	44.1	766	1	P RTP_EHV1B	Q6dlh9 equine herp
100	41	44.1	766	1	P RTP_EHVIV	Q6s6n9 equine herp
101	41	44.1	793	1	LHR2A_MOUSE	Q99kc8 mus musculu
102	41	44.1	822	1	LHR2A_RAT	Q75we7 rattus norv
103	41	44.1	822	2	Q4S8A9_TETNG	Q4s8a9 tetraodon n
104	41	44.1	837	1	SYFB_PROMA	Q7vbx6 prochloroco

105	41	44.1	925	1	YE9G_SCHPO	013776	schizosacch
106	41	44.1	929	2	Q4RW90_TETNG	Q4rw90	tetraodon n
107	41	44.1	1069	2	Q54963_RAT	Q54963	rattus norv
108	41	44.1	1117	2	Q9SED7_AEGVE	Q9sed7	aegilops ve
109	41	44.1	1203	2	Q51Y30_MAGGR	Q51y30	magnaporthe
110	41	44.1	1337	2	Q4WHR7_ASPPU	Q4whr7	aspergillus
111	41	44.1	1447	2	Q5CFG8_CRYHO	Q5cfg8	cryptospori
112	41	44.1	2270	2	Q6BGF9_PARTE	Q6bgf9	paramecium
113	41	44.1	11696	2	Q5CV09_CRYPV	Q5cv09	cryptospori
114	40.5	43.5	496	2	Q4UEB8_THEAN	Q4ueb8	theileria a
115	40.5	43.5	792	1	SYFB_CHLPN	Q9z7w0	chlamydia p
116	40.5	43.5	801	2	Q95LI3_BOVIN	Q95li3	bos taurus
117	40.5	43.5	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce
118	40.5	43.5	2274	2	Q54W13_DICDI	Q54wl3	dictyosteli
119	40	43.0	95	1	SCR23_ARATH	P82642	arabidopsi
120	40	43.0	235	1	Y559_MYCPN	P75219	mycoplasma
121	40	43.0	242	2	Q4KL96_XENLA	Q4kl96	xenopus lae
122	40	43.0	267	2	Q9D9F7_MOUSE	Q9d9f7	mus musculu
123	40	43.0	276	2	Q50TCS_ENTHI	Q50tcs	entamoeba h
124	40	43.0	277	1	LGT_BACSK	Q5wdh2	bacillus cl
125	40	43.0	312	2	Q93RA5_THETH	Q93ras	thermus the
126	40	43.0	317	1	PHEG_AGLNE	P34784	aglaothamni
127	40	43.0	332	2	Q8QFN6_ELAQU	Q8qfn6	elaphe quad
128	40	43.0	332	2	Q8QFN7_ELAQU	Q8qfn7	elaphe quad
129	40	43.0	348	2	Q61ELO_ORYSA	Q61elo	oryza sativ
130	40	43.0	348	2	Q6QHD1_ORYSA	Q6qhd1	oryza sativ
131	40	43.0	356	2	Q962C9_PODCA	Q962c9	podocoryne
132	40	43.0	369	2	Q8JV08_CSV	Q8jv08	campeletis
133	40	43.0	370	2	Q5F3Z4_CHICK	Q5f3z4	gallus gall
134	40	43.0	373	2	Q8BQU1_MOUSE	Q8bqu1	m mus muscu
135	40	43.0	390	2	Q6L5S8_STORJ	Q6l5s8	streptococc
136	40	43.0	392	2	Q4L5J4_STAHI	Q4l5j4	staphylococ
137	40	43.0	398	2	Q7SYC4_BRARE	Q7syv4	brachydanio
138	40	43.0	405	2	Q5AVS5_EMENI	Q5avs5	aspergillus
139	40	43.0	421	2	Q9NXT9_HUMAN	Q9nxt9	homo sapien
140	40	43.0	430	2	Q93KW3_STRVR	Q93kw3	streptomyce
141	40	43.0	445	2	Q86YG4_HUMAN	Q86yg4	homo sapien
142	40	43.0	446	2	Q5AD28_CANAL	Q5ad28	candida alb
143	40	43.0	456	2	Q4RR95_TETNG	Q4rr95	tetraodon n
144	40	43.0	457	2	Q99KJ4_MOUSE	Q99kj4	mus musculu
145	40	43.0	484	2	Q78J30_MOUSE	Q78j30	mus musculu
146	40	43.0	510	2	Q61LS7_CAEBR	Q61lb7	caenorhabdi
147	40	43.0	510	2	Q8JAI1_SIVCZ	Q8jai1	chimpanzee
148	40	43.0	512	2	Q8JAH2_SIVCZ	Q8jah2	chimpanzee
149	40	43.0	527	2	Q9NIV0_DICDI	Q9niv0	dictyosteli
150	40	43.0	534	2	Q6NRT8_XENLA	Q6nrt8	xenopus lae
151	40	43.0	578	2	Q57V46_9TRYP	Q57v46	trypanosoma
152	40	43.0	596	2	Q5FUU2_GLUOX	Q5fuu2	gluconobact
153	40	43.0	600	2	Q6TFL4_HUMAN	Q6tfl4	homo sapien
154	40	43.0	600	2	Q812D9_RAT	Q812d9	rattus norv
155	40	43.0	600	2	Q8BRG6_MOUSE	Q8brg6	m mus muscu
156	40	43.0	600	2	Q56A24_RAT	Q56a24	rattus norv
157	40	43.0	615	2	Q804Q2_GADMO	Q804q2	gadus morhu
158	40	43.0	616	2	Q5AR94_EMENI	Q5ar94	aspergillus
159	40	43.0	618	2	Q92200_EMENI	Q92200	emericeila
160	40	43.0	619	2	Q4RV91_TETNG	Q4rv91	tetraodon n
161	40	43.0	620	2	Q9N9D4_9DIPT	Q9n9d4	megaselia a
162	40	43.0	624	2	Q9D5K3_MOUSE	Q9d5k3	mus musculu
163	40	43.0	627	2	Q4GZ34_9TRYP	Q4gz34	trypanosoma
164	40	43.0	695	1	SYTC_RAT	Q5xhy5	rattus norv
165	40	43.0	722	1	SYTC_MOUSE	Q9d0r2	mus musculu
166	40	43.0	735	2	Q7X1P3_9LACT	Q7xip3	lactococcus
167	40	43.0	855	2	Q80TM0_MOUSE	Q80tm0	mus musculu
168	40	43.0	888	2	Q6LJF0_PHOPR	Q6ljf0	photobacter
169	40	43.0	934	2	Q7SDE7_NEUCR	Q7sde7	neurospora
170	40	43.0	943	2	Q7QE10_ANOGA	Q7qe10	anopheles g
171	40	43.0	971	2	Q5ISN1_MACFA	Q5isn1	macaca fasc
172	40	43.0	1052	2	Q5TUB0_ANOGA	Q5tub0	anopheles g
173	40	43.0	1056	2	Q4PI36_USTMA	Q4pi36	ustilago ma
174	40	43.0	1215	2	Q54AY2_DICDI	Q54ay2	dictyosteli
175	40	43.0	1222	2	Q513V5_ENTHI	Q513v5	entamoeba h
176	40	43.0	1476	1	ATP7A_CRIGR	P49015	cricetulus
177	40	43.0	1482	2	Q4F8H5_BRARE	Q4f8h5	brachydanio

178	40	43.0	1491	1	ATP7A_MOUSE	Q64430	mus musculu
179	40	43.0	1492	1	ATP7A_RAT	P70705	rattus norv
180	40	43.0	1500	1	ATP7A_HUMAN	Q04656	homo sapien
181	40	43.0	1500	2	Q5JQN4_HUMAN	Q5jqn4	homo sapien
182	40	43.0	1590	2	Q6BCX2_MOUSE	Q6bcx2	mus musculu
183	40	43.0	1591	1	UN13B_HUMAN	Q14795	homo sapien
184	40	43.0	1591	1	UN13B_MOUSE	Q9z1n9	mus musculu
185	40	43.0	1591	1	Q5VYM8_HUMAN	Q5vym8	homo sapien
186	40	43.0	1592	2	Q5RAK9_PONPY	Q5rak9	pongo pygma
187	40	43.0	1620	2	Q4LE73_HUMAN	Q4le73	homo sapien
188	40	43.0	1622	1	UN13B_RAT	Q62769	rattus norv
189	40	43.0	1622	2	Q5VYM9_HUMAN	Q5vym9	homo sapien
190	40	43.0	1944	2	Q4TBR0_TETNG	Q4tbr0	tetraodon n
191	40	43.0	1945	2	Q7RZX2_NEUCR	Q7rxz2	neurospora
192	40	43.0	2458	2	Q4Q772_LEIMA	Q4q772	leishmania
193	40	43.0	3047	2	Q4SZ59_TETNG	Q4sz59	tetraodon n
194	40	43.0	3463	2	Q7R1E2_GIALA	Q7r1e2	giardia lam
195	40	43.0	4202	2	Q8I2S8_PLAF7	Q8i2s8	plasmodium
196	39.5	42.5	794	1	NU107_SCHPO	Q10331	schizosacch
197	39.5	42.5	1137	2	Q82196_ARATH	Q82196	arabidopsi
198	39	41.9	71	2	Q84585_CHVP1	Q84585	paramecium
199	39	41.9	85	2	Q44779_CAEBL	Q44779	caenorhabdi
200	39	41.9	89	2	Q61XE2_CAEBR	Q61xe2	caenorhabdi
201	39	41.9	112	2	Q9F1P2_BURCE	Q9f1p2	burkholderi
202	39	41.9	118	2	Q50ZT6_ENTHI	Q50zt6	entamoeba h
203	39	41.9	122	2	Q4T3X8_TETNG	Q4t3x8	tetraodon n
204	39	41.9	129	2	Q4JA85_SULAC	Q4ja85	sulfolobus
205	39	41.9	132	2	Q9GV20_CIOSA	Q9gv20	ciona savig
206	39	41.9	145	2	Q7MRQ4_WOLSU	Q7mrq4	wolinella s
207	39	41.9	147	2	Q4XW43_PLACH	Q4xw43	plasmodium
208	39	41.9	151	2	Q4LZ05_9BURK	Q4lzo5	burkholderi
209	39	41.9	152	2	Q8SXQ3_DROME	Q8sxq3	drosophila
210	39	41.9	152	2	Q96067_DROME	Q96067	drosophila
211	39	41.9	157	2	Q4UE00_THEAN	Q4ue00	theileria a
212	39	41.9	165	2	Q97SM3_STRPN	Q97sm3	streptococc
213	39	41.9	193	2	Q56AQ2_9VIRU	Q56aq2	bacillus th
214	39	41.9	197	2	Q65JT8_BACLD	Q65jt8	bacillus li
215	39	41.9	198	2	Q8DT46_STRMU	Q8dt46	streptococc
216	39	41.9	199	2	Q4VXJ0_HUMAN	Q4vxj0	homo sapien
217	39	41.9	200	2	Q7PRQ6_ANOGA	Q7prq6	anopheles g
218	39	41.9	200	2	Q8I135_PLAF7	Q8i135	plasmodium
219	39	41.9	203	2	Q5L2Y1_GSOKA	Q5l2y1	geobacillus
220	39	41.9	214	2	Q9PKG5_CHLMU	Q9pkg5	chlamydia m
221	39	41.9	220	2	Q5QT25_ORYSA	Q5qt25	oryza sativ
222	39	41.9	241	2	Q63K88_BURPS	Q63k88	burkholderi
223	39	41.9	255	2	Q62CU2_BURMA	Q62cu2	burkholderi
224	39	41.9	277	1	XAPA_ECOLI	P45563	escherichia
225	39	41.9	279	2	Q731F9_BACC1	Q731f9	bacillus ce
226	39	41.9	285	2	Q6XR96_9BACT	Q6xr96	uncultured
227	39	41.9	314	1	Y207_ENCCU	Q8swh5	encephalito
228	39	41.9	316	2	Q6MJG1_BDEBA	Q6mjg1	bdellovibri
229	39	41.9	319	1	PHEG_COROI	P83592	corallina o
230	39	41.9	319	2	Q7XZS8_COROI	Q7xzs8	corallina o
231	39	41.9	324	2	Q49872_MYCLE	Q49872	mycobacteri
232	39	41.9	327	2	Q50XN8_ENTHI	Q50xn8	entamoeba h
233	39	41.9	328	2	Q9V4H8_DROME	Q9v4h8	drosophila
234	39	41.9	331	1	LDHC_PIG	Q9tsx5	sus scrofa
235	39	41.9	331	1	PLIB_AGKBL	Q93233	agkistrodon
236	39	41.9	363	2	Q7NQT2_CHRVO	Q7nqt2	chromobacte
237	39	41.9	381	2	Q8WRU3_9TRYP	Q8wru3	trypanosoma
238	39	41.9	381	2	Q505M0_XENLA	Q505m0	xenopus lae
239	39	41.9	395	2	Q7PKD4_ANOGA	Q7pkd4	anopheles g
240	39	41.9	422	2	Q5LH60_BACFN	Q5lh60	bacteroides
241	39	41.9	424	2	Q64Y19_BACFR	Q64y19	bacteroides
242	39	41.9	428	2	Q577Z9_BRUAB	Q577z9	brucella ab
243	39	41.9	428	2	Q8FW63_BRUSU	Q8fw63	brucella su
244	39	41.9	428	2	Q8YC63_BRUMB	Q8yc63	brucella me
245	39	41.9	440	2	Q4XPC4_PLACH	Q4xpc4	plasmodium
246	39	41.9	450	1	PDE7B_HUMAN	Q9np56	homo sapien
247	39	41.9	450	2	Q5VWY9_HUMAN	Q5vwy9	homo sapien
248	39	41.9	450	2	Q6LFV8_PHOPR	Q6lfv8	photobacter
249	39	41.9	458	2	Q515E5_ENTHI	Q515e5	entamoeba h
250	39	41.9	471	2	Q4IML0_GIBZE	Q4iml0	gibberella

251	39	41.9	476	2	Q8S7F0_ORYSA	Q8e7f0 oryza sativ	324	38	40.9	75	2	Q9NZG9_HUMAN	Q9nzg9 homo sapien
252	39	41.9	493	2	Q96286_PLAF7	Q96286 plasmodium	325	38	40.9	76	2	Q5TPS0_ANOGA	Q5tps0 anopheles g
253	39	41.9	505	2	Q9LFV2_ARATH	Q9lfv2 arabidopsis	326	38	40.9	81	2	Q4NCA8_9MICC	Q4ncas arthrobacte
254	39	41.9	508	2	Q5VNG4_ORYSA	Q5vng4 oryza sativ	327	38	40.9	96	2	Q6YWJ1_ORYSA	Q6ywj1 oryza sativ
255	39	41.9	508	2	Q4V398_ARATH	Q4v398 arabidopsis	328	38	40.9	100	2	Q9ZME4_HELPJ	Q9zme4 helicobacte
256	39	41.9	509	2	Q6VG50_SIVC2	Q6vg50 chimpanzee	329	38	40.9	101	2	Q5TYP9_BRARE	Q5typ9 brachydanio
257	39	41.9	516	2	Q8W385_ORYSA	Q8w385 oryza sativ	330	38	40.9	104	1	DIRC1_HUMAN	Q969h9 homo sapien
258	39	41.9	526	2	Q8QL72_NPVMC	Q8ql72 rhodospseudo	331	38	40.9	122	2	Q4WVQ2_ASPFU	Q4wvq2 aspergillus
259	39	41.9	538	2	Q6N0K3_RHOPA	Q6n0k3 rhodopseudo	332	38	40.9	122	2	Q515Y4_ENTHI	Q515y4 entamoeba h
260	39	41.9	576	1	PT1_BUCBP	Q89b04 buchnera ap	333	38	40.9	140	2	Q6ZUV6_HUMAN	Q6zuv6 homo sapien
261	39	41.9	585	2	Q9U2Y8_CAEEL	Q9u2y8 caenorhabdi	334	38	40.9	144	2	Q5V686_HALMA	Q5v686 haloarcula
262	39	41.9	586	2	Q4LE81_HUMAN	Q4le81 homo sapien	335	38	40.9	165	2	Q86U80_HUMAN	Q86u80 homo sapien
263	39	41.9	607	2	Q55WQ5_CRYNE	Q55wq5 cryptococcu	336	38	40.9	166	2	Q6LHC9_PROPR	Q6lhc9 photobacter
264	39	41.9	607	2	Q5KJJ1_CRYNE	Q5kjj1 cryptococcu	337	38	40.9	176	2	Q6CD85_YARLI	Q6cd85 yarrowia li
265	39	41.9	607	2	Q71A50_9NUCL	Q71a50 mamestra co	338	38	40.9	181	2	Q4X980_PLACH	Q4x980 plasmodium
266	39	41.9	637	2	Q5WAV1_BACSK	Q5wav1 bacillus cl	339	38	40.9	183	2	Q9D2S7_MOUSE	Q9d2s7 mus musculu
267	39	41.9	659	2	Q6FRU1_CANGA	Q6frul candida gla	340	38	40.9	186	2	Q5ZSE7_LEGPH	Q5zse7 legionella
268	39	41.9	659	2	Q8DR86_STRR6	Q8dr86 streptococc	341	38	40.9	195	2	Q4WY06_ASPFU	Q4wy06 aspergillus
269	39	41.9	662	2	Q59FJ9_HUMAN	Q59fj9 homo sapien	342	38	40.9	201	2	Q8C5I2_MOUSE	Q8c5i2 mus musculu
270	39	41.9	669	2	Q5V4P7_HALMA	Q5v4p7 haloarcula	343	38	40.9	202	2	Q8LMX9_ORYSA	Q8lmx9 oryza sativ
271	39	41.9	699	2	Q4YX57_PLABE	Q4yx57 plasmodium	344	38	40.9	205	2	Q4XCIS_PLACH	Q4xcis plasmodium
272	39	41.9	710	2	Q54J66_DICDI	Q54j66 dictyosteli	345	38	40.9	214	2	Q7S2G9_NEUCR	Q7s2g9 neurospora
273	39	41.9	714	2	Q86K58_DICDI	Q86k58 dictyosteli	346	38	40.9	215	2	Q54730_SYNP7	Q54730 synechococc
274	39	41.9	774	2	Q7RR25_PLAYO	Q7rr25 plasmodium	347	38	40.9	216	2	Q5N261_SYNP6	Q5n261 synechococc
275	39	41.9	784	2	Q4IN01_GIBZE	Q4in01 gibberella	348	38	40.9	217	2	Q9LIJ7_ARATH	Q9lij7 arabidopsis
276	39	41.9	809	2	Q9R9U6_PSEPU	Q9r9u6 pseudomonas	349	38	40.9	219	2	Q8Q0G6_METMA	Q8q0g6 methanosarc
277	39	41.9	814	2	Q4RFH4_TETNG	Q4rfh4 tetraodon n	350	38	40.9	219	2	Q8PSS8_METMA	Q8ps88 methanosarc
278	39	41.9	926	2	Q655X4_ORYSA	Q655x4 oryza sativ	351	38	40.9	224	2	Q5W400_9HIV1	Q5w400 human immun
279	39	41.9	929	2	Q32491_BACNO	Q32491 bacteroides	352	38	40.9	225	2	Q7VPY1_CHLPN	Q7vpy1 chlamydia p
280	39	41.9	999	2	Q941L1_BRANA	Q941l1 arabidopsis	353	38	40.9	225	2	Q9Z7X2_CHLPN	Q9z7x2 chlamydia p
281	39	41.9	1001	1	AHM5_ARATH	Q987f8 arabidopsis	354	38	40.9	236	2	Q57V30_9TRYP	Q57v30 trypanosoma
282	39	41.9	1001	2	Q94KD6_ARATH	Q94kd6 arabidopsis	355	38	40.9	276	2	Q92N72_RHIME	Q92n72 rhizobium m
283	39	41.9	1012	2	Q6H6Z1_ORYSA	Q6h6z1 oryza sativ	356	38	40.9	277	2	Q8FFC6_ECOL6	Q8ffc6 escherichia
284	39	41.9	1038	2	Q75E85_ASHGO	Q75e85 ashbya gosb	357	38	40.9	287	2	Q97XZ6_SULSO	Q97xz6 sulfolobus
285	39	41.9	1064	2	Q8XLD9_CLOPE	Q8xld9 clostridium	358	38	40.9	288	2	Q5HU35_CAMJR	Q5hu35 campylobact
286	39	41.9	1077	2	Q7RDA2_PLAYO	Q7rda2 plasmodium	359	38	40.9	288	2	Q9PNM5_CAMJE	Q9pnm5 campylobact
287	39	41.9	1124	2	Q9R0T2_RAT	Q9r0t2 rattus norv	360	38	40.9	297	2	Q5NGL9_FRATT	Q5ngl9 francisella
288	39	41.9	1161	2	Q5DTZ0_MOUSE	Q5dtz0 mus musculu	361	38	40.9	303	2	Q9PVG2_XENLA	Q9pvg2 xenopus lae
289	39	41.9	1177	2	Q55JP8_CRYNE	Q55jp8 cryptococcu	362	38	40.9	309	2	Q7ZAV1_9HIV1	Q7zav1 human immun
290	39	41.9	1177	2	Q5K9V4_CRYNE	Q5k9v4 cryptococcu	363	38	40.9	319	2	Q5Y172_XENTR	Q5y172 xenopus tro
291	39	41.9	1185	2	Q4QBV4_LEIMA	Q4qbv4 leishmania	364	38	40.9	324	2	Q4R6T4_MACFA	Q4r6t4 macaca fasc
292	39	41.9	1299	2	Q57YF2_9TRYP	Q57yf2 trypanosoma	365	38	40.9	331	1	LDHC_VULVU	Q29563 vulpes vulp
293	39	41.9	1334	2	Q5FFB0_EHRRG	Q5ffb0 ehrlichia r	366	38	40.9	337	2	Q5ULS2_9CAUD	Q5ula2 lactobacill
294	39	41.9	1354	2	Q4U3V3_HUMAN	Q4u3v3 homo sapien	367	38	40.9	339	1	RAD51_CRIGR	P70099 cricetulus
295	39	41.9	1368	2	Q99ZW2_STRPY	Q99zw2 streptococc	368	38	40.9	339	1	RAD51_HUMAN	Q06609 homo sapien
296	39	41.9	1413	2	Q4UJ10_THEAN	Q4uj10 theileria a	369	38	40.9	339	1	RAD51_MOUSE	Q08297 mus musculu
297	39	41.9	1432	2	Q4U3G5_CANFA	Q4u3g5 canis famil	370	38	40.9	339	2	Q5U0A5_HUMAN	Q5u0a5 homo sapien
298	39	41.9	1451	1	ATP7B_RAT	Q64535 rattus norv	371	38	40.9	339	2	Q6FHX9_HUMAN	Q6fhx9 homo sapien
299	39	41.9	1452	2	Q9QUG4_RAT	Q9qug4 rattus norv	372	38	40.9	339	2	Q8MKI8_CANFA	Q8mki8 canis famil
300	39	41.9	1462	1	ATP7B_MOUSE	Q64446 mus musculu	373	38	40.9	340	2	Q6ZNA8_HUMAN	Q6zna8 homo sapien
301	39	41.9	1465	1	ATP7B_HUMAN	P35670 homo sapien	374	38	40.9	345	1	YGN8_YEAST	P53122 saccharomyc
302	39	41.9	1465	1	Q5T7X7_HUMAN	Q5t7x7 homo sapien	375	38	40.9	351	2	Q5AF67_CANAL	Q5af67 candida alb
303	39	41.9	1505	1	ATP7B_SHEEP	Q9xt50 ovis aries	376	38	40.9	354	2	Q4WM90_ASPFU	Q4wm90 aspergillus
304	39	41.9	1626	2	Q4S7J8_TETNG	Q4s7j8 tetraodon n	377	38	40.9	361	2	Q97RN5_STRPN	Q97rn5 streptococc
305	39	41.9	1743	2	Q9XWX5_CAEEL	Q9xwx5 caenorhabdi	378	38	40.9	364	2	Q5DEP0_SCHJA	Q5dep0 schistosoma
306	39	41.9	1868	2	Q4RYG5_TETNG	Q4ryg5 tetraodon n	379	38	40.9	369	2	Q74NA2_NANEQ	Q74na2 nanoarchaeu
307	39	41.9	2202	2	Q4QEP5_LEIMA	Q4qep5 leishmania	380	38	40.9	385	2	Q93787_CAEEL	Q93787 caenorhabdi
308	39	41.9	2291	2	Q9W1A9_DROME	Q9wia9 drosophila	381	38	40.9	392	2	Q7ZVV4_BRARE	Q7zvv4 brachydanio
309	39	41.9	2943	2	Q8IK94_PLAF7	Q8ik94 plasmodium	382	38	40.9	393	2	Q5XGG8_XENTR	Q5xgg8 xenopus tro
310	39	41.9	5095	2	Q4Q3Q7_LEIMA	Q4q3q7 leishmania	383	38	40.9	395	1	TF2H2_HUMAN	Q13888 homo sapien
311	38.5	41.4	169	2	Q6C1V7_YARLI	Q6clv7 yarrowia li	384	38	40.9	395	2	Q6P1K8_HUMAN	Q6plk8 homo sapien
312	38.5	41.4	300	2	Q76EH3_GVMSI	Q76eh3 gymnodinium	385	38	40.9	395	2	Q6GR42_XENLA	Q6gr42 xenopus lae
313	38.5	41.4	300	2	Q76E15_9DINO	Q76ei5 symbiodiniu	386	38	40.9	395	2	Q4T3D5_TETNG	Q4t3d5 tetraodon n
314	38.5	41.4	355	2	Q8NXG7_STAAN	Q8nxg7 staphylococ	387	38	40.9	396	1	TF2IB4_MOUSE	Q9jib4 mus musculu
315	38.5	41.4	355	2	Q6GIG7_STAAR	Q6gig7 staphylococ	388	38	40.9	396	2	Q7TPV0_MOUSE	Q7tpv0 mus musculu
316	38.5	41.4	355	2	Q6GB05_STAAS	Q6gb05 staphylococ	389	38	40.9	398	2	Q91YN8_MOUSE	Q91yn8 mus musculu
317	38.5	41.4	355	2	Q5HHG4_STAAC	Q5hhg4 staphylococ	390	38	40.9	407	2	Q6BHM6_DEBHA	Q6bhm6 debaryomyce
318	38.5	41.4	438	2	Q9VNP8_DROME	Q9vnp8 drosophila	391	38	40.9	414	1	PP2C3_SCHPO	Q09173 schizosacch
319	38.5	41.4	514	2	Q6BZG1_DEBHA	Q6bzg1 debaryomyce	392	38	40.9	421	2	Q6GMC6_XENLA	Q6gmc6 xenopus lae
320	38.5	41.4	583	2	Q8ENC6_OCEIH	Q8enc6 oceanobacil	393	38	40.9	424	2	Q96T72_HUMAN	Q96t72 homo sapien
321	38.5	41.4	690	2	Q8IM21_PLAF7	Q8im21 plasmodium	394	38	40.9	425	2	Q4V7N9_XENLA	Q4v7n9 xenopus lae
322	38.5	41.4	873	2	Q60MQ0_CAEER	Q60mq0 caenorhabdi	395	38	40.9	426	1	PDE7A_RAT	O08593 rattus norv
323	38.5	41.4	2823	2	Q7RGM8_PLAYO	Q7rgm8 plasmodium	396	38	40.9	428	2	Q53WL0_ORYSA	Q53wl0 oryza sativ

397	38	40.9	429	2	Q5QMR2_ORYSA	Q5qmr2	oryza sativ
398	38	40.9	429	2	Q8GAH1_ARTNI	Q8gah1	arthrobacte
399	38	40.9	430	2	O31226_ARTNI	O31226	arthrobacte
400	38	40.9	432	2	Q6LZB4_METMP	Q6lzb4	methanococc
401	38	40.9	436	2	O42954_SCHPO	O42954	schizosacch
402	38	40.9	441	2	Q4Y727_PLACH	Q4y727	plasmodium
403	38	40.9	446	2	Q9C7Z9_ARATH	Q9c7z9	arabidopsis
404	38	40.9	448	1	YAP1_CHICK	P46936	gallus gall
405	38	40.9	451	2	Q4V4Z3_DROME	Q4v4z3	drosophila
406	38	40.9	455	2	Q4PDU6_USTMA	Q4pdu6	ustilago ma
407	38	40.9	455	2	Q7XUV8_ORYSA	Q7xuv8	oryza sativ
408	38	40.9	456	1	PDE7A_MOUSE	P70453	mus musculus
409	38	40.9	456	2	Q5R5B5_PONPY	Q5r5b5	pongo pygma
410	38	40.9	472	2	Q7R601_GIALA	Q7r601	giardia lam
411	38	40.9	472	2	Q92PH9_RHIME	Q92ph9	rhizobium m
412	38	40.9	482	1	PDE7A_HUMAN	Q13946	homo sapien
413	38	40.9	482	2	Q6P5G2_MOUSE	Q6p5g2	mus musculus
414	38	40.9	489	2	Q8QNN7_9PHYC	Q8qnn7	ectocarpus
415	38	40.9	503	2	O23215_ARATH	O23215	arabidopsis
416	38	40.9	504	2	Q7MXT9_PORGI	Q7mxt9	porphyromon
417	38	40.9	510	2	Q5DCH4_SCHJA	Q5dch4	schistosoma
418	38	40.9	512	2	Q4V4V2_DROME	Q4v4v2	drosophila
419	38	40.9	529	2	Q9PVG3_XENLA	Q9pvg3	xenopus lae
420	38	40.9	532	2	Q6VQV6_ORYSA	Q6vqv6	oryza sativ
421	38	40.9	535	2	Q54EK8_DICDI	Q54ek8	dictyosteli
422	38	40.9	535	2	Q7RH26_PLAYO	Q7rh26	plasmodium
423	38	40.9	542	2	Q8IQS7_DROME	Q8iqs7	drosophila
424	38	40.9	542	2	Q4T2L3_TETNG	Q4t2l3	tetraodon n
425	38	40.9	551	2	Q9SVE6_ARATH	Q9sve6	arabidopsis
426	38	40.9	551	2	Q83DR2_CXBU	Q83dr2	coxiella bu
427	38	40.9	558	2	Q9M084_ARATH	P41716	choristoneu
428	38	40.9	560	1	TATR_NPVCF	Q77df7	choristoneu
429	38	40.9	560	2	Q77DF7_NPVCF	Q50xk3	entamoeba h
430	38	40.9	562	2	Q50XK3_ENTHI	Q84sr2	oryza sativ
431	38	40.9	562	2	Q84SR2_ORYSA	Q4r9c1	macaca fasc
432	38	40.9	572	2	Q4R9C1_MACPA	Q8civ2	mus musculus
433	38	40.9	574	1	MBRL_MOUSE	Q55bh0	dictyosteli
434	38	40.9	595	2	Q55BH0_DICDI	Q6ins2	xenopus lae
435	38	40.9	605	2	Q6INS2_XENLA	Q6imp4	mus musculus
436	38	40.9	607	1	PANX2_MOUSE	Q4zin3	homo sapien
437	38	40.9	620	1	MBRL_HUMAN	Q8tle0	methanosarc
438	38	40.9	620	2	Q8TLE0_METAC	Q6t448	leishmania
439	38	40.9	623	2	Q6T448_LEIMA	Q6l542	oryza sativ
440	38	40.9	626	2	Q6L542_ORYSA	Q66j88	xenopus lae
441	38	40.9	631	2	Q66J88_XENLA	Q96rd6	homo sapien
442	38	40.9	633	1	PANX2_HUMAN	Q8mjf4	oryctolagus
443	38	40.9	641	2	Q8MJD4_RABIT	Q4i3r8	gibberella
444	38	40.9	645	2	Q4I3R8_GIBZE	Q8h7z4	oryza sativ
445	38	40.9	650	2	Q8H7Z4_ORYSA	P22459	homo sapien
446	38	40.9	653	1	KCNA4_HUMAN	Q5reb6	pongo pygma
447	38	40.9	653	2	Q5REB6_PONPY	Q61423	mus musculus
448	38	40.9	654	1	KCNA4_MOUSE	Q28527	mustela put
449	38	40.9	654	1	KCNA4_MUSPF	Q8cbf8	mus musculus
450	38	40.9	654	2	Q8CBF8_MOUSE	P15385	rattus norv
451	38	40.9	655	1	KCNA4_RAT	Q05037	bos taurus
452	38	40.9	660	1	KCNA4_BOVIN	Q9g1f1	bos taurus
453	38	40.9	661	2	Q9GLF1_BOVIN	Q5adt2	candida alb
454	38	40.9	662	2	Q5ADT2_CANAL	P60571	rattus norv
455	38	40.9	664	1	PANX2_RAT	Q4jgm2	mus musculus
456	38	40.9	667	2	Q4JGM2_MOUSE	Q4wqy0	aspergillus
457	38	40.9	684	2	Q4WQY0_ASPTU	Q7qx17	giardia lam
458	38	40.9	684	2	Q7QXI7_GIALA	Q5rg85	brachydanio
459	38	40.9	690	2	Q5RG85_BRARE	Q91fq5	chilo iride
460	38	40.9	710	2	Q91FQ5_IRV6	Q6cga7	yarrowia li
461	38	40.9	715	2	Q6CGA7_YARLI	Q5zlc2	gallus gall
462	38	40.9	723	2	Q5ZLC2_CHICK	Q6cegi	yarrowia li
463	38	40.9	726	2	Q6CEG1_YARLI	Q5lev6	entamoeba h
464	38	40.9	730	2	Q5LEV6_ENTHI	O42777	emericeila
465	38	40.9	748	1	TREB_EMENI	Q5ble5	aspergillus
466	38	40.9	748	2	Q5B1E5_EMENI	P54861	saccharomyc
467	38	40.9	757	1	DNM1_YEAST	P26659	schizosacch
468	38	40.9	772	1	RAD15_SCHPO	Q6nzf7	mus musculus
469	38	40.9	775	2	Q6NZF7_MOUSE		

470	38	40.9	776	2	Q5AFV3_CANAL	Q5afv3	candida alb
471	38	40.9	790	2	Q8CHT2_MOUSE	Q8cht2	mus musculu
472	38	40.9	790	2	O8BLY2_MOUSE	O8bly2	mus musculu
473	38	40.9	797	2	Q5AQJ4_EMENI	Q5aqj4	aspergillus
474	38	40.9	807	2	Q8K3R3_MOUSE	Q8k3r3	mus musculu
475	38	40.9	811	2	Q9FHI4_ARATH	Q9fhl4	arabidopsis
476	38	40.9	831	2	Q8CDM4_MOUSE	Q8cdm4	mus musculu
477	38	40.9	841	2	Q6MDJ4_PAROW	Q6mdj4	parachlamyd
478	38	40.9	844	2	O14147_SCHPO	O14147	schizosacch
479	38	40.9	845	2	Q6EPV3_ORYSA	Q6epv3	oryza sativ
480	38	40.9	855	2	Q50SE9_ENTHI	Q50se9	entamoeba h
481	38	40.9	882	2	Q9VZQ9_DROME	Q9vzq9	drosophila
482	38	40.9	891	2	Q8IIR1_PLAF7	Q8iir1	plasmodium
483	38	40.9	913	2	P90742_CABEL	P90742	caenorhabdi
484	38	40.9	926	2	Q7XVB0_ORYSA	Q7xvb0	oryza sativ
485	38	40.9	927	2	Q8IRD5_DROME	Q8ird5	drosophila
486	38	40.9	946	2	Q4XOP4_ASPTU	Q4xop4	aspergillus
487	38	40.9	950	2	Q8K4M9_RAT	Q8k4m9	rattus norv
488	38	40.9	969	2	Q7RMK2_PLAYO	Q7rmk2	plasmodium
489	38	40.9	976	2	Q54H51_DICDI	Q54h51	dictyosteli
490	38	40.9	984	2	Q55HV7_CRYNE	Q55hv7	cryptococcu
491	38	40.9	986	2	Q5K7E1_CRYNE	Q5k7e1	cryptococcu
492	38	40.9	992	2	Q7XRJ9_ORYSA	Q7xrj9	oryza sativ
493	38	40.9	995	2	Q4P9K4_USTMA	Q4p9k4	ustilago ma
494	38	40.9	997	1	CEBPZ_MOUSE	P53569	mus musculu
495	38	40.9	998	1	CEBPZ_HUMAN	Q03701	homo sapien
496	38	40.9	998	2	Q6NRA7_XENLA	Q6nra7	xenopus lae
497	38	40.9	1054	2	Q8NE75_HUMAN	Q8ne75	homo sapien
498	38	40.9	1068	1	PK3CA_BOVIN	P32871	bos taurus
499	38	40.9	1068	1	PK3CA_HUMAN	P42336	homo sapien
500	38	40.9	1069	1	Q4LE51_HUMAN	Q4le51	homo sapien
501	38	40.9	1073	2	Q4QOM9_LEIMA	Q4qom9	leishmania
502	38	40.9	1082	2	Q4PEH9_USTMA	Q4peh9	ustilago ma
503	38	40.9	1110	2	Q4IA83_GIBZE	Q4ia83	gibberella
504	38	40.9	1120	2	Q55QV1_CRYNE	Q55qv1	cryptococcu
505	38	40.9	1126	2	Q5KFB5_CRYNE	Q5kfb5	cryptococcu
506	38	40.9	1136	2	Q6ISB8_ORYSA	Q6isb8	oryza sativ
507	38	40.9	1176	2	Q9RC30_BACTK	Q9rc30	bacillus th
508	38	40.9	1276	2	Q03016_YEAST	Q03016	saccharomyc
509	38	40.9	1291	2	Q94I49_ORYSA	Q94i49	oryza sativ
510	38	40.9	1292	2	Q8S5Q8_ORYSA	Q8s5q8	oryza sativ
511	38	40.9	1364	2	O59757_SCHPO	O59757	schizosacch
512	38	40.9	1388	2	Q5IS90_9PRIM	Q5ie90	saimiri bol
513	38	40.9	1411	2	Q6FSJ5_CANGA	Q6fej5	candida gla
514	38	40.9	1579	2	Q9ARZ4_ORYSA	Q9arz4	oryza sativ
515	38	40.9	1607	2	Q7XS00_ORYSA	Q7xs00	oryza sativ
516	38	40.9	1727	2	Q4SDE7_TETNG	Q4sde7	tetraodon n
517	38	40.9	1752	2	Q4Z6E8_PLABE	Q4z6e8	plasmodium
518	38	40.9	1781	2	Q6BK91_DEBHA	Q6bk91	debaryomyce
519	38	40.9	1847	2	Q7XSE2_ORYSA	Q7xse2	oryza sativ
520	38	40.9	2134	2	Q8CZT9_YERPE	Q8czt9	yersinia pe
521	38	40.9	2201	2	Q8ZHV3_YERPE	Q8zhv3	yersinia pe
522	38	40.9	2367	1	POL1_RRVC	Q6w8w4	r rnal poly
523	38	40.9	3213	2	Q4HZN3_GIBZE	Q4hzn3	gibberella
524	38	40.9	3311	2	Q74QP0_YERPE	Q74qp0	yersinia pe
525	38	40.9	3577	2	Q7YV66_9TRYP	Q7yv66	trypanosoma
526	38	40.9	3886	2	Q666G1_YERPS	Q666g1	yersinia ps
527	38	40.9	4664	2	Q4QFY9_LEIMA	Q4qfy9	leishmania
528	37.5	40.3	219	2	Q6BF14_PARTE	Q6bf14	paramedium
529	37.5	40.3	344	2	Q7RL10_PLAYO	Q7rl10	plasmodium
530	37.5	40.3	372	2	Q9HQQ1_HALSA	Q9hqql	halobacteri
531	37.5	40.3	392	1	PANX3_HUMAN	Q96qz0	homo sapien
532	37.5	40.3	392	1	PANX3_MOUSE	Q8ceg0	mus musculu
533	37.5	40.3	392	1	PANX3_RAT	P60572	rattus norv
534	37.5	40.3	392	1	Q6IMP0_MOUSE	Q6imp0	mus musculu
535	37.5	40.3	804	2	Q7NAD0_PHOLL	Q7nad0	photorhabdu
536	37.5	40.3	838	2	Q9C8I5_ARATH	Q9c8i5	arabidopsis
537	37.5	40.3	900	2	Q7RMZ9_PLAYO	Q7rmz9	plasmodium
538	37.5	40.3	1021	2	Q8IDW2_PLAF7	Q8idw2	plasmodium
539	37.5	40.3	1195	2	Q6BKG7_DEBHA	Q6bkq7	debaryomyce
540	37.5	40.3	3317	2	Q7QJK9_ANOGA	Q7qjk9	anopheles g
541	37	39.8	49	2	Q7RBP3_PLAYO	Q7rbp3	plasmodium
542	37	39.8	58	2	Q85WY7_PINKO	Q85wy7	pinus korai

543	37	39.8	84	2	Q9AYP3_ORYSA	Q9AYP3_oryza sativ	616	37	39.8	331	2	Q9NDG0_TRIVA	Q9ndg0_trichomonas
544	37	39.8	95	2	Q655C6_ORYSA	Q655c6_oryza sativ	617	37	39.8	332	2	Q7QAA2_ANOGA	Q7qaa2_anopheles g
545	37	39.8	101	2	Q4MZF2_ THEPA	Q4mzf2_theileria p	618	37	39.8	332	2	Q9BIH7_ANOGA	Q9bih7_anopheles g
546	37	39.8	115	2	Q5PRO1_RAT	Q5pr01_rattus norv	619	37	39.8	333	2	Q8IHT3_PLAF7	Q8iht3_plasmodium
547	37	39.8	117	2	Q51VX2_MAGGR	Q51vx2_magnaporthe	620	37	39.8	334	2	Q81CY1_BACCR	Q81cy1_bacillus ce
548	37	39.8	124	2	Q52117_BRUAB	Q52117_brucella ab	621	37	39.8	336	2	Q8A2D9_BACTN	Q8a2d9_bacteroides
549	37	39.8	131	2	Q61QC1_CABER	Q61qc1_caenorhabdi	622	37	39.8	339	1	RAD51_RABIT	O77507_oryctolagus
550	37	39.8	132	2	Q974W6_SULTO	Q974w6_sulfolobus	623	37	39.8	341	1	APHA_MYCRA	Q48935_mycoplana r
551	37	39.8	145	2	Q41BB8_GIBZE	Q41bb8_gibberella	624	37	39.8	343	2	Q5LIA5_BACFN	Q5lia5_bacteroides
552	37	39.8	146	2	Q59S55_CANAL	Q59s55_candida alb	625	37	39.8	343	2	Q64ZB8_BACFR	Q64zb8_bacteroides
553	37	39.8	151	2	Q8J4W6_9HIV1	Q8j4w6_human immun	626	37	39.8	347	2	Q8ESK7_OCEIH	Q8esk7_oceanobacil
554	37	39.8	155	2	Q6RTW8_9HIV1	Q6rtw8_human immun	627	37	39.8	353	2	Q7Z783_HUMAN	Q7z783_homo sapien
555	37	39.8	172	2	Q95VY8_DROME	Q95vy8_drosophila	628	37	39.8	362	2	Q96S93_HUMAN	Q96s93_homo sapien
556	37	39.8	175	2	Q94JH8_ORYSA	Q94jh8_oryza sativ	629	37	39.8	364	2	Q4Y0G6_PLACH	Q4y0g6_plasmodium
557	37	39.8	176	2	Q61722_DROME	Q61722_drosophila	630	37	39.8	365	1	SERC_LACLA	Q9chw5_lactococcus
558	37	39.8	180	2	Q95KR9_SUNMU	Q95kr9_suncus muri	631	37	39.8	369	2	Q57EJ0_BRUAB	Q57ej0_brucella ab
559	37	39.8	189	2	Q80S24_BFV	Q80s24_barmah fore	632	37	39.8	369	2	Q8G211_BRUSU	Q8g211_brucella su
560	37	39.8	193	1	UGPI5_ARATH	Q9c7f7_arabidopsis	633	37	39.8	373	2	Q7Q190_ANOGA	Q7q190_anopheles g
561	37	39.8	194	2	Q8L9Q7_ARATH	Q8l9q7_arabidopsis	634	37	39.8	377	2	Q8YFW9_BRUME	Q8yfw9_brucella me
562	37	39.8	194	2	Q9KT22_VIBCH	Q9kt22_vibrio chol	635	37	39.8	378	2	Q7Q9L8_ANOGA	Q7q9l8_anopheles g
563	37	39.8	197	2	Q8PZK6_METWA	Q8pzk6_methanosarc	636	37	39.8	381	2	Q6QH99_9BACE	Q6qh99_bacteroides
564	37	39.8	198	2	Q4XQJ4_PLACH	Q4xqj4_plasmodium	637	37	39.8	381	2	Q4KGV6_PSEF5	Q4kgv6_pseudomonas
565	37	39.8	199	2	Q7RC35_PLAYO	Q7rc35_plasmodium	638	37	39.8	382	2	Q6FUL7_CANGA	Q6ful7_candida gla
566	37	39.8	203	2	Q8TK31_METAC	Q8tk31_methanosarc	639	37	39.8	385	2	Q5LRT4_SILPO	Q5lrt4_silicibacte
567	37	39.8	205	2	Q6M114_METMP	Q6m114_methanococc	640	37	39.8	386	2	O17559_CABEL	O17559_caenorhabdi
568	37	39.8	206	2	Q67YC9_ARATH	Q67yc9_arabidopsis	641	37	39.8	390	2	Q6L5Q8_STRMT	Q6l5q8_streptococc
569	37	39.8	206	2	Q8LB66_ARATH	Q8lb66_arabidopsis	642	37	39.8	393	2	Q96SK0_HUMAN	Q96sk0_homo sapien
570	37	39.8	212	2	Q5TEN0_HUMAN	Q5ten0_homo sapien	643	37	39.8	393	2	Q9BWS9_HUMAN	Q9bws9_homo sapien
571	37	39.8	223	2	Q9D9V5_MOUSE	Q9d9v5_mus musculu	644	37	39.8	393	2	Q9BY52_HUMAN	Q9by52_homo sapien
572	37	39.8	227	2	Q5A1E6_CANAL	Q5a1e6_candida alb	645	37	39.8	393	2	Q5RFF6_PONPY	Q5rff6_pongo pygma
573	37	39.8	229	2	Q9LK42_ARATH	Q9lk42_arabidopsis	646	37	39.8	393	2	Q4K2S4_STRPN	Q4k2s4_streptococc
574	37	39.8	238	2	Q68X6_ORYSA	Q68x6_oryza sativ	647	37	39.8	403	2	Q7PPS5_ANOGA	Q7pps5_anopheles g
575	37	39.8	241	2	Q7QYV5_GIALA	Q7qym3_lactobacill	648	37	39.8	409	2	Q4WYE9_PLABE	Q4ywe9_plasmodium
576	37	39.8	247	1	SCPA_LACJO	Q97fs0_clostridium	649	37	39.8	412	2	Q8MXG8_CABEL	Q8mxg8_caenorhabdi
577	37	39.8	249	2	Q97FS0_CLOAB	Q97fs0_clostridium	650	37	39.8	412	2	Q8MXG8_CABEL	Q8mxg8_caenorhabdi
578	37	39.8	255	2	Q5TMW4_ANOGA	Q5tmw4_anopheles g	651	37	39.8	413	2	Q53CX2_9GAMA	Q53cx2_macaca fusc
579	37	39.8	259	2	Q9TXQ8_CABEL	Q9txq8_caenorhabdi	652	37	39.8	414	2	Q9GNUM_PLAFA	Q9gnu8_plasmodium
580	37	39.8	265	2	Q85953_SPHAR	Q85953_sphingomona	653	37	39.8	414	2	Q8IEF6_PLAF7	Q8ief6_plasmodium
581	37	39.8	267	2	Q8BPC4_MOUSE	Q8bpc4_mus musculu	654	37	39.8	415	2	Q5R0W1_IDILO	Q5r0w1_idiomarina
582	37	39.8	271	2	Q9UYN6_PYPAB	Q9uyn6_pyrococcus	655	37	39.8	420	1	YAGA_SCHPO	Q99873_schizosacch
583	37	39.8	273	2	Q62T44_BACLD	Q62t44_bacillus li	656	37	39.8	428	2	Q7QNF7_GIALA	Q7qnf7_giardia lam
584	37	39.8	276	2	Q73Q97_TREDE	Q73q97_treponema d	657	37	39.8	429	2	Q88HM5_PSEPK	Q88hm5_pseudomonas
585	37	39.8	279	2	Q4PDY1_USTMA	Q4pdyl_ustilago ma	658	37	39.8	433	2	Q96LW3_HUMAN	Q96lw3_homo sapien
586	37	39.8	292	2	Q9FH59_ARATH	Q9fh59_arabidopsis	659	37	39.8	434	2	Q7M7M5_WOLSU	Q7m7m5_wolinella s
587	37	39.8	293	2	Q5L517_CHLAB	Q5l517_chlamydophi	660	37	39.8	436	2	Q8MXG9_CABEL	Q8mxg9_caenorhabdi
588	37	39.8	296	2	Q7RG83_PLAYO	Q7rg83_plasmodium	661	37	39.8	439	2	Q54YJ2_DICDI	Q54yj2_dictyosteli
589	37	39.8	296	2	Q5WHZ2_BACSK	Q5whz2_bacillus cl	662	37	39.8	441	2	Q6B0A1_HUMAN	Q6b0a1_homo sapien
590	37	39.8	302	2	Q9CT68_MOUSE	Q9ct68 m mus muscu	663	37	39.8	441	2	Q8C1B9_MOUSE	Q8c1b9_mus musculu
591	37	39.8	303	1	RBM13_BRARE	Q6nyd4_brachydanio	664	37	39.8	445	2	Q9KAM7_BACHD	Q9kam7_bacillus ha
592	37	39.8	303	2	Q65HP1_BACLD	Q65hp1_bacillus li	665	37	39.8	447	1	MPIP3_MOUSE	P48967_mus musculu
593	37	39.8	307	2	Q90ZT5_XENLA	Q90zt5_xenopus lae	666	37	39.8	452	2	Q8NFL8_HUMAN	Q8nfl8_homo sapien
594	37	39.8	307	2	Q6GNB0_XENLA	Q6gnb0_xenopus lae	667	37	39.8	455	2	Q4H3A9_CIOIN	Q4h3a9_ciona intes
595	37	39.8	311	2	Q5TSR8_ANOGA	Q5tsr8_anopheles g	668	37	39.8	457	2	Q821P8_CHLCV	Q821p8_chlamydophi
596	37	39.8	312	2	Q54BF6_DICDI	Q54bf6_dictyosteli	669	37	39.8	458	2	Q5L4Z6_CHLAB	Q5l4z6_chlamydophi
597	37	39.8	313	1	SPY2_CHICK	Q9ptl2_gallus gall	670	37	39.8	460	2	Q8W495_ARATH	Q8w495_arabidopsis
598	37	39.8	314	2	Q5HZA2_RAT	Q5hza2_rattus norv	671	37	39.8	463	1	GSA_CHLRE	Q39566_chlamydomon
599	37	39.8	314	2	Q90ZT6_XENLA	Q90zt6_xenopus lae	672	37	39.8	463	2	Q6C9M8_YARLI	Q6c9m8_yarrowia li
600	37	39.8	314	2	Q5Y173_XENTR	Q5y173_xenopus tro	673	37	39.8	465	2	O81046_ARATH	O81046_arabidopsis
601	37	39.8	314	2	Q5PRF7_XENTR	Q5prf7_xenopus tro	674	37	39.8	466	2	Q6IS76_HUMAN	Q6is76_homo sapien
602	37	39.8	315	1	SPY2_HUMAN	Q43597_homo sapien	675	37	39.8	466	2	Q8S7V6_ORYSA	Q8s7v6_oryza sativ
603	37	39.8	315	1	SPY2_MOUSE	Q9gxv8_mus musculu	676	37	39.8	466	2	Q9AU15_MEDTR	Q9aul5_medicago tr
604	37	39.8	315	2	Q5T6Z7_HUMAN	Q5t6z7_homo sapien	677	37	39.8	467	2	Q84UE1_MEDTR	Q84uel_medicago tr
605	37	39.8	315	2	Q5R959_PONPY	Q5r959_pongo pygma	678	37	39.8	472	2	Q5EPD8_TRIVA	Q5efd8_trichomonas
606	37	39.8	315	2	Q866R9_CERAE	Q866r9_cercopithec	679	37	39.8	474	2	Q8C150_MOUSE	Q8ci50_mus musculu
607	37	39.8	315	2	Q8KAC7_CHLTE	Q8kac7_chlorobium	680	37	39.8	476	2	Q7QDV1_ANOGA	Q7qdv1_anopheles g
608	37	39.8	316	2	Q8T221_METKA	Q8tz21_methanopyru	681	37	39.8	481	2	Q6E279_ARATH	Q6e279_arabidopsis
609	37	39.8	316	2	Q6Z0A5_ORYSA	Q6z0a5_oryza sativ	682	37	39.8	481	2	Q84WS1_ARATH	Q84ws1_arabidopsis
610	37	39.8	324	2	Q831C4_ENTFA	Q831c4_enterococcu	683	37	39.8	483	2	Q8R203_MOUSE	Q8r203_mus musculu
611	37	39.8	330	2	Q4Y677_PLACH	Q4y677_plasmodium	684	37	39.8	487	2	Q7RDX2_PLAYO	Q7rdx2_plasmodium
612	37	39.8	331	2	Q9NDF9_TRIVA	Q9ndf9_trichomonas	685	37	39.8	498	2	Q8H7L9_ORYSA	Q8h7l9_oryza sativ
613	37	39.8	331	2	Q9NDF8_TRIVA	Q9ndf8_trichomonas	686	37	39.8	499	2	Q6NQ51_ARATH	Q6nq51_arabidopsis
614	37	39.8	331	2	Q9NDF6_TRIVA	Q9ndf6_trichomonas	687	37	39.8	501	2	Q9XH61_9ASTR	Q9xh61_matricaria
615	37	39.8	331	2	Q9NDF7_TRIVA	Q9ndf7_trichomonas	688	37	39.8	505	2	O59785_SCHPO	O59785_schizosacch

689	37	39.8	506	2	Q6MM6_BDEBA	Q6mm6 bdellovibri
690	37	39.8	507	2	Q9LMF6_ARATH	Q9lmf6 arabidopsis
691	37	39.8	508	2	Q6E278_ARATH	Q6e278 arabidopsis
692	37	39.8	509	2	Q9XI85_ARATH	Q9xi85 arabidopsis
693	37	39.8	510	1	GAG_SIVNS	P31634 simian immu
694	37	39.8	510	2	Q6Z341_ORYSA	Q6z341 oryza sativ
695	37	39.8	513	2	Q6ZM76_BRARE	Q6zm76 brachydanio
696	37	39.8	514	2	Q7WUM2_ACTMI	Q7wum2 actinoplan
697	37	39.8	526	2	Q02190_CIOIN	Q02190 ciona intes
698	37	39.8	526	2	Q4H359_CIOIN	Q4h359 ciona intes
699	37	39.8	528	2	Q4YTZ2_PLABE	Q4ytz2 plasmodium
700	37	39.8	529	1	NMT_AJECA	P34763 ajellomyces
701	37	39.8	532	2	Q8GVL6_ORYSA	Q8gv16 oryza sativ
702	37	39.8	540	2	Q8K2A4_MOUSE	Q8k2a4 mus musculu
703	37	39.8	540	2	Q9JIB9_MOUSE	Q9jib9 mus musculu
704	37	39.8	542	2	Q8EW43_MYCPE	Q8ew43 mycoplasma
705	37	39.8	546	2	Q5XKG7_HUMAN	Q5xkg7 homo sapien
706	37	39.8	546	2	Q726H6_DESVH	Q726h6 desulfovibr
707	37	39.8	553	2	Q5X117_RAT	Q5xil7 rattus norv
708	37	39.8	561	2	Q86CZ6_CABEL	Q86cz6 caenorhabdi
709	37	39.8	569	2	Q5AJA6_CANAL	Q5aja6 candida alb
710	37	39.8	574	2	Q8IWH5_HUMAN	Q8iwh5 homo sapien
711	37	39.8	583	2	Q8NFL4_HUMAN	Q8nfl4 homo sapien
712	37	39.8	587	2	Q6MF24_PARUM	Q6mf24 parachlamyd
713	37	39.8	592	2	Q02191_CIOIN	Q02191 ciona intes
714	37	39.8	592	2	Q7UV94_RHOBA	Q7uv94 rhodopirell
715	37	39.8	593	2	Q73DI8_BACC1	Q73di8 bacillus ce
716	37	39.8	593	2	Q81V45_BACAN	Q81v45 bacillus an
717	37	39.8	593	2	Q63FZ0_BACCZ	Q63fz0 bacillus ce
718	37	39.8	600	2	Q605T7_METCA	Q605t7 methylococc
719	37	39.8	605	2	Q8BDR3_PAPVR	Q8bdr3 reindeer pa
720	37	39.8	606	1	ALBU1_XENLA	P08759 xenopus lae
721	37	39.8	641	2	Q68E90_AERPUP	Q68e90 aeromonas p
722	37	39.8	647	1	XBP1_YEAST	P40489 saccharomyc
723	37	39.8	651	2	Q9W7F8_BRARE	Q9w7f8 brachydanio
724	37	39.8	651	2	Q5TY81_BRARE	Q5ty81 brachydanio
725	37	39.8	652	2	Q21306_CABEL	Q21306 caenorhabdi
726	37	39.8	658	2	Q55G45_DICDI	Q55g45 dictyosteli
727	37	39.8	663	2	Q8D403_VIEVU	Q8d403 vibrio vuln
728	37	39.8	678	2	Q7QUM5_GIALA	Q7qum5 giardia lam
729	37	39.8	693	2	Q4R6C7_MACFA	Q4r6c7 macaca fasc
730	37	39.8	694	2	Q5P9E1_ANAMM	Q5p9e1 anaplasm m
731	37	39.8	695	2	Q8R428_CAVPO	Q8r428 cavia porce
732	37	39.8	701	2	Q51QK9_MAGGR	Q51qk9 magnaporthe
733	37	39.8	707	2	Q96MP4_HUMAN	Q96mp4 homo sapien
734	37	39.8	718	2	Q6C6P5_YARLI	Q6c6p5 yarrowia li
735	37	39.8	731	2	Q4T149_TETNG	Q4t149 tetraodon n
736	37	39.8	733	2	Q8NC68_HUMAN	Q8nc68 homo sapien
737	37	39.8	733	2	Q9BZQ1_HUMAN	Q9bzb1 homo sapien
738	37	39.8	733	2	Q5R5T0_PONPY	Q5r5t0 pongo pygma
739	37	39.8	749	2	Q6FZ15_BAROU	Q6fz15 bartonella
740	37	39.8	759	2	Q4P4W5_USTMA	Q4p4w5 ustilago ma
741	37	39.8	760	2	Q4MV80_BACCE	Q4mv80 bacillus ce
742	37	39.8	767	2	Q6MYA3_ASPFU	Q6mya3 aspergillus
743	37	39.8	770	2	Q4WS59_ASPFU	Q4ws59 aspergillus
744	37	39.8	774	2	Q7RTG3_PLAYO	Q7rtg3 plasmodium
745	37	39.8	783	2	Q967G0_CRYPV	Q967g0 cryptospori
746	37	39.8	796	2	Q869U8_DICDI	Q869u8 dictyosteli
747	37	39.8	799	2	Q9V964_DROME	Q9v964 drosophila
748	37	39.8	811	2	Q551L2_DICDI	Q551l2 dictyosteli
749	37	39.8	814	2	Q4HND2_CAMUP	Q4hnd2 campylobact
750	37	39.8	816	2	Q5GTP5_WOLTR	Q5gtp5 wolbachia s
751	37	39.8	816	2	Q73G34_WOLPM	Q73g34 wolbachia p
752	37	39.8	818	2	Q622U6_CABER	Q622u6 caenorhabdi
753	37	39.8	826	2	Q86S89_9CILI	Q86s89 polyplastor
754	37	39.8	866	2	Q6FY30_CANGA	Q6fy30 candida gla
755	37	39.8	870	2	Q6UAN0_TETNG	Q6uan0 tetraodon n
756	37	39.8	876	2	Q6NEQ4_CORDI	Q6neq4 corynebacte
757	37	39.8	898	2	Q8H902_ORYSA	Q8h902 oryza sativ
758	37	39.8	898	2	Q6NZG4_MOUSE	Q6nzt4 mus musculu
759	37	39.8	930	2	Q6CHP7_YARLI	Q6chp7 yarrowia li
760	37	39.8	931	2	Q519W1_CABEL	Q5i9w1 caenorhabdi
761	37	39.8	936	2	Q5CVN3_CRYPV	Q5cvn3 cryptospori

762	37	39.8	936	2	Q5CNV6_CRYHO	Q5cnv6 cryptospori
763	37	39.8	948	2	Q61XAL_CABBR	Q61xal caenorhabdi
764	37	39.8	989	1	FRQ_NEUCR	P19970 neurospora
765	37	39.8	993	2	Q81IG5_BACCR	Q81ig5 bacillus ce
766	37	39.8	998	2	Q5A8A5_CANAL	Q5a8a5 candida alb
767	37	39.8	1016	2	Q67U26_ORYSA	Q67u26 oryza sativ
768	37	39.8	1032	2	Q7RR11_PLAYO	Q7rr11 plasmodium
769	37	39.8	1047	2	Q23269_ARATH	Q23269 arabidopsis
770	37	39.8	1058	2	Q9RGV8_SALTI	Q9rgv8 salmonella
771	37	39.8	1062	2	Q8RY24_ARATH	Q8ry24 arabidopsis
772	37	39.8	1064	2	Q9MAU0_ARATH	Q9mau0 arabidopsis
773	37	39.8	1067	2	Q4L744_STAHI	Q4l744 staphylococ
774	37	39.8	1070	2	Q6BVK2_DEBHA	Q6bvk2 debaryomyce
775	37	39.8	1071	2	Q62CH9_BURMA	Q62ch9 burkholderi
776	37	39.8	1105	2	Q7MFH6_VIBVY	Q7mfh6 vibrio vuln
777	37	39.8	1114	2	Q5K7U0_CRYNE	Q5k7u0 cryptococcu
778	37	39.8	1114	2	Q55IA4_CRYNE	Q55ia4 cryptococcu
779	37	39.8	1118	2	Q4P7X3_USTMA	Q4p7x3 ustilago ma
780	37	39.8	1125	2	Q63KK6_BURPS	Q63kk6 burkholderi
781	37	39.8	1126	2	Q5TMM2_ANOGA	Q5tmm2 anopheles g
782	37	39.8	1145	2	Q7PZ65_ANOGA	Q7pz65 anopheles g
783	37	39.8	1164	2	Q4S6H5_TETNG	Q4s6h5 tetraodon n
784	37	39.8	1170	1	ITA2_BOVIN	P53710 bos taurus
785	37	39.8	1214	2	Q4N5A7_THEPA	Q4n5a7 theileria p
786	37	39.8	1230	2	Q7R656_GIALA	Q7r656 giardia lam
787	37	39.8	1256	2	Q4S276_TETNG	Q4s276 tetraodon n
788	37	39.8	1265	2	Q7G647_ORYSA	Q7g647 oryza sativ
789	37	39.8	1265	2	Q8W5E1_ORYSA	Q8w5e1 oryza sativ
790	37	39.8	1323	2	Q7XXG9_ORYSA	Q7xxg9 oryza sativ
791	37	39.8	1390	2	Q51UE4_MAGGR	Q51ue4 magnaporthe
792	37	39.8	1421	2	Q4WID6_ASPFU	Q4wid6 aspergillus
793	37	39.8	1473	2	Q54TV0_DICDI	Q54tv0 dictyosteli
794	37	39.8	1478	2	Q6CUQ0_KJULA	Q6cuq0 kluyveromyc
795	37	39.8	1492	2	Q4SJJ4_TETNG	Q4sjj4 tetraodon n
796	37	39.8	1526	2	Q6CAZ5_YARLI	Q6caz5 yarrowia li
797	37	39.8	1562	2	Q54LE5_DICDI	Q54le5 dictyosteli
798	37	39.8	1568	2	Q7Z8R6_9SACH	Q7z8r6 pichia inos
799	37	39.8	1592	2	Q4PGM7_USTMA	Q4pgm7 ustilago ma
800	37	39.8	1596	2	Q57XS0_9TRYP	Q57xs0 trypanosoma
801	37	39.8	1605	2	Q7XNT6_ORYSA	Q7xnt6 oryza sativ
802	37	39.8	1649	2	Q60K37_CABBR	Q60k37 caenorhabdi
803	37	39.8	1649	2	Q4S0X4_TETNG	Q4s0x4 tetraodon n
804	37	39.8	1703	1	UN13A_HUMAN	Q9upw8 homo sapien
805	37	39.8	1709	2	Q4SDC9_TETNG	Q4sdc9 tetraodon n
806	37	39.8	1712	2	Q4KUS2_MOUSE	Q4kus2 mus musculu
807	37	39.8	1714	2	Q4UJ04_THEAN	Q4uj04 theileria a
808	37	39.8	1722	2	Q8S636_ORYSA	Q8s636 oryza sativ
809	37	39.8	1735	1	UN13A_RAT	Q62768 rattus norv
810	37	39.8	1736	2	Q95PH7_DICDI	Q95ph7 dictyosteli
811	37	39.8	1736	2	Q86AT9_DICDI	Q86at9 dictyosteli
812	37	39.8	1864	2	Q6LFE6_PLAF7	Q6lfe6 plasmodium
813	37	39.8	1902	2	Q4RV37_TETNG	Q4rv37 tetraodon n
814	37	39.8	1931	2	Q8W2U3_ORYSA	Q8w2u3 oryza sativ
815	37	39.8	1933	2	Q7EY18_ORYSA	Q7ey18 oryza sativ
816	37	39.8	1946	2	Q4N6K9_THEPA	Q4n6k9 theileria p
817	37	39.8	1964	2	Q811X6_PLAF7	Q811x6 plasmodium
818	37	39.8	2002	2	Q5CW10_CRYPV	Q5cw10 cryptospori
819	37	39.8	2060	2	Q9P980_PICAN	Q9p980 pichia angu
820	37	39.8	2254	2	Q8ON16_9PICO	Q8on16 ljungan vir
821	37	39.8	2380	2	Q86C65_DICDI	Q86c65 dictyosteli
822	37	39.8	2380	2	Q54V59_DICDI	Q54v59 dictyosteli
823	37	39.8	3374	2	Q8JUZ3_9FLAV	Q8jjz3 montana myo
824	37	39.8	4837	2	Q54MQ5_DICDI	Q54mq5 dictyosteli
825	37	39.8	10061	2	Q813Z1_PLAF7	Q8i3z1 plasmodium
826	37	39.8	12268	2	Q8MQ08_CABEL	Q8mq08 caenorhabdi
827	37	39.8	13100	2	Q09165_CABEL	Q09165 caenorhabdi
828	36.5	39.2	78	2	Q92GA1_RICCN	Q92ga1 rickettsia
829	36.5	39.2	101	2	Q8PTP0_METMA	Q8ptp0 methanosarc
830	36.5	39.2	238	2	Q18773_CABEL	Q18773 caenorhabdi
831	36.5	39.2	274	2	Q6CZS8_ERWCT	Q6czs8 erwinia car
832	36.5	39.2	296	2	Q4R7D4_MACFA	Q4r7d4 macaca fasc
833	36.5	39.2	307	2	Q7RB95_PLAYO	Q7rb95 plasmodium
834	36.5	39.2	308	2	Q9VNL8_DROME	Q9vnl8 drosophila

835	36.5	39.2	377	2	Q64I72_HUMAN	Q64I72 homo sapien	908	36	38.7	213	2	Q57MX7_SALCH	Q57mx7 salmonella
836	36.5	39.2	433	2	Q4U8N5_THEAN	Q4u8n5 theileria a	909	36	38.7	218	1	Y363_RICPR	Q9zdg6 rickettsia
837	36.5	39.2	499	2	Q6TUH4_RAT	Q6tuh4 rattus norv	910	36	38.7	218	2	Q8NJAA_9HYPO	Q8nja4 fusarium au
838	36.5	39.2	608	2	Q86AG5_DICDI	Q86ag5 dictyosteli	911	36	38.7	218	2	Q8NIFI_9HYPO	Q8nif1 fusarium au
839	36.5	39.2	655	2	Q55IA2_DICDI	Q55ia2 dictyosteli	912	36	38.7	218	2	Q7LJG9_9HYPO	Q7ljg9 fusarium me
840	36.5	39.2	657	1	THOC1_HUMAN	Q96fv9 homo sapien	913	36	38.7	218	2	Q4XK65_PLACH	Q4xk65 plasmodium
841	36.5	39.2	657	1	THOC1_MOUSE	Q8r3n6 mus musculu	914	36	38.7	219	2	Q4SJS4_TETNG	Q4sjs4 tetraodon n
842	36.5	39.2	729	2	Q4R966_MACFA	Q4r966 macaca fasc	915	36	38.7	221	2	Q7R4V7_GIALA	Q7r4v7 giardia lam
843	36.5	39.2	803	1	GYRB_SALTY	P0a2i4 salmonella	916	36	38.7	222	2	Q4Q9I2_LEIMA	Q4q9i2 leishmania
844	36.5	39.2	803	1	GYRB_SALTY	P0a2i4 salmonella	917	36	38.7	224	2	Q5T4P8_HUMAN	Q5t4p8 homo sapien
845	36.5	39.2	804	2	Q57I03_SALCH	Q57i03 salmonella	918	36	38.7	226	2	Q5T4P9_HUMAN	Q5t4p9 homo sapien
846	36.5	39.2	804	2	Q5PKU9_SALPA	Q5pku9 salmonella	919	36	38.7	227	2	O80561_ARATH	O80561 arabidopsis
847	36.5	39.2	805	2	Q6CYR7_ERWCT	Q6cyr7 erwinia car	920	36	38.7	227	2	Q8ESPI_OCEIH	Q8esp1 oceanobacil
848	36.5	39.2	813	2	Q9JHD1_MOUSE	Q9jhd1 mus musculu	921	36	38.7	229	2	Q4RRI4_TETNG	Q4rr14 tetraodon n
849	36.5	39.2	813	2	Q640M9_MOUSE	Q640m9 mus musculu	922	36	38.7	230	2	Q4SW99_TETNG	Q4sw99 tetraodon n
850	36.5	39.2	832	1	PCAF_HUMAN	Q92831 homo sapien	923	36	38.7	232	2	Q7Z2T5_HUMAN	Q7z2t5 homo sapien
851	36.5	39.2	1056	2	Q5L7U8_BACFN	Q5l7u8 bacteroides	924	36	38.7	233	2	Q8XMB3_CLOPE	Q8xmb3 clostridium
852	36.5	39.2	1056	2	Q64N19_BACFR	Q64n19 bacteroides	925	36	38.7	234	2	Q6HZG7_BACAN	Q6hgz7 bacillus an
853	36.5	39.2	1526	2	Q8IK87_PLAF7	Q8ik87 plasmodium	926	36	38.7	235	2	Q4Q9H9_LEIMA	Q4q9h9 leishmania
854	36.5	39.2	1756	1	YCF1_PINTH	P4i647 pinus thunb	927	36	38.7	235	2	Q8KYS9_BACAN	Q8kys9 bacillus an
855	36.5	39.2	2269	2	Q54NC6_DICDI	Q54nc6 dictyosteli	928	36	38.7	235	2	Q4MP09_BACCE	Q4mp09 bacillus ce
856	36.5	39.2	3085	2	Q4SYV0_TETNG	Q4syv0 tetraodon n	929	36	38.7	235	2	Q6F006_BACAN	Q6f006 bacillus an
857	36.5	39.2	4196	1	DYHC_SCHPO	O13290 schizosacch	930	36	38.7	236	2	Q9M4D3_MAIZE	Q9m4d3 zea mays (m
858	36	38.7	15	1	ALLS_MANSE	P42559 manduca sex	931	36	38.7	237	2	Q9UL48_HUMAN	Q9ul48 homo sapien
859	36	38.7	47	2	Q5V6I6_HALMA	Q5v6i6 haloarcula	932	36	38.7	239	2	Q7U978_SYNPX	Q7u978 synechococc
860	36	38.7	49	2	Q86YZ5_HUMAN	Q86yz5 homo sapien	933	36	38.7	245	1	DERL1_DROME	Q9vg57 drosophila
861	36	38.7	53	2	Q6KEQ0_SPOFR	Q6keq0 spodoptera	934	36	38.7	245	1	Y9KL_ENCCU	Q8etk1 encephalito
862	36	38.7	61	2	Q95P88_MESMA	Q95p88 mesobuthus	935	36	38.7	246	2	Q71XK4_LISMF	Q71xk4 listeria mo
863	36	38.7	61	2	Q967L8_MESMA	Q967l8 mesobuthus	936	36	38.7	246	2	Q8Y5A6_LISMO	Q8y5a6 listeria mo
864	36	38.7	63	2	Q6JSD9_HUMAN	Q6jسد9 homo sapien	937	36	38.7	248	2	Q81R91_BACAN	Q81r91 bacillus an
865	36	38.7	68	2	Q9JW83_NEIMA	Q9jw83 neisseria m	938	36	38.7	253	2	Q4MRT9_BACCE	Q4mrt9 bacillus ce
866	36	38.7	70	2	P79261_MACMU	P79261 macaca mula	939	36	38.7	255	2	Q8EKEA_SHEON	Q8eke4 shewanella
867	36	38.7	72	2	Q8TP30_METAC	Q8tp30 methanosarc	940	36	38.7	258	1	Y706_ENCCU	Q8ev55 encephalito
868	36	38.7	94	2	Q56WL3_ARATH	Q56wl3 arabidopsis	941	36	38.7	258	2	Q64EC4_9ARCH	Q64ec4 uncultured
869	36	38.7	103	2	Q8VWY0_CUCSA	Q8vwy0 cucumis sat	942	36	38.7	262	2	Q6WZA5_STRVI	Q6wza5 streptomyce
870	36	38.7	105	2	Q5WMV0_ORYSA	Q5wmv0 oryza sativ	943	36	38.7	267	2	Q63C13_BACCZ	Q63c13 bacillus ce
871	36	38.7	108	1	Y3403_METJA	Q60302 methanococc	944	36	38.7	268	2	Q9Y7L2_SCHPO	Q9y7l2 schizosacch
872	36	38.7	111	2	Q8ZUX1_PYRAB	Q8zux1 pyrobaculum	945	36	38.7	271	1	CBIO_SALTY	Q8z5n5 salmonella
873	36	38.7	121	2	Q95NV8_DROME	Q95nv8 drosophila	946	36	38.7	271	1	CBIO_SALTY	Q05596 salmonella
874	36	38.7	122	2	Q9VKK5_DROME	Q9vkk5 drosophila	947	36	38.7	271	2	Q5PDU4_SALPA	Q5pdu4 salmonella
875	36	38.7	122	2	Q8QZZ4_MOUSE	Q8qzz4 mus musculu	948	36	38.7	272	2	Q8EJU1_SHEON	Q8eju1 shewanella
876	36	38.7	123	2	Q4Z715_PLABE	Q4z715 plasmodium	949	36	38.7	273	1	GAH6_HUMAN	Q8n8a4 homo sapien
877	36	38.7	124	2	Q4PLI0_SAMCR	Q4pli0 samia cynth	950	36	38.7	281	1	TNFI_HUMAN	P50591 homo sapien
878	36	38.7	125	1	ALLS_SPOFR	Q868f8 spodoptera	951	36	38.7	281	2	Q6IBA9_HUMAN	Q6iba9 homo sapien
879	36	38.7	125	2	Q26115_PSEUI	Q26115 pseudaletia	952	36	38.7	282	1	LRPR_STRBQ	Q54087 streptococc
880	36	38.7	150	2	Q8Q5A8_SIVCZ	Q8q5a8 chimpanzee	953	36	38.7	282	2	Q7N8Q7_PHOLL	Q7n8q7 photorhabdu
881	36	38.7	151	2	Q6ZSE1_HUMAN	Q6zse1 homo sapien	954	36	38.7	282	2	Q8NZA7_STRP8	Q8nza7 streptococc
882	36	38.7	156	2	Q8EP94_OCEIH	Q8ep94 oceanobacil	955	36	38.7	282	2	Q8KSR9_STRP3	Q8ksr9 streptococc
883	36	38.7	157	2	Q4XII0_PLACH	Q4xii0 plasmodium	956	36	38.7	289	2	Q4VSR6_PIG	Q4vsr6 sus scrofa
884	36	38.7	162	2	Q8RDM2_FUSNN	Q8rdm2 fusobacteri	957	36	38.7	289	2	P77507_ECOLI	P77507 escherichia
885	36	38.7	166	2	Q9X2X7_BACAN	Q9x2x7 bacillus an	958	36	38.7	296	2	Q877Z1_STRP3	Q877z1 streptococc
886	36	38.7	167	2	P89672_9CALI	P89672 san miguel	959	36	38.7	296	2	Q5X9T7_STRP6	Q5x9t7 streptococc
887	36	38.7	168	2	Q8YSE6_ANASP	Q8yse6 anabaena sp	960	36	38.7	297	1	YACD_BACSU	P37566 bacillus su
888	36	38.7	171	2	Q5PR44_BRARE	Q5pr44 brachydanio	961	36	38.7	298	2	Q9M4G3_MAIZE	Q9m4g3 zea mays (m
889	36	38.7	174	2	Q8LE65_ARATH	Q8le65 arabidopsis	962	36	38.7	300	2	Q5U675_HUMAN	Q5u675 homo sapien
890	36	38.7	176	2	Q9LZ14_ARATH	Q9l214 arabidopsis	963	36	38.7	300	2	Q5FL97_LACAC	Q5fl97 lactobacill
891	36	38.7	181	2	Q68236_BORBU	Q68236 borrelia bu	964	36	38.7	302	1	ICOSL_HUMAN	O75144 homo sapien
892	36	38.7	183	2	Q8SVT1_ENCCU	Q8svt1 encephalito	965	36	38.7	304	2	Q8XW55_9RHOB	Q8xw55 ruegeria sp
893	36	38.7	185	2	Q6M181_METWP	Q6m181 methanococc	966	36	38.7	309	2	Q899L3_CLOTE	Q899l3 clostridium
894	36	38.7	186	2	Q8QNF4_9PHYC	Q8qnf4 ectocarpus	967	36	38.7	309	2	Q7MP36_VIBVY	Q7mp36 vibrio vuln
895	36	38.7	187	2	Q69144_CLOPA	Q69144 clostridium	968	36	38.7	314	2	Q9BRF8_HUMAN	Q9brf8 homo sapien
896	36	38.7	189	2	Q8TP31_METAC	Q8tp31 methanosarc	969	36	38.7	314	2	Q9H9M9_HUMAN	Q9h9m9 homo sapien
897	36	38.7	194	2	Q5VTP5_BRARE	Q5vtp5 brachydanio	970	36	38.7	314	2	Q9NUT6_HUMAN	Q9nut6 homo sapien
898	36	38.7	195	2	Q79EJ3_ECOLI	Q79ej3 escherichia	971	36	38.7	314	2	Q5RCR9_PONPY	Q5rcr9 pongo pygma
899	36	38.7	196	1	ENGB_STAAR	Q69932 staphylococ	972	36	38.7	314	2	Q6LGX6_PHOPR	Q6lgx6 photobacter
900	36	38.7	203	1	CTP2_PANTR	Q6r2r2 pan troglod	973	36	38.7	315	2	Q5R6B0_PONPY	Q5r6b0 pongo pygma
901	36	38.7	204	2	Q5RGN5_BRARE	Q5rgn5 brachydanio	974	36	38.7	317	1	RPOA_MESFL	Q6fiw7 mesoplasma
902	36	38.7	207	2	Q4HF63_CAMCO	Q4h6f3 campylobact	975	36	38.7	319	2	Q5TU72_ANOGA	Q5tu72 anopheles g
903	36	38.7	208	2	Q6LYC5_METMP	Q6lyc5 methanococc	976	36	38.7	321	2	Q70KC5_EUCGU	Q70kc5 eucalyptus
904	36	38.7	212	2	Q5WXI2_LEGPL	Q5wxi2 legionella	977	36	38.7	327	2	Q5F966_NEIG1	Q5f966 neisseria g
905	36	38.7	212	2	Q5X658_LEGPA	Q5x658 legionella	978	36	38.7	327	2	Q4PZF0_NEIGO	Q4pzf0 neisseria g
906	36	38.7	212	2	Q5ZWH4_LEGPH	Q5zwh4 legionella	979	36	38.7	327	2	Q9JU60_NEIMA	Q9ju60 neisseria m
907	36	38.7	212	2	Q6MEJ5_PAROW	Q6mej5 parachlamyid	980	36	38.7	327	2	Q9JZ63_NEIMB	Q9jz63 neisseria m

981	36	38.7	331	2	Q68X12_RICTY	Q68x12 rickettsia	1054	36	38.7	470	2	Q68EK2_BRARE	Q68ek2 brachydanio
982	36	38.7	332	1	LDHA_RAT	P04642 rattus norv	1055	36	38.7	478	2	Q9ESE0_RAT	Q9ese0 rattus norv
983	36	38.7	332	2	Q7QPE7_GIALA	Q7qpe7 giardia lam	1056	36	38.7	483	1	UXAB_YERPE	Q8zic5 yersinia pe
984	36	38.7	334	2	Q6BHW7_DEBHA	Q6bhw7 debaryomyce	1057	36	38.7	483	2	Q665N9_YERPS	Q665n9 yersinia ps
985	36	38.7	335	2	Q8BPK6_OCEIH	Q8epk6 oceanobacil	1058	36	38.7	486	2	Q6BRV8_DEBHA	Q6bry8 debaryomyce
986	36	38.7	338	2	Q9P5Y4_NEUCR	Q9p5y4 neurospora	1059	36	38.7	493	2	Q6CGB7_YARLI	Q6cgb7 yarrowia li
987	36	38.7	341	2	Q5R918_PONPY	Q5r918 pongo pygma	1060	36	38.7	500	2	Q52V15_9VIRU	Q52v15 mint virus
988	36	38.7	343	2	Q6BQF7_DEBHA	Q6bqf7 debaryomyce	1061	36	38.7	501	2	Q8I5I6_PLAF7	Q8i5i6 plasmodium
989	36	38.7	349	2	Q8I4G2_CABEL	Q8i4g2 caenorhabdi	1062	36	38.7	506	1	GAG_SIWM1	P05894 simian immu
990	36	38.7	353	2	Q7VLV5_HABDU	Q7vlv5 haemophilus	1063	36	38.7	506	2	Q8H0D7_9GENT	Q8h0d7 ophiiorhiza
991	36	38.7	354	2	Q8CAZ8_MOUSE	Q8caz8 mus musculu	1064	36	38.7	509	2	Q8T3H5_DROME	Q8t3h5 drosophila
992	36	38.7	356	2	Q4UM00_RICPE	Q4um00 rickettsia	1065	36	38.7	509	2	Q9VVQ9_DROME	Q9vvq9 drosophila
993	36	38.7	356	2	Q6G5K5_BARHE	Q6g5k5 bartonella	1066	36	38.7	510	2	Q5EB91_RAT	Q5eb91 rattus norv
994	36	38.7	358	2	Q4Q0M2_LEIMA	Q4q0m2 leishmania	1067	36	38.7	514	2	Q5WQ06_9ENTR	Q5wq06 buchnera ap
995	36	38.7	359	1	PEX12_CRILLO	Q9et67 cricetulus	1068	36	38.7	521	2	Q7RZ86_NEUCR	Q7rz86 neurospora
996	36	38.7	359	1	PEX12_HUMAN	O00623 homo sapien	1069	36	38.7	531	2	Q4Q076_LEIMA	Q4q076 leishmania
997	36	38.7	359	1	PEX12_MOUSE	Q8vc48 mus musculu	1070	36	38.7	537	2	Q4YZ44_PLABE	Q4yz44 plasmodium
998	36	38.7	359	2	Q5SWQ8_MOUSE	Q5swq8 mus musculu	1071	36	38.7	541	2	Q661T7_BORGA	Q661t7 borrelia ga
999	36	38.7	361	2	Q7RU38_NEUCR	Q7ru38 neurospora	1072	36	38.7	542	2	Q5ISAS_9PRIM	Q5isa5 saimiri bol
1000	36	38.7	361	2	Q54RJ5_DICDI	Q54rj5 dictyosteli	1073	36	38.7	543	1	YDE3_SCHPO	Q10437 schizosacch
1001	36	38.7	363	2	Q93778_CABEL	Q93778 caenorhabdi	1074	36	38.7	544	2	Q6ZNA6_HUMAN	Q6zna6 homo sapien
1002	36	38.7	366	2	Q7PXM2_ANOGA	Q7pxm2 anopheles g	1075	36	38.7	545	2	Q5Z0Y3_NOCFA	Q5z0y3 nocardia fa
1003	36	38.7	368	2	Q60MW8_CABBR	Q60mw8 caenorhabdi	1076	36	38.7	550	2	Q8NXX0_YARLI	Q8nxx0 yarrowia li
1004	36	38.7	370	2	Q6NGX8_CORDI	Q6ngx8 corynebacte	1077	36	38.7	550	2	Q9VAJ7_DROME	Q9vaj7 drosophila
1005	36	38.7	373	2	Q4R318_MACFA	Q4r318 macaca fasc	1078	36	38.7	552	2	Q51H50_ENTHI	Q51h50 entamoeba h
1006	36	38.7	383	2	Q7MPQ7_VIBVY	Q7mpq7 vibrio vuln	1079	36	38.7	555	2	Q8IIC9_PLAF7	Q8iic9 plasmodium
1007	36	38.7	384	2	Q7RGG2_PLAYO	Q7rgg2 plasmodium	1080	36	38.7	555	2	Q6SZP8_PHYIN	Q6szp8 phytophthor
1008	36	38.7	387	1	TOM40_YEAST	P23644 saccharomyc	1081	36	38.7	556	2	Q91GC6_NPVEP	Q91gc6 epiphyas po
1009	36	38.7	387	2	Q6B1Q9_YEAST	Q6blq9 saccharomyc	1082	36	38.7	558	1	GLTL1_MOUSE	Q9jj61 m putative
1010	36	38.7	388	1	5HT4R_CAVPO	Q70528 cavia porce	1083	36	38.7	558	1	SYQ_BRAJA	Q89kr6 bradyrhizob
1011	36	38.7	389	2	Q9Z0F6_MOUSE	Q9z0f6 mus musculu	1084	36	38.7	558	2	Q60GT0_MOUSE	Q60gt0 mus musculu
1012	36	38.7	390	2	Q4K2Q5_STRPN	Q4k2q5 streptococc	1085	36	38.7	560	2	Q6N5R6_RHOPA	Q6n5r6 rhodopseudo
1013	36	38.7	390	2	Q5LHH7_BACFN	Q5lhh7 bacteroides	1086	36	38.7	562	1	SYQ_NEIMA	P57000 neisseria m
1014	36	38.7	390	2	Q64YF1_BACFR	Q64yf1 bacteroides	1087	36	38.7	562	1	SYQ_NEIMB	P56927 neisseria m
1015	36	38.7	391	1	OMP41_FORGI	Q983r9 porphyromon	1088	36	38.7	564	2	Q5E0C5_VIBF1	Q5e0c5 vibrio fisc
1016	36	38.7	393	2	Q60FT2_PORGI	Q60ft2 porphyromon	1089	36	38.7	564	2	Q7TP14_RAT	Q7tp14 rattus norv
1017	36	38.7	393	2	Q5CB12_9THEM	Q5cb12 thermotoga	1090	36	38.7	570	2	Q5CPZ1_CRYPV	Q5cpz1 cryptospori
1018	36	38.7	399	2	Q6BRL7_DEBHA	Q6brl7 debaryomyce	1091	36	38.7	570	2	Q5CL15_CRYHO	Q5cl15 cryptospori
1019	36	38.7	401	2	Q93408_XENLA	Q93408 xenopus lae	1092	36	38.7	573	2	Q5F7G0_NEIG1	Q5f7g0 neisseria g
1020	36	38.7	401	2	Q9YHW3_XENLA	Q9yhw3 xenopus lae	1093	36	38.7	579	1	Y751_OCEIH	Q8es91 oceanobacil
1021	36	38.7	403	1	YD87_SCHPO	Q10412 schizosacch	1094	36	38.7	579	2	Q9HRH7_HALSA	Q9hrh7 halobacteri
1022	36	38.7	408	2	Q4IC12_GIBZE	Q4ic12 gibberella	1095	36	38.7	579	2	Q4XVH9_PLACH	Q4xvh9 plasmodium
1023	36	38.7	408	2	Q5BJM5_RAT	Q5bjm5 rattus norv	1096	36	38.7	581	2	Q74485_SCHPO	O74485 schizosacch
1024	36	38.7	408	2	Q9JIY0_MOUSE	Q9jiy0 mus musculu	1097	36	38.7	584	2	Q583W8_9TRYP	Q583w8 trypanosoma
1025	36	38.7	408	2	Q9CXH2_MOUSE	Q9cxh2 mus musculu	1098	36	38.7	586	2	Q8ELJ0_OCEIH	Q8elj0 oceanobacil
1026	36	38.7	409	2	Q53GL0_HUMAN	Q53gl0 homo sapien	1099	36	38.7	586	2	Q4SDQ7_TETNG	Q4sdq7 tetraodon n
1027	36	38.7	409	2	Q9NRV3_HUMAN	Q9nrv3 homo sapien	1100	36	38.7	594	1	DCE1_FELCA	P14748 felis silve
1028	36	38.7	410	2	Q6Q2D6_BOMMO	Q6q2d6 bombyx mori	1101	36	38.7	594	1	DCE1_HUMAN	Q99259 homo sapien
1029	36	38.7	411	2	Q6FJJ4_CANGA	Q6fjj4 candida gla	1102	36	38.7	594	1	DCE1_PANTR	Q5ie68 pan troglod
1030	36	38.7	416	2	Q8SY00_DROME	Q8sy00 drosophila	1103	36	38.7	594	1	DCE1_PIG	P48319 sus scrofa
1031	36	38.7	416	2	Q4V8D6_RAT	Q4v8d6 rattus norv	1104	36	38.7	594	2	Q53TQ7_HUMAN	Q53tq7 homo sapien
1032	36	38.7	419	2	Q5V694_HALMA	Q5v694 haloarcula	1105	36	38.7	594	2	Q8IVA8_HUMAN	Q8iva8 homo sapien
1033	36	38.7	419	2	Q9H2Y3_HUMAN	Q9h2y3 homo sapien	1106	36	38.7	597	2	O16382_CABEL	O16382 caenorhabdi
1034	36	38.7	419	2	Q9HAW0_HUMAN	Q9haw0 homo sapien	1107	36	38.7	597	2	Q6DEY9_XENTR	Q6dey9 xenopus tro
1035	36	38.7	419	2	Q9NUY6_HUMAN	Q9nuy6 homo sapien	1108	36	38.7	598	2	Q6DCZ1_XENLA	Q6dcz1 xenopus lae
1036	36	38.7	420	2	Q9CZF0_MOUSE	Q9czf0 m mus muscu	1109	36	38.7	602	2	Q6CLX0_KIULA	Q6clx0 kluyveromyc
1037	36	38.7	425	2	Q4Q0L6_LEIMA	Q4q0l6 leishmania	1110	36	38.7	602	2	Q9N403_CABEL	Q9n403 caenorhabdi
1038	36	38.7	431	2	Q56XT4_ARATH	Q56xt4 arabidopsis	1111	36	38.7	605	2	Q5BE88_EMENI	Q5be88 aspergillus
1039	36	38.7	431	2	Q5LID0_BACFN	Q5lid0 bacteroides	1112	36	38.7	614	1	FBF1_CABEL	Q9n5m6 caenorhabdi
1040	36	38.7	431	2	Q64ZF0_BACFR	Q64zf0 bacteroides	1113	36	38.7	622	1	MUTL_CLOAB	Q9n120 clostridium
1041	36	38.7	431	2	Q87FT3_VIBPA	Q87ft3 vibrio para	1114	36	38.7	624	1	GLSA2_BRAJA	Q89kv2 bradyrhizob
1042	36	38.7	435	2	Q81Z51_HUMAN	Q81z51 homo sapien	1115	36	38.7	630	2	Q6BK57_DEBHA	Q6bk57 debaryomyce
1043	36	38.7	440	1	HIP4_ECOLI	P23874 escherichia	1116	36	38.7	630	2	Q6KIK0_MYCNO	Q6kik0 mycoplasma
1044	36	38.7	447	2	Q4HI19_CAMCO	Q4hi19 campylobact	1117	36	38.7	633	1	GIDA2_FUSNM	Q8ri88 fusobacteri
1045	36	38.7	448	2	Q5XGM0_XENLA	Q5xgm0 xenopus lae	1118	36	38.7	633	2	Q5E0B6_VIBF1	Q5e0b6 vibrio fisc
1046	36	38.7	449	2	O22820_ARATH	O22820 arabidopsis	1119	36	38.7	640	2	Q7RW79_NEUCR	Q7rw79 neurospora
1047	36	38.7	452	2	Q4JLP9_LACRE	Q4jlp9 lactobacill	1120	36	38.7	640	2	Q8SRH2_ENCCU	Q8srh2 encephalito
1048	36	38.7	455	2	Q7T3E7_BRARE	Q7t3e7 brachydanio	1121	36	38.7	643	2	Q8CTZ1_STAEP	Q8ctz1 staphylococ
1049	36	38.7	458	2	Q4Z5A0_PLABE	Q4z5a0 plasmodium	1122	36	38.7	643	2	Q9ERV6_MOUSE	Q9erv6 mus musculu
1050	36	38.7	461	2	Q86KZ2_DICDI	Q86kz2 dictyosteli	1123	36	38.7	644	2	Q9CGW3_LACLA	Q9cgw3 lactococcus
1051	36	38.7	463	2	Q4UER5_THEAN	Q4uer5 theileria a	1124	36	38.7	646	1	SRP72_YEAST	P38688 saccharomyc
1052	36	38.7	466	2	Q84UE2_MEDTR	Q84ue2 medicago tr	1125	36	38.7	649	2	Q4HA25_9DEIO	Q4ha25 deinococcus
1053	36	38.7	470	2	Q9LUI1_ARATH	Q9lui1 arabidopsis	1126	36	38.7	652	2	Q6AI46_HUMAN	Q6ai46 homo sapien

1127	36	38.7	654	2	Q9RYI7_DEIRA	Q9ryi7 deinococcus
1128	36	38.7	655	2	Q692R3_MOUSE	Q69zr3 mus musculus
1129	36	38.7	655	2	Q9WVF5_MOUSE	Q9wvf5 m epidermal
1130	36	38.7	656	2	Q5FC33_CABEL	Q5fc33 caenorhabdi
1131	36	38.7	657	2	Q8C191_MOUSE	Q8c191 mus musculus
1132	36	38.7	662	2	Q9QW36_COLLI	Q9Qw36 columba liv
1133	36	38.7	662	2	Q9YGX8_CHICK	Q9ygx8 gallus gall
1134	36	38.7	670	2	Q9LW73_ARATH	Q9lW73 arabidopsis
1135	36	38.7	670	2	Q896X0_CLOTE	Q896x0 clostridium
1136	36	38.7	671	2	Q6GW04_DICDI	Q6gw04 dictyosteli
1137	36	38.7	671	2	Q5RBH7_PONPY	Q5rbh7 pongo pygma
1138	36	38.7	676	1	RPOC1_HUPLU	Q5scx9 huperzia lu
1139	36	38.7	684	2	Q86D2I_CAEEL	Q86d2i caenorhabdi
1140	36	38.7	694	2	Q7SEV8_NEUCR	Q7sev8 neurospora
1141	36	38.7	695	2	Q9UT10_SCHPO	Q9ut10 schizosacch
1142	36	38.7	703	2	Q6DI76_MOUSE	Q6di76 mus musculus
1143	36	38.7	704	2	Q61ZE4_CAEBR	Q61ze4 caenorhabdi
1144	36	38.7	705	2	Q4W276_9CALI	Q4w276 rabbit vesi
1145	36	38.7	714	2	Q7UPF6_RHOBA	Q7upf6 rhodopirell
1146	36	38.7	719	2	Q4IMH1_GIBZE	Q4imh1 gibberella
1147	36	38.7	725	1	SYTC_CAEEL	P52709 caenorhabdi
1148	36	38.7	729	2	Q94400_ORYSA	Q94400 caenorhabdi
1149	36	38.7	735	2	Q6H5M0_MOUSE	Q6h5m0 oryza sativ
1150	36	38.7	741	1	RN5A_HUMAN	Q05823 homo sapien
1151	36	38.7	741	2	Q5W0L2_HUMAN	Q5w0l2 homo sapien
1152	36	38.7	741	2	Q5RAY3_PONPY	Q5ray3 pongo pygma
1153	36	38.7	752	2	Q9PKZ9_ARATH	Q9fkz9 arabidopsis
1154	36	38.7	770	2	Q96H55_HUMAN	Q96h55 homo sapien
1155	36	38.7	770	2	Q64QD3_BACFR	Q64qd3 bacteroides
1156	36	38.7	783	2	Q86ZJ7_PODAN	Q86zj7 podospora a
1157	36	38.7	783	2	Q9WJ22_9VIRU	Q9wj22 ophiostoma
1158	36	38.7	784	2	Q5NCP0_MOUSE	Q5ncp0 mus musculus
1159	36	38.7	787	2	Q4YXU8_PLABE	Q4yxu8 plasmodium
1160	36	38.7	788	2	Q7S4U7_NEUCR	Q7s4u7 neurospora
1161	36	38.7	792	2	Q74XG5_YERPE	Q74xg5 yersinia pe
1162	36	38.7	792	2	Q66FH7_YERPE	Q66fh7 yersinia ps
1163	36	38.7	792	2	Q8ZJ27_YERPE	Q8zj27 yersinia pe
1164	36	38.7	797	2	Q8IKP0_PLAF7	Q8ikp0 plasmodium
1165	36	38.7	801	2	Q51X13_MAGGR	Q51xi3 magnaporthe
1166	36	38.7	817	2	Q21854_CAEEL	Q21854 caenorhabdi
1167	36	38.7	818	2	Q5WA51_CHICK	Q5wa51 gallus gall
1168	36	38.7	818	2	Q5ZIH8_CHICK	Q5zlh8 gallus gall
1169	36	38.7	819	2	Q6YR62_ONYPE	Q6yr62 onion yello
1170	36	38.7	825	2	Q7SHP1_NEUCR	Q7shp1 neurospora
1171	36	38.7	833	2	Q93HU8_ENTPA	Q93hu8 enterococcu
1172	36	38.7	836	2	Q6BL30_DEBHA	Q6bl30 debaryomyce
1173	36	38.7	846	2	Q6BUQ8_DEBHA	Q6buq8 debaryomyce
1174	36	38.7	852	1	SSY1_YEAST	Q03770 saccharomyc
1175	36	38.7	856	2	Q9CZ62_MOUSE	Q9cz62 m mus muscu
1176	36	38.7	860	2	Q8DIX1_SYNEL	Q8dix1 synechococc
1177	36	38.7	861	2	Q53SM6_HUMAN	Q53sm6 homo sapien
1178	36	38.7	861	2	Q55CT4_DICDI	Q55ct4 dictyosteli
1179	36	38.7	865	1	GLND_BORBR	Q7wj96 bordetella
1180	36	38.7	865	1	GLND_BORPA	Q7wa62 bordetella
1181	36	38.7	865	1	GLND_BORPE	Q7vyd2 bordetella
1182	36	38.7	870	1	EPAS1_HUMAN	Q99814 homo sapien
1183	36	38.7	870	2	Q9XTA4_BOVIN	Q9xta4 bos taurus
1184	36	38.7	871	2	Q5H726_FUGRU	Q5h726 fugu rubrip
1185	36	38.7	884	2	Q5OUK8_ENTHI	Q5ouk8 entamoeba h
1186	36	38.7	886	2	Q8IEN6_PLAF7	Q8ien6 plasmodium
1187	36	38.7	889	2	Q4P917_USTMA	Q4p917 ustilago ma
1188	36	38.7	891	2	Q75DC4_ASHGO	Q75dc4 ashbya goss
1189	36	38.7	892	2	Q8NQ92_CORGL	Q8nq92 corynebacte
1190	36	38.7	894	2	Q6MV75_NEUCR	Q6mv75 neurospora
1191	36	38.7	904	2	Q9W6G1_PROAT	Q9w6g1 protopterus
1192	36	38.7	911	2	Q7Z1H8_APLCA	Q7zlh8 aplysia cal
1193	36	38.7	912	2	Q9SUE7_ARATH	Q9sue7 arabidopsis
1194	36	38.7	916	2	Q5F807_NEIG1	Q5f807 neisseria g
1195	36	38.7	920	2	Q7S094_NEUCR	Q7s094 neurospora
1196	36	38.7	926	2	Q4UEX6_THEAN	Q4uex6 theileria a
1197	36	38.7	928	1	ATC1_YARLI	Q43l08 yarrowia li
1198	36	38.7	967	2	Q9X085_THEMEA	Q9x085 thermotoga
1199	36	38.7	978	2	Q874G6_KLUJLA	Q874g6 kluyveromyc

1200	36	38.7	980	2	Q5VPE8_ORYSA	Q5vpe8 oryza sativ
1201	36	38.7	983	2	Q874C2_TRAVE	Q874c2 trametes ve
1202	36	38.7	1004	2	Q6H5Y7_ORYSA	Q6h5y7 oryza sativ
1203	36	38.7	1012	2	Q96757_DROME	Q96757 drosophila
1204	36	38.7	1012	2	Q9VFH9_DROME	Q9vfh9 drosophila
1205	36	38.7	1014	2	Q4WQD5_ASPTU	Q4wqd5 aspergillus
1206	36	38.7	1016	2	Q6TFU0_ERWAM	Q6tfu0 erwinia amy
1207	36	38.7	1016	2	Q8GFR7_CITPR	Q8gfr7 citrobacter
1208	36	38.7	1017	2	Q9LKV5_ARATH	Q9lkv5 arabidopsis
1209	36	38.7	1027	2	Q6CL64_KLUJLA	Q6cl64 kluyveromyc
1210	36	38.7	1051	2	Q6FR16_CANGA	Q6fr16 candida gla
1211	36	38.7	1053	2	Q7Q3D3_ANOGA	Q7q3d3 anopheles g
1212	36	38.7	1055	2	Q5K722_CRYNE	Q5k722 cryptococcu
1213	36	38.7	1055	2	Q55HI4_CRYNE	Q55hi4 cryptococcu
1214	36	38.7	1060	2	Q6CPI0_KLUJLA	Q6cpi0 kluyveromyc
1215	36	38.7	1067	2	Q874G3_SACEX	Q874g3 saccharomyc
1216	36	38.7	1070	2	Q874G2_SACEX	Q874g2 saccharomyc
1217	36	38.7	1072	2	Q71Z25_LISMF	Q71z25 listeria mo
1218	36	38.7	1072	2	Q8Y6P0_LISMO	Q8y6p0 listeria mo
1219	36	38.7	1072	2	Q92B65_LISIN	Q92b65 listeria in
1220	36	38.7	1078	2	Q5CI20_CRYHO	Q5ci20 cryptospori
1221	36	38.7	1093	2	Q54GV1_DICDI	Q54gv1 dictyosteli
1222	36	38.7	1098	2	Q6FKL7_CANGA	Q6fkl7 candida gla
1223	36	38.7	1099	2	Q54KF6_DICDI	Q54kf6 dictyosteli
1224	36	38.7	1112	1	SENP6_HUMAN	Q9gzr1 homo sapien
1225	36	38.7	1141	2	Q4I3Q3_GIBZE	Q4i3q3 gibberella
1226	36	38.7	1146	2	Q9VF10_DROME	Q9vfi0 drosophila
1227	36	38.7	1147	2	Q96758_DROME	Q96758 drosophila
1228	36	38.7	1160	2	Q7QB81_ANOGA	Q7qb81 anopheles g
1229	36	38.7	1173	2	Q868R0_ANOGA	Q868r0 anopheles g
1230	36	38.7	1181	1	CR1AE_BACTL	Q03748 bacillus th
1231	36	38.7	1188	2	Q9VUL6_DROME	Q9vul6 drosophila
1232	36	38.7	1188	2	Q8EJ91_SHEON	Q8ej91 shewanella
1233	36	38.7	1204	2	Q9S9K0_ARATH	Q9s9k0 arabidopsis
1234	36	38.7	1209	2	Q9QX70_RAT	Q9qx70 rattus norv
1235	36	38.7	1210	1	EGFR_MOUSE	Q01279 mus musculu
1236	36	38.7	1210	2	Q9EP98_MOUSE	Q9ep98 mus musculu
1237	36	38.7	1210	2	Q5SVE8_MOUSE	Q5sve8 mus musculu
1238	36	38.7	1219	2	Q9VYT4_DROME	Q9vyt4 drosophila
1239	36	38.7	1231	2	Q7SBC4_NEUCR	Q7sbc4 neurospora
1240	36	38.7	1249	2	Q4MZQ0_THEPA	Q4mzq0 theileria p
1241	36	38.7	1249	2	Q6IDF6_DROME	Q6idf6 drosophila
1242	36	38.7	1257	2	Q6BM72_DEBHA	Q6bm72 debaryomyce
1243	36	38.7	1303	2	Q4SD07_TETNG	Q4sd07 tetraodon n
1244	36	38.7	1314	2	Q6C4H8_YARLI	Q6c4h8 yarrowia li
1245	36	38.7	1318	2	Q5F7J4_NEIG1	Q5f7j4 neisseria g
1246	36	38.7	1320	1	PUR4_NEIMA	Q9jwc5 neisseria m
1247	36	38.7	1345	2	Q6ZS01_HUMAN	Q6zs01 homo sapien
1248	36	38.7	1357	2	Q4ITJ2_AZOV1	Q4itj2 azotobacter
1249	36	38.7	1378	2	Q5KIC0_CRYNE	Q5kic0 cryptococcu
1250	36	38.7	1409	2	Q5U22_CRYNE	Q5u22 cryptococcu
1251	36	38.7	1451	2	Q67WN2_ORYSA	Q67wn2 oryza sativ
1252	36	38.7	1476	2	Q8WRF4_WONBE	Q8wrf4 monosiga br
1253	36	38.7	1500	2	Q6ALB9_DESPS	Q6alb9 desulfotale
1254	36	38.7	1536	2	Q86AL7_DICDI	Q86al7 dictyosteli
1255	36	38.7	1581	2	Q5RES4_PONPY	Q5res4 pongo pygma
1256	36	38.7	1624	2	Q7Z3L7_HUMAN	Q7z3l7 homo sapien
1257	36	38.7	1645	2	Q8YYW3_ANASP	Q8yyw3 anabaena sp
1258	36	38.7	1688	2	Q4WQ98_ASPTU	Q4wq98 aspergillus
1259	36	38.7	1704	1	VILD_DICDI	Q8wq85 dictyosteli
1260	36	38.7	1704	2	Q54IR2_DICDI	Q54ir2 dictyosteli
1261	36	38.7	1722	2	Q19350_CABEL	Q19350 caenorhabdi
1262	36	38.7	1746	2	Q54T88_DICDI	Q54t88 dictyosteli
1263	36	38.7	1755	2	Q6CPF6_KLUJLA	Q6cpf6 kluyveromyc
1264	36	38.7	1833	2	Q5BF38_EMENI	Q5bf38 aspergillus
1265	36	38.7	1861	2	Q4WRV0_ASPTU	Q4wrvo aspergillus
1266	36	38.7	1969	1	ZN292_HUMAN	Q60281 homo sapien
1267	36	38.7	2152	2	Q80DP6_9VIRU	Q80dp6 andes virus
1268	36	38.7	2153	2	Q89709_9VIRU	Q89709 sin nombre
1269	36	38.7	2153	2	Q916F6_9VIRU	Q916f6 convict cre
1270	36	38.7	2153	2	Q9E005_9VIRU	Q9e005 andes virus
1271	36	38.7	2156	1	RRPL_PUUMH	P27176 puumala vir
1272	36	38.7	2195	1	SEC16_YEAST	P48415 saccharomyc

1273	36	38.7	2222	2	Q4PAX7_USTMA	Q4pax7	ustilago ma	1346	35	37.6	130	2	Q9YEK2_ABRPE	O9yek2	aeropyrum p
1274	36	38.7	2254	2	Q6ZM94_BRARE	Q6zm94	brachydanio	1347	35	37.6	131	2	Q4H5G0_9DEIO	Q4h5g0	deinococcus
1275	36	38.7	2301	2	Q6BG00_PARTE	Q6bg00	paramedion	1348	35	37.6	132	2	Q54I88_DICDI	Q54i88	dictyosteli
1276	36	38.7	2470	2	Q4RV69_TETNG	Q4rv69	tetradon n	1349	35	37.6	136	2	Q62492_MOUSE	Q62492	mus musculu
1277	36	38.7	2497	2	Q7RJM2_PLAYO	Q7rjm2	plasmodium	1350	35	37.6	139	2	Q9WBL1_9HIV1	Q9wbl1	human immun
1278	36	38.7	2578	2	Q5W0B2_HUMAN	Q5w0b2	homo sapien	1351	35	37.6	147	2	Q9ZBB8_AZOVI	Q9zbb8	azotobacter
1279	36	38.7	2789	2	Q9BXT5_HUMAN	Q9bxt5	homo sapien	1352	35	37.6	147	2	Q4IUI1_AZOVI	Q4iui1	azotobacter
1280	36	38.7	3417	2	Q4SXF9_TETNG	Q4sxf9	tetradon n	1353	35	37.6	147	2	Q8R2K8_MOUSE	Q8r2k8	mus musculu
1281	36	38.7	3834	2	Q600K9_MYCHY	Q600k9	mycoplasma	1354	35	37.6	148	2	Q8K3T8_MOUSE	Q8k3t8	mus musculu
1282	36	38.7	3855	2	Q8IDL5_PLAF7	Q8idl5	plasmodium	1355	35	37.6	154	2	Q7NHS4_GLOVI	Q7nhs4	gloeobacter
1283	36	38.7	4727	2	Q8GR92_MYCMO	Q8gr92	mycoplasma	1356	35	37.6	155	2	Q8SQX9_ENCCU	Q8sqx9	encephalito
1284	36	38.7	4753	1	LRP_CABEL	Q04833	caenorhabdi	1357	35	37.6	155	2	Q4I6Z0_GIBZE	Q4i6z0	gibberella
1285	36	38.7	7191	2	Q6XA09_9PLEO	Q6xa09	alternaria	1358	35	37.6	156	2	Q93D85_STRMU	Q93d85	streptococc
1286	35.5	38.2	99	2	O55556_NPVLS	O55556	leucania se	1359	35	37.6	157	1	GYRI_ECOLI	P33012	escherichia
1287	35.5	38.2	110	2	O5XV44_ARATH	O5xv44	arabidopsis	1360	35	37.6	157	2	Q8FG58_ECOL6	Q8fg58	escherichia
1288	35.5	38.2	134	2	Q7P9W5_RICSI	Q7p9w5	rickettsia	1361	35	37.6	157	2	Q8X8U1_ECO57	Q8x8u1	escherichia
1289	35.5	38.2	161	2	Q71AB7_9NUCL	Q71ab7	namestra co	1362	35	37.6	160	2	Q44535_AZOVI	Q44535	azotobacter
1290	35.5	38.2	161	2	Q8JM58_9NUCL	Q8jm58	namestra co	1363	35	37.6	160	2	Q4IZU5_AZOVI	Q4izu5	azotobacter
1291	35.5	38.2	161	2	Q8QLD9_NPVMC	Q8qld9	namestra co	1364	35	37.6	161	2	Q20424_CABEL	Q20424	caenorhabdi
1292	35.5	38.2	181	2	Q5XV45_ARATH	Q5xv45	arabidopsis	1365	35	37.6	161	2	O92453_NPVBW	O92453	bombyx mori
1293	35.5	38.2	270	2	Q9NQ88_HUMAN	Q9nq88	homo sapien	1366	35	37.6	167	2	O5C6R2_SCHJA	Q5c6r2	schistosoma
1294	35.5	38.2	278	2	Q9KKS3_VTBCH	Q9kks3	vibrio chol	1367	35	37.6	170	2	O5WKN0_BACSK	Q5wkn0	bacillus cl
1295	35.5	38.2	297	2	Q5CNL1_CRYHO	Q5cnl7	cryptospori	1368	35	37.6	172	2	Q4Q869_LEIMA	Q4q869	leishmania
1296	35.5	38.2	319	2	Q8DAC7_VTBVU	Q8dac1	vibrio vuln	1369	35	37.6	172	2	Q9CRU8_MOUSE	Q9cru8	mus musculu
1297	35.5	38.2	319	2	Q7MJV0_VTBVY	Q7mjv0	vibrio vuln	1370	35	37.6	172	2	Q9PWQ3_CHICK	Q9pwq3	gallus gall
1298	35.5	38.2	349	2	Q64469_ARATH	O64469	arabidopsis	1371	35	37.6	173	2	Q973Y0_SULTO	Q973y0	sulfolobus
1299	35.5	38.2	353	2	Q6DFK1_XENLA	Q6dfk1	xenopus lae	1372	35	37.6	175	2	Q4UGR5_THEAN	Q4ugr5	theileria a
1300	35.5	38.2	356	1	CHLI_PORPU	P51394	porphyra pu	1373	35	37.6	176	2	O567L5_BRARE	Q567l5	brachydanio
1301	35.5	38.2	367	2	Q8DIS0_SYNEL	Q8dis0	synechococc	1374	35	37.6	181	2	Q9PWQ2_CHICK	Q9pwq2	gallus gall
1302	35.5	38.2	380	2	Q6ETT0_ORYSA	Q6ett0	oryza sativ	1375	35	37.6	182	2	Q57U02_9TRYP	Q57u02	trypanosoma
1303	35.5	38.2	387	2	Q6ETT3_ORYSA	Q6ett3	oryza sativ	1376	35	37.6	185	1	BMF_RAT	Q8k589	rattus norv
1304	35.5	38.2	388	2	Q4IST0_GIBZE	Q4ist0	gibberella	1377	35	37.6	189	2	Q4IJF9_GIBZE	Q4ijf9	gibberella
1305	35.5	38.2	401	2	Q9CGQ8_LACLA	Q9cgq8	lactococcus	1378	35	37.6	201	2	Q67XT3_ARATH	Q67xt3	arabidopsis
1306	35.5	38.2	413	2	Q9AZY7_9CAUD	Q9azy7	bacterioph	1379	35	37.6	202	2	Q5Q0A6_ARATH	Q5q0a6	arabidopsis
1307	35.5	38.2	453	2	Q8BUQU_MOUSE	Q8buq6	mus musculu	1380	35	37.6	203	2	Q5E0A3_VIBF1	Q5e0a3	vibrio fisc
1308	35.5	38.2	537	2	Q60XU0_CABER	Q60xu0	caenorhabdi	1381	35	37.6	204	2	Q7MVA4_PORGI	Q7mva4	porphyromon
1309	35.5	38.2	589	1	SYD2_STRMU	Q8drv9	streptococc	1382	35	37.6	204	2	P89134_SHFV	P89134	simian hemo
1310	35.5	38.2	591	1	VATA_CHLMU	Q9pk85	chlamydia m	1383	35	37.6	206	2	Q4YMC7_PLABE	Q4ymc7	plasmodium
1311	35.5	38.2	591	1	VATA_CHLTR	O84310	chlamydia t	1384	35	37.6	218	2	Q9YUQ3_PADEN	Q9yuq3	turkey aden
1312	35.5	38.2	657	2	Q7Q2Y1_ANOGA	Q7q2y1	anopheles g	1385	35	37.6	219	1	ATPD_CHLRE	Q42687	chlamydomon
1313	35.5	38.2	742	1	CDCH_HALSA	Q9hpf0	halobacteri	1386	35	37.6	219	2	Q9SBM2_VOLCA	Q9sbm2	volvox cart
1314	35.5	38.2	881	2	Q6CA84_YARLI	Q6ca84	yarrowia li	1387	35	37.6	220	2	Q4G133_HUMAN	Q4g133	homo sapien
1315	35.5	38.2	920	2	Q5B4L3_EMENI	Q5b4l3	aspergillus	1388	35	37.6	223	2	Q63211_RAT	Q63211	rattus norv
1316	35.5	38.2	1256	2	Q8NEN5_HUMAN	Q8nen5	homo sapien	1389	35	37.6	224	2	Q6DRS0_BORGA	Q6drs0	borrelia ga
1317	35.5	38.2	1258	2	Q9SSP0_ARATH	Q9ssp0	arabidopsis	1390	35	37.6	224	2	Q5WLB8_BACSK	Q5wlb8	bacillus cl
1318	35.5	38.2	1633	2	Q615D4_CABER	Q615d4	caenorhabdi	1391	35	37.6	224	2	Q662K6_BORGA	Q662k6	borrelia ga
1319	35.5	38.2	1779	2	Q6TYB9_CABER	Q6tyb9	caenorhabdi	1392	35	37.6	226	2	Q8C6I7_MOUSE	Q8c6i7	mus musculu
1320	35.5	38.2	1901	2	Q9DHH8_YLDV	Q9dhh8	yaba-like d	1393	35	37.6	227	2	O5QPL2_HUMAN	Q5qpl2	homo sapien
1321	35	37.6	35	2	Q65VF2_MANSW	Q65vf2	mannheimia	1394	35	37.6	228	2	Q898N4_CLOTE	Q898n4	clostridium
1322	35	37.6	58	2	Q5T909_HUMAN	Q5t909	homo sapien	1395	35	37.6	231	2	Q71B79_9HIV1	Q71b79	human immun
1323	35	37.6	69	2	Q4L4M9_STAHI	Q4l4m9	staphylococ	1396	35	37.6	233	2	Q4TDI6_TETNG	Q4tdi6	tetradodon n
1324	35	37.6	70	2	Q58LS6_9CAUD	Q58ls6	cyanothode n	1397	35	37.6	234	2	Q9MZ06_BOVIN	Q9mz06	bos taurus
1325	35	37.6	74	2	Q4RBD2_TETNG	Q4rbd2	tetradodon n	1398	35	37.6	235	2	Q60ZX7_CABER	Q60zx7	caenorhabdi
1326	35	37.6	76	2	Q5Z8Z9_ORYSA	Q5z8z9	oryza sativ	1399	35	37.6	236	2	Q7P8A1_FUSNV	Q7p8a1	fusobacteri
1327	35	37.6	80	2	Q54BZ6_DICDI	Q54bz6	dictyosteli	1400	35	37.6	237	2	Q7ZX78_XENLA	Q7zx78	xenopus lae
1328	35	37.6	84	2	Q8PYH8_METWA	Q8pyh8	methanosarc	1401	35	37.6	240	2	Q4ZVB7_PSESY	Q4zvb7	pseudomonas
1329	35	37.6	84	2	Q8TIW2_METAC	Q8tiw2	methanosarc	1402	35	37.6	241	2	Q73QJ9_TREDE	Q73qj9	treponema d
1330	35	37.6	89	1	SEM1_YEAST	O94742	saccharomyc	1403	35	37.6	241	2	Q9YWR4_9HIV1	Q9ywr4	human immun
1331	35	37.6	93	2	Q6AW53_COTJA	Q6aw53	coturnix co	1404	35	37.6	244	2	Q8TI96_DICDI	Q8ti96	dictyosteli
1332	35	37.6	93	2	Q6AW54_COTJA	Q6aw54	coturnix co	1405	35	37.6	245	1	NUK_WHEAT	P26304	trititicum ae
1333	35	37.6	93	2	Q6AW55_COTJA	Q6aw55	coturnix co	1406	35	37.6	245	2	Q55BY1_DICDI	Q55by1	dictyosteli
1334	35	37.6	101	2	Q8ZMY2_PYRAE	Q8zwy2	pyrobaculum	1407	35	37.6	245	2	Q8S034_ORYSA	Q8s034	oryza sativ
1335	35	37.6	104	2	Q6NXW3_MOUSE	Q6nxw3	mus musculu	1408	35	37.6	245	2	Q85XC3_HORVU	Q85xc3	hordeum vul
1336	35	37.6	105	2	Q5FTU2_GLUOX	Q5ftu2	gluconobact	1409	35	37.6	247	2	Q4XT75_PLACH	Q4xt75	plasmodium
1337	35	37.6	107	2	Q5C412_SCHJA	O5c412	schistosoma	1410	35	37.6	250	2	Q4S582_TETNG	Q4s582	tetradodon n
1338	35	37.6	107	2	Q4VS17_BOVIN	Q4vsl7	bos taurus	1411	35	37.6	251	2	Q8GF12_EDWTA	Q8gfi2	edwardsiell
1339	35	37.6	107	2	Q6Z6I7_ORYSA	Q6z6i7	oryza sativ	1412	35	37.6	252	2	Q95RQ2_DROME	Q95rq2	drosophila
1340	35	37.6	111	2	Q5BFFN5_EMENI	Q5bfm5	aspergillus	1413	35	37.6	254	1	CYSH_MYCBO	P65669	mycobacteri
1341	35	37.6	118	2	Q6OM15_CABER	Q6om15	caenorhabdi	1414	35	37.6	254	1	CYSH_MYCTU	P65668	mycobacteri
1342	35	37.6	119	2	Q9QH59_9ALPH	Q9qh59	gallid herp	1415	35	37.6	255	2	Q9VYM8_DROME	Q9vym8	drosophila
1343	35	37.6	125	2	Q8TR09_METAC	Q8tr09	methanosarc	1416	35	37.6	258	1	PSB1_CABEL	P34286	caenorhabdi
1344	35	37.6	126	2	Q5HVU4_CAMJR	Q5hvu4	campylobact	1417	35	37.6	258	2	Q60IX4_CABER	Q60ix4	caenorhabdi
1345	35	37.6	126	2	Q99MH4_CRIGR	Q99mh4	cricetulus	1418	35	37.6	259	2	Q76LJ3_COTJA	Q76lj3	coturnix co

RA Waterston R.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25075 MW; 1718E0594997A1A1 CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCPE 18
|||||
Db 32 VSLVEEDQFSQNPISCPE 49

RESULT 3

Q6UWS1 HUMAN
ID Q6UWS1_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q6UWS1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TCCE518.
GN ORFNames=UNQ518;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358671; AAQ89034.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 229 AA; 25109 MW; 1718ED342C58C903 CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCPE 18
|||||
Db 32 VSLVEEDQFSQNPISCPE 49

RESULT 4

Q5U609 HUMAN
ID Q5U609_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q5U609;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Transmembrane 4 L six family member 20.
GN Name=TM4SF20;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC035754; AAH35754.1; -; mRNA.
DR Ensembl; ENSG00000168955; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
KW Transmembrane.
SQ SEQUENCE 229 AA; 25137 MW; B750504AFD7C247D CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCPE 18
|||||
Db 32 VSLVEEDQFSQNPISCPE 49

RESULT 5

Q9CQY8 MOUSE
ID Q9CQY8_MOUSE PRELIMINARY; PRT; 226 AA.
AC Q9CQY8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033426G15 product:similar
DE to CDNA: FLJ22800 FIS, CLONE KAI2630 (Mus musculus 10 day old male
DE pancreas cDNA, RIKEN full-length enriched library, clone:1810018L02
DE product:similar to CDNA: FLJ22800 FIS, CLONE KAI2630).
GN Name=Tm4sf20;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCPE 18
|||||
Db 32 VSLVEEDQFSQNPISCPE 49

RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

[5]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK017195; BAB30629.1; -; mRNA.
DR EMBL; AK007532; BAB25093.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; Tm4sf20.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;

Query Match 75.3%; Score 70; DB 2; Length 226;
Best Local Similarity 72.2%; Pred.No. 0.00094;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VSLVEDQFSQNPISCFE 18
:||||| | |||||:|
Db 32 ISLVEADSTSQNPISCYE 49

RESULT 6
Q9D3R0 MOUSE
ID Q9D3R0_MOUSE PRELIMINARY; PRT; 226 AA.
AC Q9D3R0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033405M13 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI2630.
GN Name=Tm4sf20; Synonyms=1810018L02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RP NUCLEOTIDE SEQUENCE.

OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Perteau M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Perteau M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGK01000002; EAN32582.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 143 AA; 16977 MW; 500D0921D3856550 CRC64;

Query Match 48.4%; Score 45; DB 2; Length 143;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 LVEEDQFSQNPFSCFE 18
Db 39 LVDDDDQFRNDIDIYE 54
||:||||:|:|
||:||||:|:|

RESULT 11
Q7T301 BRARE
ID Q7T301 BRARE PRELIMINARY; PRT; 238 AA.
AC Q7T301;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Basic helix-loop-helix domain containing, class B, 5.
GN Name=bhlhb5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; BC053312; AAH53312.1; -; mRNA.
DR Ensembl; ENSDARG0000025861; Danio rerio.
DR ZFIN; ZDB-GENE-040426-1411; bhlhb5.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS50888; HLH; 1.
SQ SEQUENCE 238 AA; 25499 MW; 4F3D0949829EBF99 CRC64;

Query Match 48.4%; Score 45; DB 2; Length 238;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SQNPISCFE 18
Db 17 SQSPISCFE 25
||:|||||
||:|||||

RESULT 12
Q9VDK6 DROME
ID Q9VDK6 DROME PRELIMINARY; PRT; 410 AA.
AC Q9VDK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG4159-PA.
GN Name=CG4159; ORFNames=CG4159;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,


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DE Hypothetical protein.
GN ORFNames=DDB0201744;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1] _NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Tivey A.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000011; EAL72619.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine_P1.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF00515; TPR_1; 1.
DR SMART; SM00028; TPR; 2.
DR PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
DR KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 805 AA; 93914 MW; 6BE0153F294B8C17 CRC64;

Query Match 48.4%; Score 45; DB 2; Length 805;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISC 16
Db 424 VNMLERDQLFSNPWSC 439
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RESULT 15
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ID _GYRA MYCLE STANDARD; PRT; 1273 AA.
AC Q57532; Q50209; Q9CDF2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DNA gyrase subunit A (EC 5.99.1.3) [Contains: Mle gyra intein].
GN Name=gyrA; OrderedLocusNames=ML0006;
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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96194983; PubMed=8622949; DOI=10.1073/pnas.93.8.3410;
RA Fsihi H., Vincent V., Cole S.T.;
RT "Homing events in the gyrA gene of some mycobacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3410-3415(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=TN;
MEDLINE=211128732; PubMed=11234002; DOI=10.1038/35059006;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
[3]
NUCLEOTIDE SEQUENCE OF 75-114.
MEDLINE=96050760; PubMed=8540734;
Guillemin I., Cambau E., Jarlier V.;
"Sequences of conserved region in the A subunit of DNA gyrase from
nine species of the genus Mycobacterium: phylogenetic analysis and
implication for intrinsic susceptibility to quinolones.";
Antimicrob. Agents Chemother. 39:2145-2149(1995).
-1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
DNA rings, including catenanes and knotted rings.
-1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA.
-1- SUBUNIT: Made up of two chains. The A chain is responsible for DNA
breakage and rejoining; the B chain catalyzes ATP hydrolysis. The
enzyme forms an A2B2 tetramer.
-1- PTM: This protein undergoes a protein self splicing that involves
a post-translational excision of the intervening region (intein)
followed by peptide ligation (Potential).
-1- SIMILARITY: Belongs to the topoisomerase gyrA/parC subunit family.
-1- SIMILARITY: Contains 1 DOD-type homing endonuclease domain.
-1- CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 1247.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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EMBL; Z70722; CAA94713.1; -; Genomic DNA.
EMBL; Z68206; CAA92430.1; -; Genomic DNA.
EMBL; AL583917; CAC29514.1; ALT_FRAME; Genomic_DNA.
EMBL; X87124; CAA60608.1; -; Genomic_DNA.
PIR; T10006; T10006.
HSSP; P72065; 1AM2.
SMR; Q57532; 494-550.
Leproma; ML0006; -.
InterPro; IPR005743; DNA_gyrA.
InterPro; IPR006691; DNA_gyraseA_C.
InterPro; IPR002205; DNA_topoisoIV.
InterPro; IPR003586; Hedgehog_hint_C.
InterPro; IPR003587; Hedgehog_hint_N.
InterPro; IPR006142; INTEIN.
InterPro; IPR004042; Intein_endonuc.
InterPro; IPR006141; Intein_S.
Pfam; PF03989; DNA_gyraseA_C; 6.
Pfam; PF00521; DNA_topoisoIV; 2.
PRINTS; PR00379; INTEIN.
ProDom; PD000742; DNA_topoisoIV; 2.
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SMART; SM00306; HintN; 1.
SMART; SM00434; TOP4C; 1.
TIGRFAMS; TIGR01063; gyrA; 1.
TIGRFAMS; TIGR01443; intein_Cterm; 1.
TIGRFAMS; TIGR01445; intein_Nterm; 1.
PROSITE; PS50818; INTEIN_C_TER; 1.
PROSITE; PS50819; INTEIN_ENDONUCLEASE; 1.
PROSITE; PS50817; INTEIN_N_TER; 1.
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KW Autocatalytic cleavage; Complete proteome; DNA-binding; Isomerase;
KW Protein splicing; Topoisomerase.
FT CHAIN 1 130 DNA gyrase subunit A, 1st part (By
FT similarity).
FT CHAIN 131 550 Mle gyrA intein (By similarity).
FT CHAIN 551 1273 DNA gyrase subunit A, 2nd part (By
FT similarity).
FT DOMAIN 256 396 DOD-type homing endonuclease.
FT ACT_SITE 130 130 O-(5'-phospho-DNA)-tyrosine intermediate
FT (By similarity).
FT CONFLICT 267 267 F -> S (in Ref. 1).
SQ SEQUENCE 1273 AA; 141218 MW; 4B6FFB5BD7AEF53 CRC64;

Query Match 47.3%; Score 44; DB 1; Length 1273;
Best Local Similarity 46.7%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VEEDQFSQNPISCFE 18
Db ||||| |:|:|:|:
469 VEEDSFNQHNVDVCVQ 483

Search completed: December 22, 2005, 03:00:16
Job time : 128 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:46:28 ; Search time 12.4898 Seconds
(without alignments)
119.150 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49

Perfect score: 93

Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	93	100.0	229	2	US-09-992-598-258
5	43	46.2	1110	1	US-08-118-441-29
6	43	46.2	1110	2	US-08-338-579A-29
7	43	46.2	1110	4	PCT-US94-09851-29
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10	42	45.2	676	2	US-08-894-997-50
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13	42	45.2	1147	2	US-09-949-016-8616
14	42	45.2	1464	1	US-08-231-193A-11
15	42	45.2	1464	1	US-08-486-273A-11
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20	42	45.2	1464	2	US-09-648-797-11
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					Sequence 258, App
					Sequence 258, App
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					Sequence 11, Appl
					Sequence 11, Appl
					Sequence 2, Appli
					Sequence 11, Appl
					Sequence 8311, Ap
					Sequence 11, Appl
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					Sequence 11, Appl
					Sequence 6, Appli

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102	37	39.8	363	2	US-10-004-860-278	Sequence 278, App	175	36	38.7	490	2	US-09-667-135-28	Sequence 28, Appl
103	37	39.8	370	2	US-09-205-258-558	Sequence 558, App	176	36	38.7	558	2	US-09-667-135-31	Sequence 31, Appl
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114	37	39.8	579	1	US-08-448-196A-8	Sequence 8, Appli	187	36	38.7	640	2	US-09-134-000C-5035	Sequence 5035, App
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116	36.5	39.2	657	2	US-09-653-465B-2	Sequence 2, Appli	189	36	38.7	648	2	US-09-949-016-11296	Sequence 11296, A
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122	36	38.7	101	2	US-09-320-424-4	Sequence 4, Appli	195	36	38.7	741	1	US-08-487-797-2	Sequence 2, Appli
123	36	38.7	101	2	US-09-374-454-17	Sequence 17, Appl	196	36	38.7	741	1	US-08-487-797-4	Sequence 4, Appli
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137	36	38.7	225	2	US-09-949-016-11298	Sequence 11298, A	210	35	37.6	93	2	US-09-248-796A-25316	Sequence 25316, A
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145	36	38.7	261	2	US-09-270-767-47059	Sequence 47059, A	218	35	37.6	199	2	US-09-232-200-85	Sequence 85, Appl
146	36	38.7	266	2	US-09-645-415A-10	Sequence 10, Appl	219	35	37.6	199	2	US-09-232-197-85	Sequence 85, Appl
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151	36	38.7	281	2	US-08-780-496-1	Sequence 1, Appli	224	35	37.6	253	2	US-09-248-796A-14363	Sequence 14363, A
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154	36	38.7	281	2	US-09-333-593A-6	Sequence 6, Appli	227	35	37.6	261	1	US-08-446-822-15	Sequence 15, Appl
155	36	38.7	281	2	US-09-157-864-11	Sequence 11, Appl	228	35	37.6	261	2	US-09-328-314-15	Sequence 15, Appl
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157	36	38.7	281	2	US-09-919-039-118	Sequence 118, App	230	35	37.6	264	2	US-09-270-767-44841	Sequence 44841, A
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165	36	38.7	309	2	US-09-620-461-7	Sequence 7, Appli	238	35	37.6	336	1	US-08-442-043A-16	Sequence 16, Appl
166	36	38.7	352	2	US-09-710-279-216	Sequence 216, App	239	35	37.6	336	2	US-08-441-893A-16	Sequence 16, Appl
167	36	38.7	359	2	US-09-949-016-5912	Sequence 5912, Ap	240	35	37.6	352	2	US-09-248-796A-18408	Sequence 18408, A
168	36	38.7	377	2	US-09-489-039A-12546	Sequence 12546, A	241	35	37.6	360	2	US-09-555-313B-4	Sequence 4, Appli
169	36	38.7	403	2	US-09-540-236-2573	Sequence 2573, Ap	242	35	37.6	360	2	US-09-826-509-443	Sequence 443, App
170	36	38.7	411	2	US-09-188-930-302	Sequence 302, App	243	35	37.6	362	2	US-09-146-980-2	Sequence 2, Appli
171	36	38.7	411	2	US-09-312-283C-302	Sequence 302, App	244	35	37.6	364	2	US-09-270-767-43337	Sequence 43337, A
172	36	38.7	450	2	US-09-949-016-8496	Sequence 8496, Ap	245	35	37.6	377	2	US-10-164-595-64	Sequence 64, Appl
173	36	38.7	478	2	US-09-570-454-2	Sequence 2, Appli	246	35	37.6	378	2	US-09-826-509-445	Sequence 445, App

247	35	37.6	380	2	US-09-555-313B-24	Sequence 24, Appl	320	34	36.6	120	2	US-09-248-796A-16151	Sequence 16151, A
248	35	37.6	380	2	US-09-826-509-441	Sequence 441, App	321	34	36.6	130	2	US-09-621-976-4013	Sequence 4013, Ap
249	35	37.6	387	2	US-09-826-509-436	Sequence 436, App	322	34	36.6	141	2	US-09-489-039A-11896	Sequence 11896, A
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251	35	37.6	388	2	US-09-328-314-8	Sequence 8, Appli	324	34	36.6	154	2	US-08-845-623-22	Sequence 22, Appl
252	35	37.6	388	2	US-09-826-509-439	Sequence 439, App	325	34	36.6	154	2	US-08-815-927-22	Sequence 22, Appl
253	35	37.6	388	4	PCT-US93-12586-8	Sequence 8, Appli	326	34	36.6	154	2	US-09-103-330-22	Sequence 22, Appl
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259	35	37.6	548	1	US-09-270-767-49793	Sequence 49793, A	332	34	36.6	188	2	US-09-710-279-152	Sequence 152, App
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261	35	37.6	569	1	US-08-381-603-2	Sequence 2, Appli	334	34	36.6	224	2	US-09-270-767-33261	Sequence 33261, A
262	35	37.6	569	2	US-08-924-376-2	Sequence 2, Appli	335	34	36.6	224	2	US-09-830-230A-349	Sequence 349, App
263	35	37.6	569	2	US-08-685-212-2	Sequence 2, Appli	336	34	36.6	245	2	US-09-602-787A-22	Sequence 22, Appl
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270	35	37.6	580	2	US-09-367-583-2	Sequence 2, Appli	343	34	36.6	309	2	US-09-723-677B-5	Sequence 5, Appli
271	35	37.6	588	2	US-09-949-016-8572	Sequence 2, Appli	344	34	36.6	315	2	US-09-252-991A-24352	Sequence 24352, A
272	35	37.6	593	2	US-09-124-141-7	Sequence 8572, Ap	345	34	36.6	317	2	US-09-949-016-8193	Sequence 8193, Ap
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274	35	37.6	616	2	US-09-393-529-2	Sequence 2, Appli	347	34	36.6	323	1	US-08-475-637-4	Sequence 4, Appli
275	35	37.6	616	2	US-09-396-149-7	Sequence 7, Appli	348	34	36.6	323	2	US-08-706-281A-12	Sequence 12, Appl
276	35	37.6	652	2	US-09-134-001C-3517	Sequence 3517, Ap	349	34	36.6	323	2	US-09-191-359-4	Sequence 4, Appli
277	35	37.6	758	2	US-09-198-452A-996	Sequence 996, App	350	34	36.6	323	2	US-09-097-231-12	Sequence 12, Appl
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279	35	37.6	760	2	US-09-555-313B-2	Sequence 2, Appli	352	34	36.6	323	2	US-09-709-066-2	Sequence 2, Appli
280	35	37.6	826	2	US-09-252-991A-22143	Sequence 22143, A	353	34	36.6	330	2	US-09-301-666A-10	Sequence 10, Appl
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284	35	37.6	902	2	US-10-282-162-36	Sequence 36, Appl	357	34	36.6	390	2	US-09-543-681A-5753	Sequence 5753, Ap
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286	35	37.6	902	2	US-10-282-162-42	Sequence 42, Appl	359	34	36.6	422	2	US-08-492-459-4	Sequence 4, Appli
287	35	37.6	902	2	US-10-282-162-44	Sequence 44, Appl	360	34	36.6	422	2	US-08-423-752-2	Sequence 2, Appli
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289	35	37.6	910	2	US-10-282-162-28	Sequence 28, Appl	362	34	36.6	422	2	US-08-716-873-7	Sequence 7, Appli
290	35	37.6	959	2	US-09-248-796A-20776	Sequence 20776, A	363	34	36.6	422	2	US-08-716-873-16	Sequence 16, Appl
291	35	37.6	1070	2	US-10-164-595-18	Sequence 18, Appl	364	34	36.6	422	2	US-08-716-873-18	Sequence 18, Appl
292	35	37.6	1073	2	US-10-164-595-22	Sequence 22, Appl	365	34	36.6	422	2	US-09-368-431-7	Sequence 7, Appli
293	35	37.6	1092	2	US-09-543-681A-7058	Sequence 7058, Ap	366	34	36.6	422	2	US-09-368-431-16	Sequence 16, Appl
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296	35	37.6	1175	1	US-08-639-923A-36	Sequence 36, Appl	369	34	36.6	422	2	US-09-414-006-4	Sequence 4, Appli
297	35	37.6	1279	2	US-09-170-496D-293	Sequence 293, App	370	34	36.6	422	2	US-09-447-223-2	Sequence 2, Appli
298	35	37.6	1279	2	US-09-364-425B-58	Sequence 58, Appl	371	34	36.6	422	2	US-09-447-223-4	Sequence 4, Appli
299	35	37.6	1372	2	US-09-902-540-14099	Sequence 14099, A	372	34	36.6	422	2	US-09-951-217-7	Sequence 7, Appli
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305	34.5	37.1	826	2	US-09-949-016-9212	Sequence 9212, Ap	378	34	36.6	451	2	US-09-215-649A-4	Sequence 4, Appli
306	34.5	37.1	826	2	US-09-949-016-9213	Sequence 9213, Ap	379	34	36.6	451	2	US-09-577-780-4	Sequence 4, Appli
307	34.5	37.1	826	2	US-09-949-016-9214	Sequence 9214, Ap	380	34	36.6	451	2	US-09-577-800-4	Sequence 4, Appli
308	34.5	37.1	950	2	US-09-328-352-4668	Sequence 4668, Ap	381	34	36.6	451	2	US-09-466-496-4	Sequence 4, Appli
309	34.5	37.1	1073	2	US-09-134-000C-6356	Sequence 6356, Ap	382	34	36.6	451	2	US-09-871-856-4	Sequence 4, Appli
310	34.5	37.1	1297	1	US-08-290-731C-4	Sequence 4, Appli	383	34	36.6	451	2	US-09-871-291-4	Sequence 4, Appli
311	34	36.6	21	2	US-09-555-313B-6	Sequence 6, Appli	384	34	36.6	451	2	US-09-107-532A-6652	Sequence 6652, Ap
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313	34	36.6	43	1	US-08-558-107-16	Sequence 16, Appl	386	34	36.6	451	2	US-09-865-363-4	Sequence 4, Appli
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315	34	36.6	75	2	US-09-248-796A-24803	Sequence 24803, A	388	34	36.6	483	2	US-09-252-991A-27020	Sequence 27020, A
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395	34	36.6	574	1	US-08-756-317-4	Sequence 4, Appli	468	34	36.6	1155	1	US-08-349-867-19	Sequence 19, Appl
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399	34	36.6	591	2	US-09-577-780-2	Sequence 2, Appli	472	34	36.6	1155	1	US-07-951-715A-9	Sequence 9, Appli
400	34	36.6	591	2	US-09-577-800-2	Sequence 2, Appli	473	34	36.6	1155	1	US-08-463-308-2	Sequence 2, Appli
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402	34	36.6	591	2	US-09-871-856-2	Sequence 2, Appli	475	34	36.6	1155	1	US-08-598-305A-33	Sequence 33, Appl
403	34	36.6	591	2	US-09-871-291-2	Sequence 2, Appli	476	34	36.6	1155	1	US-08-639-923A-19	Sequence 19, Appl
404	34	36.6	591	2	US-09-877-650-2	Sequence 2, Appli	477	34	36.6	1155	1	US-08-459-448A-9	Sequence 9, Appli
405	34	36.6	591	2	US-09-865-363-2	Sequence 2, Appli	478	34	36.6	1155	2	US-08-459-595A-9	Sequence 9, Appli
406	34	36.6	591	2	US-09-688-459-2	Sequence 2, Appli	479	34	36.6	1155	2	US-09-021-203-2	Sequence 2, Appli
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410	34	36.6	616	2	US-09-215-649A-6	Sequence 6, Appli	483	34	36.6	1155	2	US-09-053-549-6	Sequence 6, Appli
411	34	36.6	616	2	US-09-577-780-6	Sequence 6, Appli	484	34	36.6	1155	2	US-09-547-422-9	Sequence 9, Appli
412	34	36.6	616	2	US-09-577-800-6	Sequence 6, Appli	485	34	36.6	1155	2	US-09-988-462-9	Sequence 9, Appli
413	34	36.6	616	2	US-09-466-496-6	Sequence 6, Appli	486	34	36.6	1155	4	PCT-US95-05431-19	Sequence 19, Appl
414	34	36.6	616	2	US-09-871-856-6	Sequence 6, Appli	487	34	36.6	1155	6	5254799-4	Patent No. 5254799
415	34	36.6	616	2	US-09-871-291-6	Sequence 6, Appli	488	34	36.6	1156	2	US-09-178-252-15	Sequence 15, Appl
416	34	36.6	616	2	US-09-877-650-6	Sequence 6, Appli	489	34	36.6	1156	2	US-09-826-660-15	Sequence 15, Appl
417	34	36.6	616	2	US-09-865-363-6	Sequence 6, Appli	490	34	36.6	1162	2	US-09-134-001C-4008	Sequence 4008, Ap
418	34	36.6	616	2	US-09-949-016-6421	Sequence 6421, Ap	491	34	36.6	1163	1	US-08-239-474A-11	Sequence 11, Appl
419	34	36.6	616	2	US-09-688-459-6	Sequence 6, Appli	492	34	36.6	1163	1	US-08-732-495-11	Sequence 11, Appl
420	34	36.6	616	2	US-09-957-944-2	Sequence 2, Appli	493	34	36.6	1163	2	US-09-178-252-21	Sequence 21, Appl
421	34	36.6	619	2	US-10-104-047-2497	Sequence 2497, Ap	494	34	36.6	1163	2	US-09-826-660-21	Sequence 21, Appl
422	34	36.6	620	2	US-09-134-000C-5867	Sequence 5867, Ap	495	34	36.6	1165	1	US-07-828-788A-14	Sequence 14, Appl
423	34	36.6	622	2	US-09-957-944-10	Sequence 10, Appl	496	34	36.6	1165	1	US-08-239-476-33	Sequence 33, Appl
424	34	36.6	632	2	US-09-328-352-5495	Sequence 5495, Ap	497	34	36.6	1165	1	US-08-356-034-4	Sequence 4, Appli
425	34	36.6	638	1	US-08-756-317-2	Sequence 2, Appli	498	34	36.6	1165	1	US-08-639-923A-33	Sequence 33, Appl
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427	34	36.6	672	2	US-09-363-708-2	Sequence 2, Appli	500	34	36.6	1165	2	US-09-176-320-6	Sequence 6, Appli
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429	34	36.6	719	1	US-08-082-849B-31	Sequence 31, Appl	502	34	36.6	1165	2	US-09-837-961A-4	Sequence 4, Appli
430	34	36.6	719	4	PCT-US94-01624-31	Sequence 31, Appl	503	34	36.6	1165	2	US-09-661-016-6	Sequence 6, Appli
431	34	36.6	735	1	US-08-021-601-4	Sequence 4, Appli	504	34	36.6	1165	4	PCT-US92-11337-14	Sequence 14, Appl
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433	34	36.6	735	4	PCT-US94-01624-4	Sequence 4, Appli	506	34	36.6	1165	6	5188960-4	Patent No. 5188960
434	34	36.6	736	2	US-09-350-729A-7	Sequence 7, Appli	507	34	36.6	1171	1	US-07-828-788A-6	Sequence 6, Appli
435	34	36.6	757	2	US-09-823-038A-52	Sequence 52, Appl	508	34	36.6	1171	1	US-08-278-685-2	Sequence 2, Appli
436	34	36.6	763	2	US-09-350-729A-5	Sequence 5, Appli	509	34	36.6	1171	1	US-08-277-721-2	Sequence 2, Appli
437	34	36.6	764	2	US-09-350-729A-6	Sequence 6, Appli	510	34	36.6	1171	1	US-08-277-721-4	Sequence 4, Appli
438	34	36.6	903	1	US-08-021-601-12	Sequence 12, Appl	511	34	36.6	1171	1	US-08-602-737-4	Sequence 4, Appli
439	34	36.6	903	1	US-08-082-849B-12	Sequence 12, Appl	512	34	36.6	1171	2	US-09-001-982-4	Sequence 4, Appli
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441	34	36.6	924	2	US-09-489-039A-8842	Sequence 8842, Ap	514	34	36.6	1171	4	PCT-US92-11337-6	Sequence 6, Appli
442	34	36.6	1046	2	US-09-199-637A-13	Sequence 13, Appl	515	34	36.6	1174	1	US-07-828-788A-10	Sequence 10, Appl
443	34	36.6	1049	2	US-09-252-991A-26475	Sequence 26475, A	516	34	36.6	1174	1	US-08-349-867-25	Sequence 25, Appl
444	34	36.6	1129	6	5164180-6	Patent No. 5164180	517	34	36.6	1174	1	US-08-349-867-29	Sequence 29, Appl
445	34	36.6	1148	1	US-08-349-867-23	Sequence 23, Appl	518	34	36.6	1174	1	US-08-349-867-32	Sequence 32, Appl
446	34	36.6	1148	1	US-08-349-867-27	Sequence 27, Appl	519	34	36.6	1174	1	US-08-239-476-25	Sequence 25, Appl
447	34	36.6	1148	1	US-08-239-476-23	Sequence 23, Appl	520	34	36.6	1174	1	US-08-239-476-29	Sequence 29, Appl
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449	34	36.6	1148	1	US-08-598-305A-23	Sequence 23, Appl	522	34	36.6	1174	1	US-08-598-305A-25	Sequence 25, Appl
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452	34	36.6	1148	1	US-08-598-305A-37	Sequence 37, Appl	525	34	36.6	1174	1	US-08-639-923A-25	Sequence 25, Appl
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456	34	36.6	1148	1	US-08-639-923A-35	Sequence 35, Appl	529	34	36.6	1174	2	US-09-521-344-8	Sequence 8, Appli
457	34	36.6	1148	1	US-08-639-923A-37	Sequence 37, Appl	530	34	36.6	1174	2	US-09-826-660-6	Sequence 6, Appli
458	34	36.6	1148	1	US-08-639-923A-38	Sequence 38, Appl	531	34	36.6	1174	2	US-09-837-961A-8	Sequence 8, Appli
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460	34	36.6	1148	2	US-09-826-660-2	Sequence 2, Appli	533	34	36.6	1174	4	PCT-US92-11337-10	Sequence 10, Appl
461	34	36.6	1148	4	PCT-US95-05431-23	Sequence 23, Appl	534	34	36.6	1174	4	PCT-US95-05431-25	Sequence 25, Appl
462	34	36.6	1148	4	PCT-US95-05431-27	Sequence 27, Appl	535	34	36.6	1174	4	PCT-US95-05431-29	Sequence 29, Appl
463	34	36.6	1150	1	US-08-349-867-21	Sequence 21, Appl	536	34	36.6	1174	6	5188960-8	Patent No. 5188960
464	34	36.6	1150	1	US-08-239-476-21	Sequence 21, Appl	537	34	36.6	1176	1	US-07-828-788A-12	Sequence 12, Appl
465	34	36.6	1150	1	US-08-598-305A-21	Sequence 21, Appl	538	34	36.6	1176	1	US-08-257-999-2	Sequence 2, Appli

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543	34	36.6	1176	2	US-09-521-344-2	Sequence 2, Appli	616	34	36.6	1189	2	US-09-314-093-6	Sequence 6, Appli
544	34	36.6	1176	2	US-09-837-961A-2	Sequence 2, Appli	617	34	36.6	1189	2	US-09-314-093-8	Sequence 8, Appli
545	34	36.6	1176	4	PCT-US92-11337-12	Sequence 12, Appl	618	34	36.6	1189	2	US-09-314-093-10	Sequence 10, Appl
546	34	36.6	1179	1	US-08-040-751-1	Sequence 1, Appli	619	34	36.6	1189	2	US-09-314-093-12	Sequence 12, Appl
547	34	36.6	1179	6	518960-2	Patent No. 518960	620	34	36.6	1189	2	US-09-314-093-59	Sequence 59, Appl
548	34	36.6	1181	1	US-07-951-715A-11	Sequence 11, Appl	621	34	36.6	1189	2	US-09-314-093-61	Sequence 61, Appl
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551	34	36.6	1181	1	US-07-951-715A-17	Sequence 17, Appl	624	34	36.6	1189	2	US-09-250-848-4	Sequence 4, Appli
552	34	36.6	1181	1	US-07-951-715A-28	Sequence 28, Appl	625	34	36.6	1189	2	US-09-250-848-6	Sequence 6, Appli
553	34	36.6	1181	1	US-08-459-448A-11	Sequence 11, Appl	626	34	36.6	1189	2	US-09-250-848-8	Sequence 8, Appli
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557	34	36.6	1181	1	US-08-459-448A-28	Sequence 28, Appl	630	34	36.6	1189	2	US-09-251-885-2	Sequence 2, Appli
558	34	36.6	1181	2	US-08-459-595A-11	Sequence 11, Appl	631	34	36.6	1189	2	US-09-251-885-4	Sequence 4, Appli
559	34	36.6	1181	2	US-08-459-595A-13	Sequence 13, Appl	632	34	36.6	1189	2	US-09-251-885-6	Sequence 6, Appli
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564	34	36.6	1181	2	US-08-459-504B-13	Sequence 13, Appl	637	34	36.6	1189	2	US-09-337-635-2	Sequence 2, Appli
565	34	36.6	1181	2	US-08-459-504B-15	Sequence 15, Appl	638	34	36.6	1189	2	US-09-337-635-4	Sequence 4, Appli
566	34	36.6	1181	2	US-08-459-504B-17	Sequence 17, Appl	639	34	36.6	1189	2	US-09-337-635-6	Sequence 6, Appli
567	34	36.6	1181	2	US-08-459-504B-28	Sequence 28, Appl	640	34	36.6	1189	2	US-09-337-635-8	Sequence 8, Appli
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573	34	36.6	1181	2	US-09-547-422-13	Sequence 13, Appl	646	34	36.6	1189	2	US-09-337-280-4	Sequence 4, Appli
574	34	36.6	1181	2	US-09-547-422-15	Sequence 15, Appl	647	34	36.6	1189	2	US-09-337-280-6	Sequence 6, Appli
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581	34	36.6	1181	2	US-09-988-462-28	Sequence 28, Appl	654	34	36.6	1189	2	US-09-837-961A-6	Sequence 6, Appli
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583	34	36.6	1182	1	US-08-598-305A-34	Sequence 34, Appl	656	34	36.6	1189	2	US-09-972-175-2	Sequence 2, Appli
584	34	36.6	1184	1	US-08-239-476-32	Sequence 32, Appl	657	34	36.6	1189	2	US-09-972-175-4	Sequence 4, Appli
585	34	36.6	1184	1	US-08-639-923A-32	Sequence 32, Appl	658	34	36.6	1189	2	US-09-972-175-6	Sequence 6, Appli
586	34	36.6	1184	4	PCT-US95-05431-32	Sequence 32, Appl	659	34	36.6	1189	2	US-09-972-175-8	Sequence 8, Appli
587	34	36.6	1186	1	US-08-602-737-6	Sequence 6, Appli	660	34	36.6	1189	2	US-09-972-175-10	Sequence 10, Appl
588	34	36.6	1186	2	US-09-001-982-6	Sequence 6, Appli	661	34	36.6	1189	2	US-09-972-175-12	Sequence 12, Appl
589	34	36.6	1186	2	US-09-178-252-23	Sequence 23, Appl	662	34	36.6	1189	2	US-09-972-175-59	Sequence 59, Appl
590	34	36.6	1186	2	US-09-826-660-23	Sequence 23, Appl	663	34	36.6	1189	2	US-09-972-175-61	Sequence 61, Appl
591	34	36.6	1186	2	US-09-668-650-6	Sequence 6, Appli	664	34	36.6	1189	2	US-10-200-522-2	Sequence 2, Appli
592	34	36.6	1186	2	US-08-239-476-34	Sequence 34, Appl	665	34	36.6	1189	2	US-10-200-522-4	Sequence 4, Appli
593	34	36.6	1188	1	US-08-639-923A-34	Sequence 34, Appl	666	34	36.6	1189	2	US-10-200-522-6	Sequence 6, Appli
594	34	36.6	1188	1	PCT-US95-05431-34	Sequence 34, Appl	667	34	36.6	1189	2	US-10-200-522-8	Sequence 8, Appli
595	34	36.6	1188	4	5254799-7	Patent No. 5254799	668	34	36.6	1189	2	US-10-200-522-10	Sequence 10, Appl
596	34	36.6	1188	6	US-07-828-788A-16	Sequence 16, Appl	669	34	36.6	1189	2	US-10-200-522-12	Sequence 12, Appl
597	34	36.6	1189	1	US-08-356-034-6	Sequence 6, Appli	670	34	36.6	1189	2	US-10-200-522-59	Sequence 59, Appl
598	34	36.6	1189	1	US-08-602-737-2	Sequence 2, Appli	671	34	36.6	1189	2	US-10-200-522-61	Sequence 61, Appl
599	34	36.6	1189	1	US-08-980-071-2	Sequence 2, Appli	672	34	36.6	1189	2	US-09-661-016-8	Sequence 8, Appli
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603	34	36.6	1189	1	US-08-980-071-10	Sequence 10, Appl	676	34	36.6	1190	1	US-08-732-495-12	Sequence 12, Appl
604	34	36.6	1189	1	US-08-980-071-12	Sequence 12, Appl	677	34	36.6	1193	1	US-08-602-737-8	Sequence 8, Appli
605	34	36.6	1189	1	US-08-980-071-59	Sequence 59, Appl	678	34	36.6	1193	2	US-08-754-490-30	Sequence 30, Appl
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686	34	36.6	1193	2	US-09-916-956A-30	Sequence 30, Appl	759	33	35.5	188	2	US-09-438-185A-957	Sequence 957, App
687	34	36.6	1193	2	US-09-873-873-30	Sequence 30, Appl	760	33	35.5	192	2	US-09-828-310-11	Sequence 11, Appl
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689	34	36.6	1193	2	US-09-636-746B-30	Sequence 30, Appl	762	33	35.5	193	2	US-09-540-236-2960	Sequence 2960, Ap
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692	34	36.6	1193	2	US-10-817-182-30	Sequence 30, Appl	765	33	35.5	212	2	US-09-248-335-20	Sequence 20, Appl
693	34	36.6	1193	2	US-10-071-900-4	Sequence 4, Appli	766	33	35.5	215	2	US-09-270-767-62476	Sequence 62476, A
694	34	36.6	1193	2	US-10-672-163-30	Sequence 30, Appl	767	33	35.5	218	2	US-10-034-500A-2	Sequence 2, Appli
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704	34	36.6	2074	2	US-09-491-356C-9	Sequence 9, Appli	777	33	35.5	258	2	US-09-270-767-44625	Sequence 44625, A
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709	33.5	36.0	838	2	US-09-564-805-229	Sequence 229, App	782	33	35.5	283	2	US-09-248-796A-19476	Sequence 19476, A
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711	33.5	36.0	1942	2	US-09-949-016-8135	Sequence 8135, Ap	784	33	35.5	291	2	US-09-107-532A-4763	Sequence 4763, Ap
712	33	35.5	27	2	US-09-406-781-14	Sequence 14, Appl	785	33	35.5	294	2	US-09-949-016-6097	Sequence 6097, Ap
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715	33	35.5	28	2	US-09-880-132-11	Sequence 11, Appl	788	33	35.5	302	2	US-09-270-767-44347	Sequence 44347, A
716	33	35.5	29	2	US-09-406-781-52	Sequence 52, Appl	789	33	35.5	303	2	US-09-489-039A-11552	Sequence 11552, A
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725	33	35.5	74	2	US-09-187-789-63	Sequence 63, Appl	798	33	35.5	338	2	US-08-961-536-2	Sequence 2, Appli
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727	33	35.5	74	2	US-09-989-903-63	Sequence 63, Appl	800	33	35.5	338	2	US-09-432-682-2	Sequence 2, Appli
728	33	35.5	80	2	US-09-248-796A-23878	Sequence 23878, A	801	33	35.5	346	2	US-09-107-433-4305	Sequence 4305, Ap
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753	33	35.5	162	2	US-09-605-703B-814	Sequence 814, App	826	33	35.5	443	1	US-08-226-486-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 258, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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RESULT 2
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
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; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLVEEDQFSQNPISCFE 18

Db 32 VSLVEEDQFSQNPISCFE 49
RESULT 3
US-09-997-333-258
; Sequence 258, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 4
US-09-992-598-258
; Sequence 258, Application US/09992598

Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730PlC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 5
US-08-118-441-29
; Sequence 29, Application US/08118441
; Patent No. 5578493
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S DISEASE
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 29

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,441
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-118-441-29

Query Match 46.2%; Score 43; DB 1; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNP 13
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Db 590 VKLVERAQMKNP 602

RESULT 6
US-08-338-579A-29
; Sequence 29, Application US/08338579A
; Patent No. 6068975
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,579A
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400

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; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-579A-29

Query Match 46.2%; Score 43; DB 2; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNP 13
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Db 590 VKLVEEAQMSKNP 602

RESULT 7
PCT-US94-09851-29
; Sequence 29, Application PC/TUS9409851
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09851
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09851-29

Query Match 46.2%; Score 43; DB 4; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNP 13
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Db 590 VKLVEEAQMSKNP 602

RESULT 8
US-08-398-590A-40
; Sequence 40, Application US/08398590A
; Patent No. 5935811
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; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Schoenherr, Christopher J.
; TITLE OF INVENTION: Neuron-Restrictive Silencer Factor
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,590A
; FILING DATE: 03-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,445
; FILING DATE: 06-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-60897/RPT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-590A-40

Query Match 45.2%; Score 42; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLVEEDQFSQNPISC 16
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Db 284 STAEEDFSKGPIRC 298

RESULT 9
US-08-894-997-40
; Sequence 40, Application US/08894997A
; Patent No. 6270990
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Schoenherr, Christopher J.
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NRSF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
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; LOCATION: (1)..(676)
; OTHER INFORMATION: Human NSRF (partial)
US-08-894-997-40

Query Match          45.2%; Score 42; DB 2; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      2 SLVEEDQFSQNPISC 16
Db      284 STAEEDGFSKGPIRC 298

RESULT 10
US-09-873-155A-40
; Sequence 40, Application US/09873155A
; Patent No. 6824774
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: Antibodies That Bind Neuron Restrictive Silencer Factor
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 17810-502 CIPCON
; CURRENT APPLICATION NUMBER: US/09/873,155A
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 08/894,997
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: PCT/US96/02817
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 08/398,590
; PRIOR FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(676)
; OTHER INFORMATION: Human NSRF (partial)
US-09-873-155A-40

Query Match          45.2%; Score 42; DB 2; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      2 SLVEEDQFSQNPISC 16
Db      284 STAEEDGFSKGPIRC 298

RESULT 11
US-08-894-997-50
; Sequence 50, Application US/08894997A
; Patent No. 6270990
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NSRF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-08-894-997-50

Query Match          45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2 SLVEEDQFSQNPISC 16
Db      199 SPAEEDGFSKGPIRC 213

RESULT 12
US-09-873-155A-50
; Sequence 50, Application US/09873155A
; Patent No. 6824774
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: Antibodies That Bind Neuron Restrictive Silencer Factor
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 17810-502 CIPCON
; CURRENT APPLICATION NUMBER: US/09/873,155A
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 08/894,997
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: PCT/US96/02817
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 08/398,590
; PRIOR FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-09-873-155A-50

Query Match          45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2 SLVEEDQFSQNPISC 16
Db      199 SPAEEDGFSKGPIRC 213

RESULT 13
US-09-949-016-8616
; Sequence 8616, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8616
;; LENGTH: 1147
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8616

Query Match 45.2%; Score 42; DB 2; Length 1147;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLVEEDQFSQNPISC 16
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Db 254 STAEEDGFSKGPIRC 268

RESULT 14
US-08-231-193A-11
; Sequence 11, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-231-193A-11

Query Match 45.2%; Score 42; DB 1; Length 1464;
Best Local Similarity 46.7%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPIS 15
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Db 1018 VDSIRQDSLQNPVS 1032

RESULT 15
US-08-486-273A-11
; Sequence 11, Application US/08486273A
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-273A-11

Query Match 45.2%; Score 42; DB 1; Length 1464;
Best Local Similarity 46.7%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPIS 15
| : ||||: |
Db 1018 VDSIRQDSLQNPVS 1032

Search completed: December 22, 2005, 03:00:29
Job time : 26.4898 secs

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OM protein - protein search, using sw model

Run on: December 22, 2005, 03:01:15 ; Search time 21.6735 Seconds
(without alignments)
347.011 Million cell updates/sec

Perfect score: 93

Sequence: 1 VSLVEEDQFSQNPISCFE 18

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Minimum DB seq length: 0
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Listing first 1500 summaries

Database : Published Applications AA Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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28	93	100.0	229	3	US-09-997-428-258
75	93	100.0	229	4	US-10-087-192-66
564	93	100.0	229	4	US-10-174-587-198
628	93	100.0	229	4	US-10-063-742-48
743	93	100.0	229	4	US-10-755-889-508
744	93	100.0	229	5	US-10-972-317-48
746	93	100.0	229	5	US-10-950-374-258
749	70	75.3	228	4	US-10-331-053-33
750	70	75.3	230	4	US-10-087-192-63
751	45	48.4	410	6	US-11-097-143-8163
752	44	47.3	122	4	US-10-424-599-274225
753	44	47.3	1249	4	US-10-282-122A-63637
754	43	46.2	232	4	US-10-243-552-414
755	43	46.2	601	5	US-10-732-923-1910
756	43	46.2	601	5	US-10-732-923-1911
757	43	46.2	846	4	US-10-425-115-251730
758	42	45.2	104	4	US-10-425-115-239301
759	42	45.2	149	4	US-10-156-932-28
760	42	45.2	222	3	US-09-864-761-43249
761	42	45.2	222	5	US-10-473-127-239
762	42	45.2	564	6	US-11-051-668A-4
763	42	45.2	676	3	US-09-873-155-40
764	42	45.2	704	4	US-10-424-599-193941
765	42	45.2	875	5	US-10-450-763-50201
766	42	45.2	900	4	US-10-437-963-160639
767	42	45.2	926	6	US-11-051-668A-2
768	42	45.2	948	5	US-10-732-923-18695
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					Sequence 63637, A
					Sequence 414, App
					Sequence 1910, Ap
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					Sequence 251730,
					Sequence 239301,
					Sequence 28, Appl
					Sequence 43249, A
					Sequence 239, App
					Sequence 4, Appli
					Sequence 40, Appl
					Sequence 193941,
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					Sequence 160639,
					Sequence 2, Appli
					Sequence 18695, A

769	42	45.2	976	3	US-09-873-155-50	Sequence 50, Appl
770	42	45.2	1464	3	US-09-945-901-11	Sequence 11, Appl
771	42	45.2	1464	4	US-10-007-747-11	Sequence 11, Appl
772	42	45.2	1464	4	US-10-038-937-11	Sequence 11, Appl
773	42	45.2	1464	4	US-10-243-740-2	Sequence 2, Appli
774	42	45.2	1464	5	US-10-473-127-236	Sequence 236, App
775	42	45.2	1464	5	US-10-473-127-237	Sequence 237, App
776	42	45.2	1464	5	US-10-473-127-238	Sequence 238, App
777	42	45.2	1464	5	US-10-473-127-240	Sequence 240, App
778	42	45.2	1464	5	US-10-473-127-241	Sequence 241, App
779	42	45.2	1464	5	US-10-473-127-242	Sequence 242, App
780	42	45.2	1464	5	US-10-473-127-243	Sequence 243, App
781	42	45.2	1464	5	US-10-473-127-244	Sequence 244, App
782	42	45.2	1464	5	US-10-473-127-245	Sequence 245, App
783	42	45.2	1464	5	US-10-473-127-246	Sequence 246, App
784	42	45.2	1547	4	US-10-437-963-138161	Sequence 138161,
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786	41.5	44.6	93	4	US-10-424-599-169800	Sequence 169800,
787	41.5	44.6	355	4	US-10-282-122A-44248	Sequence 44248, A
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789	41	44.1	288	4	US-10-424-599-237495	Sequence 237495,
790	41	44.1	315	4	US-10-204-887-156	Sequence 156, App
791	41	44.1	559	4	US-10-437-963-153454	Sequence 153454,
792	41	44.1	597	4	US-10-369-493-3265	Sequence 3265, Ap
793	41	44.1	775	5	US-10-626-832-38	Sequence 38, Appl
794	41	44.1	925	4	US-10-055-569A-59	Sequence 59, Appl
795	40.5	43.5	374	4	US-10-424-599-175708	Sequence 175708,
796	40.5	43.5	792	4	US-10-282-122A-54746	Sequence 54746, A
797	40.5	43.5	797	4	US-10-289-762-636	Sequence 636, App
798	40	43.0	37	4	US-10-425-115-314304	Sequence 314304,
799	40	43.0	78	4	US-10-425-115-222565	Sequence 222565,
800	40	43.0	158	4	US-10-104-047-3221	Sequence 3221, Ap
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804	40	43.0	358	4	US-10-425-114-67490	Sequence 67490, A
805	40	43.0	430	4	US-10-107-431-45	Sequence 45, Appl
806	40	43.0	430	4	US-10-084-846A-62	Sequence 62, Appl
807	40	43.0	633	5	US-10-450-763-50620	Sequence 50620, A
808	40	43.0	712	4	US-10-425-115-301230	Sequence 301230,
809	40	43.0	735	4	US-10-471-601-1	Sequence 1, Appli
810	40	43.0	1591	4	US-10-408-765A-692	Sequence 692, App
811	40	43.0	1591	5	US-10-719-993-574	Sequence 574, App
812	40	43.0	19723	4	US-10-084-846A-5	Sequence 5, Appli
813	39	41.9	59	4	US-10-425-115-249658	Sequence 249658,
814	39	41.9	81	4	US-10-424-599-149221	Sequence 149221,
815	39	41.9	86	4	US-10-437-963-175906	Sequence 175906,
816	39	41.9	114	4	US-10-425-115-290441	Sequence 290441,
817	39	41.9	114	4	US-10-425-115-290442	Sequence 290442,
818	39	41.9	114	5	US-10-739-930-8234	Sequence 8234, Ap
819	39	41.9	115	4	US-10-425-115-185779	Sequence 185779,
820	39	41.9	152	6	US-11-097-143-2823	Sequence 2823, Ap
821	39	41.9	156	4	US-10-437-963-134249	Sequence 134249,
822	39	41.9	165	5	US-10-472-928-446	Sequence 446, App
823	39	41.9	183	4	US-10-424-599-206967	Sequence 206967,
824	39	41.9	189	4	US-10-767-701-34628	Sequence 34628, A
825	39	41.9	192	4	US-10-767-701-34049	Sequence 34049, A
826	39	41.9	198	4	US-10-282-122A-72375	Sequence 72375, A
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828	39	41.9	215	4	US-10-437-963-204025	Sequence 204025,
829	39	41.9	231	4	US-10-424-599-237693	Sequence 237693,
830	39	41.9	239	4	US-10-424-599-145085	Sequence 145085,
831	39	41.9	266	4	US-10-282-122A-59074	Sequence 59074, A
832	39	41.9	271	4	US-10-282-122A-72970	Sequence 72970, A
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834	39	41.9	300	5	US-10-450-763-56301	Sequence 56301, A
835	39	41.9	313	4	US-10-425-115-203474	Sequence 203474,
836	39	41.9	320	4	US-10-386-414-6	Sequence 6, Appli
837	39	41.9	328	6	US-11-097-143-29190	Sequence 29190, A
838	39	41.9	335	5	US-10-771-833-23	Sequence 23, Appl
839	39	41.9	335	5	US-10-886-949-23	Sequence 23, Appl
840	39	41.9	391	5	US-10-204-268A-4	Sequence 4, Appli
841	39	41.9	450	4	US-10-781-181-5	Sequence 5, Appli

842	39	41.9	450	5	US-10-204-268A-2	Sequence 2, Appli	915	38	40.9	653	4	US-10-029-386-33075	Sequence 33075, A
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844	39	41.9	502	4	US-10-386-414-4	Sequence 4, Appli	917	38	40.9	670	4	US-10-600-070-196	Sequence 196, App
845	39	41.9	502	4	US-10-311-104-1	Sequence 1, Appli	918	38	40.9	695	4	US-10-437-963-138212	Sequence 138212,
846	39	41.9	502	6	US-11-048-744-1	Sequence 1, Appli	919	38	40.9	709	4	US-10-424-599-160622	Sequence 160622,
847	39	41.9	502	6	US-11-048-068-1	Sequence 1, Appli	920	38	40.9	712	4	US-10-369-493-13008	Sequence 13008, A
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850	39	41.9	524	4	US-10-369-493-20784	Sequence 20784, A	923	38	40.9	772	4	US-10-369-493-2075	Sequence 2075, Ap
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853	39	41.9	661	5	US-10-617-320-3700	Sequence 3700, Ap	926	38	40.9	811	5	US-10-739-930-5643	Sequence 5643, Ap
854	39	41.9	739	4	US-10-425-114-50080	Sequence 50080, A	927	38	40.9	822	4	US-10-369-493-13052	Sequence 13052, A
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858	39	41.9	929	4	US-10-437-963-144160	Sequence 144160,	931	38	40.9	1068	5	US-10-951-579-3	Sequence 3, Appli
859	39	41.9	993	4	US-10-424-599-145074	Sequence 145074,	932	38	40.9	1192	4	US-10-437-963-192718	Sequence 192718,
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861	39	41.9	1012	4	US-10-437-963-115924	Sequence 115924,	934	38	40.9	1415	4	US-10-437-963-138129	Sequence 138129,
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863	39	41.9	2271	6	US-11-097-143-23640	Sequence 23640, A	936	38	40.9	1573	4	US-10-437-963-192716	Sequence 192716,
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865	38.5	41.4	355	5	US-10-616-550-8	Sequence 48, Appli	938	38	40.9	1609	4	US-10-437-963-138054	Sequence 138054,
866	38.5	41.4	355	5	US-10-616-550-48	Sequence 48, Appli	939	38	40.9	1678	4	US-10-437-963-138217	Sequence 138217,
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869	38.5	41.4	393	4	US-10-329-624-5248	Sequence 5248, Ap	942	38	40.9	1790	4	US-10-437-963-138166	Sequence 138166,
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871	38	40.9	70	4	US-10-330-051A-48	Sequence 48, Appli	944	37.5	40.3	15	4	US-10-213-821-184	Sequence 184, App
872	38	40.9	70	4	US-10-330-051A-60	Sequence 60, Appli	945	37.5	40.3	15	5	US-10-486-234-16	Sequence 16, Appl
873	38	40.9	100	4	US-10-335-977-9323	Sequence 9323, Ap	946	37	39.8	29	5	US-10-450-763-53068	Sequence 53068, A
874	38	40.9	100	4	US-10-335-977-9324	Sequence 9324, Ap	947	37	39.8	39	4	US-10-425-115-281144	Sequence 281144,
875	38	40.9	142	4	US-10-784-880-26	Sequence 26, Appli	948	37	39.8	42	3	US-09-864-761-42853	Sequence 42853, A
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883	38	40.9	228	4	US-10-424-599-228931	Sequence 228931,	956	37	39.8	85	4	US-10-437-963-154813	Sequence 154813,
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885	38	40.9	302	4	US-10-282-122A-45207	Sequence 45207, A	958	37	39.8	94	4	US-10-425-115-290655	Sequence 290655,
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889	38	40.9	334	5	US-10-886-949-22	Sequence 22, Appli	962	37	39.8	109	4	US-10-424-599-227209	Sequence 227209,
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898	38	40.9	424	5	US-10-380-437-53	Sequence 53, Appli	971	37	39.8	205	4	US-10-425-115-317163	Sequence 317163,
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912	38	40.9	591	5	US-10-644-765-195	Sequence 195, App	985	37	39.8	314	4	US-10-425-114-57186	Sequence 57186, A
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1002	37	39.8	370	4	US-10-004-860-558	Sequence 558, App	1075	36	38.7	14	4	US-10-283-423-184	Sequence 184, App
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1004	37	39.8	383	4	US-10-424-599-146603	Sequence 146603,	1077	36	38.7	15	4	US-10-283-423-185	Sequence 185, App
1005	37	39.8	393	3	US-09-840-787-11	Sequence 11, Appl	1078	36	38.7	15	4	US-10-213-821-185	Sequence 185, App
1006	37	39.8	393	3	US-09-977-418-12	Sequence 12, Appl	1079	36	38.7	29	4	US-10-323-069A-133	Sequence 133, App
1007	37	39.8	393	3	US-09-977-033A-12	Sequence 12, Appl	1080	36	38.7	29	5	US-10-851-965-133	Sequence 133, App
1008	37	39.8	393	3	US-09-977-751C-12	Sequence 12, Appl	1081	36	38.7	47	4	US-10-424-599-279991	Sequence 279991,
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1016	37	39.8	416	4	US-10-004-860-461	Sequence 461, App	1089	36	38.7	98	4	US-10-367-094-20	Sequence 20, Appl
1017	37	39.8	416	4	US-10-023-282-461	Sequence 461, App	1090	36	38.7	101	4	US-10-121-235-17	Sequence 17, Appl
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1019	37	39.8	435	4	US-10-276-774-1760	Sequence 1760, Ap	1092	36	38.7	101	5	US-10-900-399-4	Sequence 4, Appli
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1195	36	38.7	281	5	US-10-986-376-66	Sequence 66, Appl	1268	36	38.7	473	4	US-10-250-533-4	Sequence 4, Appli
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1500 35 37.6 443 4 US-10-369-493-2139 Sequence 2139, Ap

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Job time : 22.6735 secs

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OM protein - protein search, using sw model

Run on: December 22, 2005, 03:04:50 ; Search time 1.65306 Seconds
(without alignments)
77.661 Million cell updates/sec

Perfect score: 93

Sequence: 1 VSLVEDQFSQNPISCFE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:

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- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	36	38.7	281	6	US-10-821-234-1288
6	36	38.7	281	7	US-11-077-272-2
7	36	38.7	335	6	US-10-467-657-3818
8	36	38.7	352	6	US-10-793-626-216
9	36	38.7	573	6	US-10-467-657-684
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11	36	38.7	892	7	US-11-082-389-396
12	36	38.7	1259	6	US-10-467-657-5510
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19	35	37.6	902	7	US-11-144-987-12
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95	31	33.3	208	6	US-10-467-657-3050
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99	31	33.3	404	6	US-10-467-657-9211
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108	31	33.3	550	7	US-11-113-837-17	Sequence 17, Appl	184	30	32.3	1096	6	US-10-995-561-710	Sequence 710, App
109	31	33.3	577	6	US-10-623-155-500	Sequence 500, App	185	30	32.3	1210	7	US-11-113-202-6	Sequence 6, Appli
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121	31	33.3	3960	6	US-10-995-561-771	Sequence 771, App	196	29.5	31.7	346	6	US-10-467-657-5946	Sequence 5946, Ap
122	31	33.3	5335	6	US-10-995-561-777	Sequence 777, App	197	29.5	31.7	606	6	US-10-624-932-16	Sequence 16, Appl
123	31	33.3	5406	6	US-10-995-561-774	Sequence 774, App	198	29.5	31.7	606	6	US-10-624-932-18	Sequence 18, Appl
124	31	33.3	5415	6	US-10-995-561-779	Sequence 779, App	199	29.5	31.7	728	6	US-10-467-657-8376	Sequence 8376, Ap
125	31	33.3	5464	6	US-10-995-561-775	Sequence 775, App	200	29.5	31.7	864	7	US-11-194-246-343	Sequence 343, App
126	30.5	32.8	35	6	US-10-467-657-2610	Sequence 2610, Ap	201	29	31.2	38	7	US-11-068-783-78	Sequence 78, Appl
127	30.5	32.8	423	6	US-10-467-962B-85	Sequence 85, Appl	202	29	31.2	41	7	US-11-027-111-13	Sequence 13, Appl
128	30.5	32.8	1150	6	US-10-821-234-1083	Sequence 1083, Ap	203	29	31.2	41	7	US-11-027-111-18	Sequence 18, Appl
129	30	32.3	41	7	US-11-027-111-19	Sequence 19, Appl	204	29	31.2	66	6	US-10-467-657-7418	Sequence 7418, Ap
130	30	32.3	86	6	US-10-467-657-3962	Sequence 3962, Ap	205	29	31.2	125	6	US-10-793-626-1454	Sequence 1454, Ap
131	30	32.3	95	6	US-10-467-657-2136	Sequence 2136, Ap	206	29	31.2	158	7	US-11-055-822-730	Sequence 730, App
132	30	32.3	164	6	US-10-793-626-3040	Sequence 3040, Ap	207	29	31.2	176	6	US-10-467-657-1880	Sequence 1880, Ap
133	30	32.3	168	6	US-10-467-657-1066	Sequence 1066, Ap	208	29	31.2	189	6	US-10-793-626-2976	Sequence 2976, Ap
134	30	32.3	180	7	US-11-165-697-47	Sequence 47, Appl	209	29	31.2	189	6	US-10-793-626-3000	Sequence 3000, Ap
135	30	32.3	189	6	US-10-467-657-4902	Sequence 4902, Ap	210	29	31.2	192	5	US-09-940-308-4	Sequence 4, Appli
136	30	32.3	205	6	US-10-793-626-2510	Sequence 2510, Ap	211	29	31.2	196	6	US-10-793-626-778	Sequence 778, App
137	30	32.3	236	7	US-11-170-653-46	Sequence 46, Appl	212	29	31.2	230	7	US-11-055-822-1068	Sequence 1068, Ap
138	30	32.3	237	7	US-11-170-653-47	Sequence 47, Appl	213	29	31.2	236	7	US-11-091-100-15	Sequence 15, Appl
139	30	32.3	244	6	US-10-793-626-566	Sequence 566, App	214	29	31.2	237	6	US-10-454-437-310	Sequence 310, App
140	30	32.3	275	7	US-11-000-463-868	Sequence 868, App	215	29	31.2	242	6	US-10-467-657-5676	Sequence 5676, Ap
141	30	32.3	291	7	US-11-000-463-396	Sequence 396, App	216	29	31.2	254	6	US-10-878-556A-177	Sequence 177, App
142	30	32.3	317	6	US-10-689-742-166	Sequence 166, App	217	29	31.2	259	7	US-11-056-621-6	Sequence 6, Appli
143	30	32.3	318	6	US-10-632-150-42	Sequence 42, Appl	218	29	31.2	265	6	US-10-485-517-154	Sequence 154, App
144	30	32.3	318	7	US-11-073-457-42	Sequence 42, Appl	219	29	31.2	266	6	US-10-508-263-104	Sequence 104, App
145	30	32.3	318	7	US-11-073-460-42	Sequence 42, Appl	220	29	31.2	269	6	US-10-793-626-880	Sequence 880, App
146	30	32.3	320	6	US-10-793-626-2938	Sequence 2938, Ap	221	29	31.2	269	7	US-11-074-176-210	Sequence 210, App
147	30	32.3	331	7	US-11-167-856-6	Sequence 6, Appli	222	29	31.2	289	6	US-10-793-626-234	Sequence 234, App
148	30	32.3	339	6	US-10-485-517-367	Sequence 367, App	223	29	31.2	325	5	US-09-940-308-8	Sequence 8, Appli
149	30	32.3	352	6	US-10-467-657-2438	Sequence 2438, Ap	224	29	31.2	332	6	US-10-793-626-540	Sequence 540, App
150	30	32.3	360	6	US-10-995-561-547	Sequence 547, App	225	29	31.2	332	6	US-10-793-626-2562	Sequence 2562, Ap
151	30	32.3	366	7	US-11-091-334-9	Sequence 9, Appli	226	29	31.2	348	6	US-10-793-626-2866	Sequence 2866, Ap
152	30	32.3	387	7	US-11-137-465-57	Sequence 57, Appl	227	29	31.2	367	7	US-11-012-762-60	Sequence 60, Appli
153	30	32.3	388	6	US-10-467-657-58	Sequence 58, Appl	228	29	31.2	389	5	US-09-940-308-6	Sequence 6, Appli
154	30	32.3	388	6	US-10-467-657-1864	Sequence 1864, Ap	229	29	31.2	392	6	US-10-467-657-1784	Sequence 1784, Ap
155	30	32.3	391	7	US-11-055-822-60	Sequence 60, Appl	230	29	31.2	393	5	US-09-940-308-7	Sequence 7, Appli
156	30	32.3	391	7	US-11-055-822-300	Sequence 300, App	231	29	31.2	398	7	US-11-132-142-7	Sequence 7, Appli
157	30	32.3	391	7	US-11-055-822-328	Sequence 328, App	232	29	31.2	406	6	US-10-821-234-1026	Sequence 1026, Ap
158	30	32.3	404	6	US-10-793-626-1130	Sequence 1130, Ap	233	29	31.2	408	6	US-10-467-657-2848	Sequence 2848, Ap
159	30	32.3	406	7	US-11-167-856-14	Sequence 14, Appl	234	29	31.2	410	6	US-10-793-626-3258	Sequence 3258, Ap
161	30	32.3	516	7	US-11-135-604-2	Sequence 2, Appli	236	29	31.2	437	6	US-10-967-648A-4	Sequence 4, Appli
162	30	32.3	532	7	US-11-135-604-4	Sequence 4, Appli	237	29	31.2	445	6	US-10-793-626-2858	Sequence 2858, Ap
163	30	32.3	534	7	US-11-082-389-348	Sequence 348, App	238	29	31.2	445	6	US-10-858-730-4	Sequence 4, Appli
164	30	32.3	537	7	US-11-135-604-6	Sequence 6, Appli	239	29	31.2	476	6	US-10-999-866-39	Sequence 39, Appl
166	30	32.3	670	6	US-10-995-561-528	Sequence 528, App	240	29	31.2	476	7	US-11-061-821-39	Sequence 39, Appl
167	30	32.3	727	6	US-10-793-626-2862	Sequence 2862, Ap	241	29	31.2	477	6	US-10-793-626-3250	Sequence 3250, Ap
168	30	32.3	753	7	US-11-137-465-51	Sequence 51, Appl	242	29	31.2	479	7	US-11-024-251-33	Sequence 33, Appl
169	30	32.3	766	6	US-10-793-626-420	Sequence 420, App	243	29	31.2	497	6	US-10-793-626-1624	Sequence 1624, Ap
170	30	32.3	782	6	US-10-793-626-2352	Sequence 2352, Ap	244	29	31.2	532	6	US-10-467-657-820	Sequence 820, App
171	30	32.3	783	7	US-11-082-389-354	Sequence 354, App	245	29	31.2	540	6	US-10-821-234-1395	Sequence 1395, Ap
172	30	32.3	821	7	US-11-087-227-90	Sequence 90, Appl	246	29	31.2	543	6	US-10-858-730-221	Sequence 221, App
173	30	32.3	845	7	US-11-147-047-46	Sequence 46, Appl	247	29	31.2	557	6	US-10-793-626-1486	Sequence 1486, Ap
174	30	32.3	852	6	US-10-645-441-15	Sequence 15, Appl	248	29	31.2	590	5	US-09-940-308-2	Sequence 2, Appli
175	30	32.3	853	6	US-10-420-192-6	Sequence 6, Appli	249	29	31.2	680	6	US-10-467-962B-101	Sequence 101, Appl
176	30	32.3	859	7	US-11-188-743-16	Sequence 16, Appl	250	29	31.2	697	6	US-10-485-517-202	Sequence 202, App

251	29	31.2	701	7	US-11-055-822-1066	Sequence 1066, Ap	324	28	30.1	175	6	US-10-821-234-1543	Sequence 1543, Ap
252	29	31.2	777	6	US-10-821-234-1658	Sequence 1658, Ap	325	28	30.1	197	5	US-09-940-308-3	Sequence 3, Appli
253	29	31.2	782	6	US-10-821-234-1592	Sequence 1592, Ap	327	28	30.1	200	6	US-10-878-556A-64	Sequence 64, Appl
254	29	31.2	791	7	US-11-056-621-4	Sequence 4, Appli	328	28	30.1	200	7	US-11-069-642-131	Sequence 131, App
255	29	31.2	805	6	US-10-518-599-24	Sequence 24, Appl	329	28	30.1	204	6	US-10-793-626-692	Sequence 692, App
256	29	31.2	810	6	US-10-995-561-761	Sequence 761, App	330	28	30.1	207	6	US-10-793-626-3290	Sequence 3290, Ap
257	29	31.2	810	6	US-10-220-824-2	Sequence 2, Appli	331	28	30.1	210	6	US-10-467-657-4386	Sequence 4386, Ap
258	29	31.2	812	7	US-11-010-874-1	Sequence 1, Appli	332	28	30.1	211	6	US-10-493-864A-1	Sequence 1, Appli
259	29	31.2	866	7	US-11-147-047-32	Sequence 32, Appl	333	28	30.1	211	6	US-10-493-864A-2	Sequence 2, Appli
260	29	31.2	924	6	US-10-857-780-20	Sequence 20, Appl	334	28	30.1	212	6	US-10-793-626-1128	Sequence 1128, Ap
261	29	31.2	924	7	US-11-107-028-26	Sequence 26, Appl	335	28	30.1	218	6	US-10-467-657-7818	Sequence 7818, Ap
262	29	31.2	983	7	US-11-113-424-59	Sequence 59, Appl	336	28	30.1	218	7	US-11-060-920-2	Sequence 2, Appli
263	29	31.2	1065	7	US-11-191-374-16	Sequence 16, Appl	337	28	30.1	240	7	US-11-170-653-38	Sequence 38, Appl
264	29	31.2	1065	7	US-11-191-375-16	Sequence 16, Appl	338	28	30.1	257	7	US-11-135-855-42	Sequence 42, Appl
265	29	31.2	1069	7	US-11-191-374-17	Sequence 17, Appl	339	28	30.1	257	7	US-11-159-597-6	Sequence 6, Appli
266	29	31.2	1069	7	US-11-191-375-17	Sequence 17, Appl	340	28	30.1	268	6	US-10-467-657-1564	Sequence 1564, Ap
267	29	31.2	1169	6	US-10-995-561-609	Sequence 609, App	341	28	30.1	269	6	US-10-467-657-330	Sequence 330, App
268	29	31.2	1386	7	US-11-091-643-6	Sequence 6, Appli	342	28	30.1	275	7	US-11-159-597-8	Sequence 8, Appli
269	29	31.2	1481	7	US-11-077-386-30	Sequence 30, Appl	343	28	30.1	277	7	US-11-159-597-4	Sequence 4, Appli
270	29	31.2	1618	6	US-10-984-645-2	Sequence 2, Appli	344	28	30.1	279	7	US-11-159-597-10	Sequence 10, Appl
271	29	31.2	1798	7	US-11-080-991-96	Sequence 96, Appl	345	28	30.1	288	6	US-10-793-626-2914	Sequence 2914, Ap
272	29	31.2	1960	7	US-11-077-386-29	Sequence 29, Appl	346	28	30.1	289	6	US-10-793-626-3254	Sequence 3254, Ap
273	29	31.2	2061	7	US-11-077-386-27	Sequence 27, Appl	347	28	30.1	289	6	US-10-467-657-3878	Sequence 3878, Ap
274	29	31.2	2314	7	US-11-097-728-2	Sequence 2, Appli	348	28	30.1	293	7	US-11-092-168-11	Sequence 11, Appl
275	29	31.2	2353	7	US-11-097-728-6	Sequence 6, Appli	349	28	30.1	300	6	US-10-793-626-1900	Sequence 1900, Ap
276	28.5	30.6	107	7	US-11-107-028-40	Sequence 40, Appl	350	28	30.1	313	6	US-10-793-626-2892	Sequence 2892, Ap
277	28.5	30.6	107	7	US-11-107-028-42	Sequence 42, Appl	351	28	30.1	313	6	US-10-793-626-3146	Sequence 3146, Ap
278	28.5	30.6	165	6	US-10-467-657-1444	Sequence 1444, Ap	352	28	30.1	316	7	US-11-074-176-358	Sequence 358, App
279	28.5	30.6	213	7	US-11-172-320-4	Sequence 4, Appli	353	28	30.1	320	6	US-10-454-437-252	Sequence 252, App
280	28.5	30.6	213	7	US-11-173-969-4	Sequence 8, Appli	354	28	30.1	327	6	US-10-512-184-64	Sequence 64, Appl
281	28.5	30.6	213	7	US-11-173-969-8	Sequence 8, Appli	355	28	30.1	330	6	US-10-689-742-82	Sequence 82, Appl
282	28.5	30.6	213	7	US-11-173-969-8	Sequence 8, Appli	356	28	30.1	332	7	US-11-074-176-230	Sequence 230, App
283	28.5	30.6	221	6	US-10-793-626-2216	Sequence 2216, Ap	357	28	30.1	334	6	US-10-467-657-2542	Sequence 2542, Ap
284	28.5	30.6	592	7	US-11-135-855-24	Sequence 24, Appl	358	28	30.1	339	6	US-10-467-657-4318	Sequence 4318, Ap
285	28.5	30.6	693	6	US-10-995-561-632	Sequence 632, App	359	28	30.1	354	7	US-11-053-100-27	Sequence 27, Appl
286	28.5	30.6	847	6	US-10-995-561-634	Sequence 634, App	360	28	30.1	356	7	US-11-053-100-36	Sequence 36, Appl
287	28.5	30.6	919	6	US-10-858-730-206	Sequence 206, App	361	28	30.1	357	7	US-11-053-100-30	Sequence 30, Appl
288	28.5	30.6	1259	6	US-10-995-561-625	Sequence 625, App	362	28	30.1	357	7	US-11-053-100-33	Sequence 33, Appl
289	28.5	30.6	1286	6	US-10-995-561-628	Sequence 628, App	363	28	30.1	360	7	US-11-069-185-7	Sequence 7, Appli
290	28.5	30.6	1315	6	US-10-995-561-630	Sequence 630, App	364	28	30.1	362	7	US-11-010-874-18	Sequence 18, Appl
291	28.5	30.6	1341	6	US-10-995-561-621	Sequence 621, App	365	28	30.1	370	6	US-10-821-234-1502	Sequence 1502, Ap
292	28.5	30.6	1348	6	US-10-995-561-624	Sequence 624, App	366	28	30.1	379	6	US-10-793-626-2810	Sequence 2810, Ap
293	28.5	30.6	2296	6	US-10-995-561-633	Sequence 633, App	367	28	30.1	380	6	US-10-793-626-702	Sequence 702, App
294	28.5	30.6	2355	6	US-10-995-561-623	Sequence 623, App	368	28	30.1	383	6	US-10-793-626-2426	Sequence 2426, Ap
295	28.5	30.6	2355	6	US-10-995-561-627	Sequence 627, App	369	28	30.1	399	6	US-10-467-657-1672	Sequence 1672, Ap
296	28.5	30.6	2384	6	US-10-821-234-1545	Sequence 1545, Ap	370	28	30.1	402	6	US-10-454-437-282	Sequence 282, App
297	28.5	30.6	2386	6	US-10-995-561-626	Sequence 626, App	371	28	30.1	410	6	US-10-821-234-1180	Sequence 1180, Ap
298	28	30.1	14	6	US-10-632-645-15	Sequence 15, Appl	372	28	30.1	416	6	US-10-793-626-2402	Sequence 2402, Ap
299	28	30.1	15	7	US-11-045-024-13396	Sequence 13396, A	373	28	30.1	418	6	US-10-821-234-1331	Sequence 1331, Ap
300	28	30.1	20	7	US-11-022-562-290	Sequence 290, App	374	28	30.1	418	7	US-11-077-716-2	Sequence 2, Appli
301	28	30.1	20	7	US-11-022-562-291	Sequence 291, App	375	28	30.1	431	7	US-11-092-140-6	Sequence 6, Appli
302	28	30.1	34	7	US-11-112-277-6	Sequence 6, Appli	376	28	30.1	433	7	US-11-082-389-332	Sequence 332, App
303	28	30.1	34	7	US-11-112-277-8	Sequence 8, Appli	377	28	30.1	439	6	US-10-467-657-3034	Sequence 3034, Ap
304	28	30.1	34	7	US-11-112-277-36	Sequence 36, Appl	378	28	30.1	451	6	US-10-467-657-516	Sequence 516, App
305	28	30.1	34	7	US-11-112-277-38	Sequence 38, Appl	379	28	30.1	466	7	US-11-074-176-58	Sequence 58, Appl
306	28	30.1	35	7	US-11-112-277-7	Sequence 7, Appli	380	28	30.1	495	6	US-10-467-657-3844	Sequence 3844, Ap
307	28	30.1	35	7	US-11-112-277-37	Sequence 37, Appl	381	28	30.1	504	7	US-11-053-100-28	Sequence 28, Appl
308	28	30.1	36	7	US-11-029-003-1	Sequence 1, Appli	382	28	30.1	506	7	US-11-053-100-37	Sequence 37, Appl
309	28	30.1	37	7	US-11-112-277-33	Sequence 33, Appl	383	28	30.1	507	7	US-11-053-100-31	Sequence 31, Appl
310	28	30.1	41	6	US-10-986-501-311	Sequence 311, App	384	28	30.1	507	7	US-11-053-100-34	Sequence 34, Appl
311	28	30.1	41	7	US-11-027-111-15	Sequence 15, Appl	385	28	30.1	524	7	US-11-069-642-13	Sequence 13, Appl
312	28	30.1	44	7	US-11-089-426-10	Sequence 10, Appl	386	28	30.1	543	7	US-11-106-672A-10	Sequence 10, Appl
313	28	30.1	52	6	US-10-512-184-39	Sequence 39, Appl	387	28	30.1	565	6	US-10-793-626-2608	Sequence 2608, Ap
314	28	30.1	57	6	US-10-467-657-5780	Sequence 5780, Ap	388	28	30.1	591	6	US-10-485-517-332	Sequence 332, App
315	28	30.1	62	6	US-10-493-864A-9	Sequence 9, Appli	389	28	30.1	592	7	US-11-106-672A-14	Sequence 14, Appl
316	28	30.1	115	6	US-10-493-864A-4	Sequence 4, Appli	392	28	30.1	620	7	US-11-055-822-460	Sequence 460, App
317	28	30.1	117	6	US-10-821-234-1253	Sequence 1253, Ap	393	28	30.1	620	7	US-11-055-822-702	Sequence 702, App
318	28	30.1	138	6	US-10-467-657-6758	Sequence 6758, Ap	394	28	30.1	639	7	US-11-113-837-21	Sequence 21, Appl
319	28	30.1	159	6	US-10-467-657-6756	Sequence 6756, Ap	395	28	30.1	645	6	US-10-793-626-1770	Sequence 1770, Ap
320	28	30.1	174	6	US-10-984-376-9	Sequence 9, Appli	396	28	30.1	651	6	US-10-821-234-1666	Sequence 1666, Ap
321	28	30.1	174	6	US-10-984-376-10	Sequence 10, Appl	397	28	30.1	654	7	US-11-053-100-29	Sequence 29, Appl
322	28	30.1	174	6	US-10-984-376-11	Sequence 11, Appl	398	28	30.1	656	7	US-11-053-100-38	Sequence 38, Appl
323	28	30.1	174	6	US-10-984-376-12	Sequence 12, Appl	399	28	30.1	657	7	US-11-053-100-32	Sequence 32, Appl

400	28	30.1	657	7	US-11-053-100-35	Sequence 35, Appl	475	27.5	29.6	1099	6	US-10-873-528-11	Sequence 11, Appl
402	28	30.1	747	7	US-11-182-592-2	Sequence 2, Appl1	476	27.5	29.6	1263	6	US-10-485-517-127	Sequence 127, App
403	28	30.1	752	7	US-11-080-991-52	Sequence 52, Appl	477	27	29.0	15	7	US-11-022-562-39	Sequence 39, Appl
404	28	30.1	756	7	US-11-188-743-20	Sequence 20, Appl	478	27	29.0	15	7	US-11-045-024-13399	Sequence 13399, A
405	28	30.1	783	7	US-11-186-284-59	Sequence 59, Appl	479	27	29.0	35	7	US-11-148-108-48	Sequence 48, Appl
406	28	30.1	801	6	US-10-454-437-278	Sequence 278, App	480	27	29.0	51	6	US-10-467-657-5132	Sequence 5132, Ap
407	28	30.1	807	7	US-11-102-240-98	Sequence 98, Appl	481	27	29.0	53	6	US-10-467-657-2666	Sequence 2666, Ap
408	28	30.1	843	6	US-10-645-441-7	Sequence 7, Appl1	482	27	29.0	61	7	US-11-157-049-34	Sequence 34, Appl
409	28	30.1	856	6	US-10-510-947-8	Sequence 8, Appl1	483	27	29.0	70	6	US-10-821-234-1394	Sequence 1394, Ap
410	28	30.1	856	7	US-11-042-988-13	Sequence 13, Appl	484	27	29.0	70	6	US-10-467-657-9208	Sequence 9208, Ap
411	28	30.1	863	6	US-10-793-626-2010	Sequence 2010, Ap	485	27	29.0	73	7	US-11-157-049-35	Sequence 35, Appl
412	28	30.1	872	7	US-11-077-550-145	Sequence 145, App	486	27	29.0	75	6	US-10-467-657-8895	Sequence 8895, Ap
413	28	30.1	879	7	US-11-077-550-143	Sequence 143, App	487	27	29.0	78	6	US-10-467-657-4846	Sequence 4846, Ap
414	28	30.1	881	7	US-11-191-374-12	Sequence 12, Appl	488	27	29.0	97	7	US-11-157-049-26	Sequence 26, Appl
415	28	30.1	881	7	US-11-191-375-12	Sequence 12, Appl	489	27	29.0	99	7	US-11-090-439-56	Sequence 56, Appl
416	28	30.1	887	7	US-11-077-550-147	Sequence 147, App	490	27	29.0	105	7	US-11-096-074-55	Sequence 55, Appl
417	28	30.1	896	7	US-11-192-219-3	Sequence 3, Appl1	491	27	29.0	116	7	US-11-194-246-389	Sequence 389, App
418	28	30.1	898	7	US-11-166-730-3	Sequence 3, Appl1	492	27	29.0	123	7	US-11-082-389-110	Sequence 110, App
419	28	30.1	923	7	US-11-192-219-4	Sequence 4, Appl1	493	27	29.0	128	7	US-11-157-049-42	Sequence 42, Appl
420	28	30.1	934	7	US-11-108-864-19	Sequence 19, Appl	494	27	29.0	142	6	US-10-821-234-1235	Sequence 1235, Ap
421	28	30.1	937	7	US-11-017-550-66	Sequence 66, Appl	495	27	29.0	148	6	US-10-995-561-678	Sequence 678, App
422	28	30.1	979	6	US-10-636-320-6	Sequence 6, Appl1	496	27	29.0	150	6	US-10-793-626-2324	Sequence 2324, Ap
423	28	30.1	998	6	US-10-510-524-1	Sequence 1, Appl1	497	27	29.0	150	6	US-10-467-657-8879	Sequence 8879, Ap
424	28	30.1	1006	6	US-10-793-626-154	Sequence 154, App	499	27	29.0	151	7	US-11-082-389-108	Sequence 108, App
425	28	30.1	1068	7	US-11-191-374-45	Sequence 45, Appl	500	27	29.0	151	7	US-11-082-389-372	Sequence 372, App
426	28	30.1	1068	7	US-11-191-375-45	Sequence 45, Appl	501	27	29.0	151	7	US-11-157-049-38	Sequence 38, Appl
427	28	30.1	1165	7	US-11-192-219-2	Sequence 2, Appl1	502	27	29.0	153	7	US-11-157-049-41	Sequence 41, Appl
429	28	30.1	1315	7	US-11-077-550-141	Sequence 141, App	503	27	29.0	154	7	US-11-157-049-37	Sequence 37, Appl
430	28	30.1	1388	6	US-10-821-234-1143	Sequence 1143, Ap	504	27	29.0	156	6	US-10-467-657-5798	Sequence 5798, Ap
431	28	30.1	1493	7	US-11-004-057-4	Sequence 4, Appl1	505	27	29.0	157	7	US-11-157-049-43	Sequence 43, Appl
432	28	30.1	1493	7	US-11-080-991-56	Sequence 56, Appl	506	27	29.0	158	7	US-11-157-049-36	Sequence 36, Appl
433	28	30.1	2011	7	US-11-080-991-56	Sequence 56, Appl	507	27	29.0	158	7	US-11-157-049-40	Sequence 40, Appl
434	28	30.1	2769	7	US-11-113-424-14	Sequence 14, Appl	508	27	29.0	160	7	US-11-157-049-14	Sequence 14, Appl
435	28	30.1	5024	6	US-10-793-626-2964	Sequence 2964, Ap	509	27	29.0	160	7	US-11-157-049-15	Sequence 15, Appl
436	27.5	29.6	60	7	US-11-000-463-363	Sequence 363, App	510	27	29.0	160	7	US-11-157-049-16	Sequence 16, Appl
437	27.5	29.6	60	7	US-11-000-463-835	Sequence 835, App	511	27	29.0	160	7	US-11-157-049-17	Sequence 17, Appl
438	27.5	29.6	102	7	US-11-053-076-289	Sequence 289, App	512	27	29.0	160	7	US-11-157-049-18	Sequence 18, Appl
439	27.5	29.6	103	7	US-11-053-076-206	Sequence 206, App	513	27	29.0	160	7	US-11-157-049-19	Sequence 19, Appl
440	27.5	29.6	109	6	US-10-793-626-2540	Sequence 2540, Ap	514	27	29.0	160	7	US-11-157-049-20	Sequence 20, Appl
441	27.5	29.6	117	7	US-11-053-076-292	Sequence 292, App	515	27	29.0	160	7	US-11-157-049-21	Sequence 21, Appl
442	27.5	29.6	122	7	US-11-053-076-290	Sequence 290, App	516	27	29.0	160	7	US-11-157-049-22	Sequence 22, Appl
443	27.5	29.6	125	7	US-11-053-076-291	Sequence 291, App	517	27	29.0	160	7	US-11-157-049-23	Sequence 23, Appl
444	27.5	29.6	141	6	US-10-467-657-2620	Sequence 2620, Ap	518	27	29.0	160	7	US-11-157-049-24	Sequence 24, Appl
445	27.5	29.6	243	6	US-10-467-657-4442	Sequence 4442, Ap	519	27	29.0	160	7	US-11-157-049-25	Sequence 25, Appl
446	27.5	29.6	249	7	US-11-054-515-1160	Sequence 1160, Ap	520	27	29.0	160	7	US-11-157-049-39	Sequence 39, Appl
447	27.5	29.6	250	7	US-11-054-515-1159	Sequence 1159, Ap	521	27	29.0	172	6	US-10-821-234-1588	Sequence 1588, Ap
448	27.5	29.6	251	7	US-11-054-515-890	Sequence 890, App	522	27	29.0	174	6	US-10-984-376-7	Sequence 7, Appl1
449	27.5	29.6	251	7	US-11-054-515-891	Sequence 891, App	523	27	29.0	174	6	US-10-984-376-8	Sequence 8, Appl1
450	27.5	29.6	251	7	US-11-054-515-894	Sequence 894, App	525	27	29.0	180	7	US-11-157-049-2	Sequence 2, Appl1
451	27.5	29.6	251	7	US-11-054-515-903	Sequence 903, App	526	27	29.0	180	7	US-11-157-049-12	Sequence 12, Appl
452	27.5	29.6	251	7	US-11-054-515-910	Sequence 910, App	527	27	29.0	196	6	US-10-353-783-40	Sequence 40, Appl
453	27.5	29.6	251	7	US-11-054-515-1121	Sequence 1121, Ap	528	27	29.0	197	6	US-10-699-742-11	Sequence 11, Appl
454	27.5	29.6	251	7	US-11-054-515-1126	Sequence 1126, Ap	529	27	29.0	198	6	US-10-793-626-2792	Sequence 2792, Ap
455	27.5	29.6	251	7	US-11-054-515-1127	Sequence 1127, Ap	530	27	29.0	199	6	US-10-821-234-950	Sequence 950, App
456	27.5	29.6	251	7	US-11-054-515-1140	Sequence 1140, Ap	531	27	29.0	207	6	US-10-878-556A-93	Sequence 93, Appl
457	27.5	29.6	251	7	US-11-054-515-1141	Sequence 1141, Ap	532	27	29.0	221	7	US-11-067-425A-74	Sequence 74, Appl
458	27.5	29.6	251	7	US-11-054-515-1147	Sequence 1147, Ap	533	27	29.0	224	7	US-11-055-822-858	Sequence 858, App
459	27.5	29.6	251	7	US-11-054-515-1148	Sequence 1148, Ap	534	27	29.0	227	6	US-10-467-657-2624	Sequence 2624, Ap
460	27.5	29.6	251	7	US-11-054-515-1149	Sequence 1149, Ap	535	27	29.0	228	6	US-10-793-626-1862	Sequence 1862, Ap
461	27.5	29.6	251	7	US-11-054-515-1151	Sequence 1151, Ap	536	27	29.0	228	7	US-10-793-626-1862	Sequence 136, App
462	27.5	29.6	251	7	US-11-054-515-1152	Sequence 1152, Ap	537	27	29.0	231	6	US-10-467-657-1084	Sequence 1084, Ap
463	27.5	29.6	251	7	US-11-054-515-1157	Sequence 1157, Ap	538	27	29.0	234	7	US-11-100-183-36	Sequence 36, Appl
464	27.5	29.6	251	7	US-11-054-515-1162	Sequence 1162, Ap	539	27	29.0	238	6	US-10-793-626-3126	Sequence 3126, Ap
465	27.5	29.6	251	7	US-11-054-515-1166	Sequence 1166, Ap	540	27	29.0	238	6	US-10-793-626-3152	Sequence 3152, Ap
466	27.5	29.6	251	7	US-11-054-515-1373	Sequence 1373, Ap	541	27	29.0	241	7	US-11-082-389-20	Sequence 20, Appl
467	27.5	29.6	279	6	US-10-467-657-1310	Sequence 1310, Ap	542	27	29.0	242	6	US-10-821-234-1078	Sequence 1078, Ap
468	27.5	29.6	279	7	US-11-102-497-8	Sequence 8, Appl1	543	27	29.0	251	6	US-10-663-794-4	Sequence 4, Appl1
469	27.5	29.6	397	7	US-11-060-008-8	Sequence 8, Appl1	544	27	29.0	257	6	US-10-467-657-5118	Sequence 5118, Ap
470	27.5	29.6	420	6	US-10-992-577-6	Sequence 6, Appl1	545	27	29.0	261	7	US-11-000-463-715	Sequence 715, App
471	27.5	29.6	522	6	US-10-510-018-2	Sequence 2, Appl1	546	27	29.0	263	6	US-10-793-626-332	Sequence 332, App
472	27.5	29.6	540	6	US-10-770-726-80	Sequence 80, Appl	547	27	29.0	263	6	US-10-793-626-2750	Sequence 2750, Ap
473	27.5	29.6	641	6	US-10-821-234-1519	Sequence 1519, Ap	548	27	29.0	268	7	US-11-055-822-314	Sequence 314, App
474	27.5	29.6	641	6	US-10-491-096-189	Sequence 189, App	549	27	29.0	269	6	US-10-495-597-3	Sequence 3, Appl1

550	27	29.0	269	7	US-11-055-822-856	Sequence 856, App	625	27	29.0	725	6	US-10-995-561-938	Sequence 938, App
551	27	29.0	273	6	US-10-353-783-42	Sequence 42, Appl	626	27	29.0	743	6	US-10-467-657-4082	Sequence 4082, Ap
552	27	29.0	273	6	US-10-353-783-54	Sequence 54, Appl	627	27	29.0	751	7	US-11-012-762-26	Sequence 26, Appl
553	27	29.0	284	6	US-10-793-626-1426	Sequence 1426, Ap	628	27	29.0	758	6	US-10-467-962B-12	Sequence 12, Appl
554	27	29.0	284	6	US-10-793-626-2790	Sequence 2790, Ap	629	27	29.0	760	6	US-10-821-234-1141	Sequence 1141, Ap
555	27	29.0	289	6	US-10-467-657-1762	Sequence 1762, Ap	630	27	29.0	766	7	US-11-147-047-27	Sequence 27, Appl
557	27	29.0	301	7	US-11-055-822-1062	Sequence 1062, Ap	631	27	29.0	771	7	US-11-147-047-34	Sequence 34, Appl
558	27	29.0	307	6	US-10-793-626-522	Sequence 522, App	632	27	29.0	799	7	US-11-074-176-348	Sequence 348, App
559	27	29.0	315	6	US-10-467-657-7848	Sequence 7848, Ap	633	27	29.0	805	7	US-11-074-176-172	Sequence 172, App
560	27	29.0	317	6	US-10-821-234-1529	Sequence 1529, Ap	634	27	29.0	829	7	US-11-090-739-122	Sequence 122, App
561	27	29.0	319	6	US-10-467-657-3252	Sequence 3252, Ap	635	27	29.0	829	7	US-11-186-284-18	Sequence 18, Appl
562	27	29.0	325	7	US-11-074-176-368	Sequence 368, App	636	27	29.0	830	6	US-10-995-561-899	Sequence 899, App
563	27	29.0	339	6	US-10-957-569-61	Sequence 61, Appl	637	27	29.0	863	7	US-11-097-749-2	Sequence 2, Appli
564	27	29.0	344	7	US-11-055-822-516	Sequence 516, App	638	27	29.0	865	6	US-10-467-962B-33	Sequence 33, Appl
565	27	29.0	356	6	US-10-980-388-70	Sequence 70, Appl	639	27	29.0	903	6	US-10-689-742-142	Sequence 142, App
566	27	29.0	356	6	US-10-467-657-1210	Sequence 1210, Ap	640	27	29.0	914	7	US-11-108-172-1066	Sequence 1066, Ap
567	27	29.0	357	7	US-11-194-246-282	Sequence 282, App	641	27	29.0	914	7	US-11-148-108-41	Sequence 41, Appl
568	27	29.0	359	6	US-10-995-561-712	Sequence 712, App	642	27	29.0	918	6	US-10-995-561-696	Sequence 696, App
569	27	29.0	359	6	US-10-995-561-716	Sequence 716, App	643	27	29.0	950	6	US-10-467-657-854	Sequence 854, App
570	27	29.0	361	7	US-11-012-762-54	Sequence 54, Appl	644	27	29.0	984	7	US-11-113-424-60	Sequence 60, Appl
571	27	29.0	362	7	US-11-012-762-56	Sequence 56, Appl	645	27	29.0	987	6	US-10-770-726-61	Sequence 61, Appl
572	27	29.0	374	6	US-10-467-657-3786	Sequence 3786, Ap	646	27	29.0	995	7	US-11-113-424-62	Sequence 62, Appl
573	27	29.0	382	6	US-10-995-561-926	Sequence 926, App	647	27	29.0	1022	7	US-11-186-284-163	Sequence 163, App
574	27	29.0	383	6	US-10-793-626-3110	Sequence 3110, Ap	648	27	29.0	1032	7	US-11-014-367-3	Sequence 3, Appli
575	27	29.0	388	6	US-10-995-561-713	Sequence 713, App	649	27	29.0	1035	6	US-10-995-561-557	Sequence 557, App
576	27	29.0	391	7	US-11-084-624-14	Sequence 14, Appl	650	27	29.0	1070	7	US-11-147-047-49	Sequence 49, Appl
577	27	29.0	394	6	US-10-995-561-714	Sequence 714, App	651	27	29.0	1113	7	US-11-067-811-4	Sequence 4, Appli
578	27	29.0	394	6	US-10-995-561-715	Sequence 715, App	652	27	29.0	1151	7	US-11-128-420-10	Sequence 10, Appl
579	27	29.0	396	6	US-10-793-626-3222	Sequence 3222, Ap	653	27	29.0	1170	6	US-10-831-997-2	Sequence 2, Appli
580	27	29.0	401	6	US-10-821-234-881	Sequence 881, App	654	27	29.0	1170	6	US-10-995-561-594	Sequence 594, App
581	27	29.0	401	7	US-11-097-749-3	Sequence 3, Appli	655	27	29.0	1170	6	US-10-995-561-595	Sequence 595, App
582	27	29.0	410	6	US-10-467-657-2312	Sequence 2312, Ap	656	27	29.0	1170	6	US-10-995-561-596	Sequence 596, App
583	27	29.0	417	6	US-10-793-626-196	Sequence 196, App	657	27	29.0	1170	7	US-10-995-561-595	Sequence 595, App
584	27	29.0	417	6	US-10-821-234-1639	Sequence 1639, Ap	658	27	29.0	1170	7	US-11-046-456-28	Sequence 28, Appl
585	27	29.0	417	6	US-10-878-556A-52	Sequence 52, Appl	659	27	29.0	1170	7	US-11-046-644-28	Sequence 28, Appl
586	27	29.0	431	6	US-10-467-657-1322	Sequence 1322, Ap	660	27	29.0	1210	7	US-11-058-727-4	Sequence 4, Appli
587	27	29.0	438	7	US-11-140-417-2	Sequence 2, Appli	661	27	29.0	1210	7	US-11-108-389-4	Sequence 4, Appli
588	27	29.0	472	6	US-10-689-742-68	Sequence 68, Appl	662	27	29.0	1311	6	US-10-509-422-5	Sequence 5, Appli
589	27	29.0	477	7	US-11-055-822-98	Sequence 98, Appl	663	27	29.0	1390	7	US-11-063-343-35	Sequence 35, Appl
590	27	29.0	479	7	US-11-147-047-44	Sequence 44, Appl	664	27	29.0	1451	7	US-11-046-346-1	Sequence 1, Appli
591	27	29.0	485	6	US-10-485-517-136	Sequence 136, App	665	27	29.0	1841	7	US-11-057-058-63	Sequence 63, Appl
592	27	29.0	491	6	US-10-467-657-5316	Sequence 5316, Ap	666	27	29.0	2214	7	US-11-080-991-94	Sequence 94, Appl
593	27	29.0	510	7	US-11-194-246-442	Sequence 442, App	667	27	29.0	2630	7	US-11-186-731-2	Sequence 2, Appl
594	27	29.0	530	6	US-10-858-730-67	Sequence 67, Appl	668	27	29.0	2644	6	US-10-770-726-45	Sequence 45, Appl
595	27	29.0	531	7	US-11-060-914-4	Sequence 67, Appl	669	27	29.0	2764	6	US-10-995-561-691	Sequence 691, App
596	27	29.0	532	7	US-11-184-380-6	Sequence 4, Appli	670	27	29.0	2813	6	US-10-995-561-688	Sequence 688, App
597	27	29.0	533	6	US-10-467-657-9063	Sequence 9063, Ap	671	27	29.0	2919	6	US-10-821-234-1133	Sequence 1133, Ap
598	27	29.0	533	7	US-11-147-047-33	Sequence 33, Appl	672	27	29.0	3623	6	US-10-995-561-593	Sequence 593, App
599	27	29.0	537	6	US-10-467-657-4136	Sequence 4136, Ap	673	27	29.0	4868	7	US-11-044-111-24	Sequence 24, Appl
600	27	29.0	538	6	US-10-793-626-260	Sequence 260, App	674	27	29.0	7102	7	US-11-143-980-48	Sequence 48, Appl
601	27	29.0	538	6	US-10-763-712A-58	Sequence 58, Appl	675	26.5	28.5	7968	7	US-11-186-731-5	Sequence 5, Appli
602	27	29.0	550	7	US-11-055-822-866	Sequence 866, App	676	26.5	28.5	125	6	US-10-467-657-3488	Sequence 3488, Ap
603	27	29.0	554	7	US-11-000-463-240	Sequence 240, App	677	26.5	28.5	132	6	US-10-467-657-8176	Sequence 8176, Ap
604	27	29.0	567	6	US-10-793-626-3184	Sequence 3184, Ap	678	26.5	28.5	289	7	US-11-060-008-12	Sequence 12, Appl
605	27	29.0	588	7	US-11-184-380-5	Sequence 5, Appli	679	26.5	28.5	317	6	US-10-995-561-798	Sequence 798, App
606	27	29.0	594	7	US-11-012-762-4	Sequence 4, Appli	680	26.5	28.5	332	6	US-10-949-720-405	Sequence 405, App
607	27	29.0	619	6	US-10-821-234-1150	Sequence 1150, Ap	681	26.5	28.5	401	6	US-10-949-720-419	Sequence 419, App
608	27	29.0	619	6	US-10-999-886-3	Sequence 3, Appli	682	26.5	28.5	431	6	US-10-949-720-410	Sequence 410, App
609	27	29.0	625	7	US-11-021-441-37	Sequence 37, Appl	683	26.5	28.5	488	6	US-10-467-657-6264	Sequence 6264, Ap
610	27	29.0	628	6	US-10-467-657-4030	Sequence 4030, Ap	684	26.5	28.5	511	6	US-10-878-556A-104	Sequence 104, App
611	27	29.0	628	7	US-11-147-047-45	Sequence 45, Appl	685	26.5	28.5	522	6	US-10-949-720-425	Sequence 425, App
612	27	29.0	635	6	US-10-821-234-927	Sequence 927, App	686	26.5	28.5	537	6	US-10-949-720-424	Sequence 424, App
613	27	29.0	640	6	US-10-999-886-4	Sequence 4, Appli	687	26.5	28.5	555	6	US-10-949-720-387	Sequence 387, App
614	27	29.0	644	6	US-10-821-234-1107	Sequence 1107, Ap	688	26.5	28.5	567	7	US-11-000-463-400	Sequence 400, App
615	27	29.0	648	6	US-10-467-657-2802	Sequence 2802, Ap	689	26.5	28.5	570	6	US-10-949-720-386	Sequence 386, App
616	27	29.0	650	6	US-10-873-528-95	Sequence 95, Appl	690	26.5	28.5	724	6	US-10-793-626-3082	Sequence 3082, Ap
617	27	29.0	655	6	US-10-467-657-3168	Sequence 3168, Ap	691	26.5	28.5	771	6	US-10-949-720-412	Sequence 412, App
618	27	29.0	657	6	US-10-873-528-57	Sequence 57, Appl	692	26.5	28.5	771	6	US-10-793-626-3082	Sequence 3082, Ap
619	27	29.0	673	7	US-11-058-727-14	Sequence 14, Appl	693	26.5	28.5	797	6	US-10-821-234-1271	Sequence 1271, Ap
620	27	29.0	673	7	US-11-108-389-14	Sequence 14, Appl	694	26.5	28.5	874	7	US-10-995-561-802	Sequence 802, App
622	27	29.0	698	6	US-10-995-561-939	Sequence 939, App	695	26.5	28.5	882	7	US-11-012-762-8	Sequence 8, Appli
623	27	29.0	724	7	US-11-109-156-19	Sequence 19, Appl	696	26.5	28.5	944	6	US-11-012-762-34	Sequence 34, Appl
624	27	29.0	724	7	US-11-184-380-4	Sequence 4, Appli	697	26.5	28.5	987	6	US-10-793-626-3324	Sequence 3324, Ap
												US-10-949-720-395	Sequence 395, App

698	26.5	28.5	990	6	US-10-821-234-1201	Sequence 1201, Ap
699	26.5	28.5	1142	7	US-11-109-156-22	Sequence 22, Appl
700	26.5	28.5	1210	7	US-11-108-172-692	Sequence 692, App
701	26.5	28.5	1548	7	US-11-108-172-1095	Sequence 1095, Ap
702	26.5	28.5	1554	7	US-11-186-284-93	Sequence 93, Appl
703	26	28.0	13	6	US-10-511-559-410	Sequence 410, App
704	26	28.0	31	6	US-10-467-657-8808	Sequence 8808, Ap
705	26	28.0	42	6	US-10-656-894-6	Sequence 6, Appli
706	26	28.0	42	6	US-10-656-894-22	Sequence 22, Appl
707	26	28.0	42	6	US-10-656-894-23	Sequence 23, Appl
708	26	28.0	43	6	US-10-467-657-2656	Sequence 2656, Ap
709	26	28.0	45	7	US-11-198-847-280	Sequence 280, App
710	26	28.0	46	6	US-10-467-657-4096	Sequence 4096, Ap
711	26	28.0	54	6	US-10-467-657-7188	Sequence 7188, Ap
712	26	28.0	57	7	US-11-082-389-370	Sequence 370, App
713	26	28.0	60	6	US-10-467-657-6136	Sequence 6136, Ap
714	26	28.0	69	6	US-10-467-657-1680	Sequence 1680, Ap
715	26	28.0	71	6	US-10-467-657-5618	Sequence 5618, Ap
716	26	28.0	77	6	US-10-467-657-3496	Sequence 3496, Ap
717	26	28.0	77	7	US-11-006-119-23	Sequence 23, Appl
718	26	28.0	79	7	US-11-077-386-21	Sequence 21, Appl
719	26	28.0	95	7	US-11-198-847-89	Sequence 89, Appl
720	26	28.0	98	6	US-10-467-657-6988	Sequence 6988, Ap
721	26	28.0	105	6	US-10-467-657-1678	Sequence 1678, Ap
722	26	28.0	107	6	US-10-467-657-3832	Sequence 3832, Ap
723	26	28.0	116	6	US-10-793-626-136	Sequence 136, App
724	26	28.0	123	6	US-10-467-657-4690	Sequence 4690, Ap
725	26	28.0	124	6	US-10-467-657-294	Sequence 294, App
726	26	28.0	124	6	US-10-467-657-5944	Sequence 5944, Ap
727	26	28.0	128	6	US-10-467-657-5268	Sequence 5268, Ap
728	26	28.0	135	6	US-10-467-657-8348	Sequence 8348, Ap
729	26	28.0	136	6	US-10-793-626-1852	Sequence 1852, Ap
730	26	28.0	156	6	US-10-467-657-2864	Sequence 2864, Ap
731	26	28.0	160	6	US-10-846-172A-10	Sequence 10, Appl
732	26	28.0	163	7	US-11-102-240-160	Sequence 160, App
733	26	28.0	165	6	US-10-454-437-58	Sequence 58, Appl
735	26	28.0	174	6	US-10-485-517-301	Sequence 301, App
736	26	28.0	177	7	US-11-068-717-8	Sequence 8, Appli
737	26	28.0	178	7	US-11-055-822-118	Sequence 118, App
738	26	28.0	178	7	US-11-055-822-488	Sequence 488, App
739	26	28.0	181	7	US-11-000-463-890	Sequence 890, App
740	26	28.0	182	7	US-11-000-463-418	Sequence 418, App
741	26	28.0	195	6	US-10-467-657-8594	Sequence 8594, Ap
742	26	28.0	195	7	US-11-055-822-914	Sequence 914, App
743	26	28.0	196	6	US-10-467-657-8288	Sequence 8288, Ap
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745	26	28.0	206	6	US-10-467-657-2550	Sequence 2550, Ap
746	26	28.0	216	6	US-10-118-590-2	Sequence 2, Appli
747	26	28.0	217	7	US-11-170-653-48	Sequence 48, Appl
748	26	28.0	220	7	US-11-082-389-72	Sequence 72, Appl
749	26	28.0	225	6	US-10-793-626-1452	Sequence 1452, Ap
750	26	28.0	226	6	US-10-467-657-2162	Sequence 2162, Ap
751	26	28.0	232	6	US-10-467-657-4338	Sequence 4338, Ap
752	26	28.0	234	7	US-11-102-240-14	Sequence 14, Appl
753	26	28.0	236	6	US-10-878-556A-96	Sequence 96, Appl
754	26	28.0	237	6	US-10-793-626-162	Sequence 162, App
755	26	28.0	244	6	US-10-454-437-238	Sequence 238, App
756	26	28.0	244	6	US-10-454-437-240	Sequence 240, App
757	26	28.0	251	7	US-11-054-515-151	Sequence 151, App
758	26	28.0	252	6	US-10-510-386-104	Sequence 104, App
759	26	28.0	255	7	US-11-054-515-863	Sequence 863, App
760	26	28.0	255	7	US-11-054-515-866	Sequence 866, App
761	26	28.0	256	6	US-10-118-590-36	Sequence 36, Appl
762	26	28.0	257	6	US-10-663-794-2	Sequence 2, Appli
764	26	28.0	259	7	US-11-182-946-2	Sequence 464, App
765	26	28.0	266	7	US-11-000-463-464	Sequence 5806, Ap
766	26	28.0	270	6	US-10-467-657-5806	Sequence 85, Appl
767	26	28.0	277	6	US-10-667-295-85	Sequence 310, App
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769	26	28.0	280	6	US-10-467-657-1806	Sequence 1118, Ap
770	26	28.0	288	6	US-10-793-626-1118	Sequence 316, App
771	26	28.0	292	7	US-11-194-246-316	

772	26	28.0	293	6	US-10-793-626-1634	Sequence 1634, Ap
773	26	28.0	302	6	US-10-793-626-1552	Sequence 1552, Ap
774	26	28.0	303	6	US-10-770-726-52	Sequence 52, Appl
775	26	28.0	304	6	US-10-467-657-506	Sequence 506, App
776	26	28.0	305	7	US-11-113-424-58	Sequence 58, Appl
777	26	28.0	306	6	US-10-467-657-7672	Sequence 7672, Ap
778	26	28.0	308	7	US-11-055-822-822	Sequence 822, App
779	26	28.0	312	6	US-10-793-626-2186	Sequence 2186, Ap
780	26	28.0	314	6	US-10-793-626-2552	Sequence 2552, Ap
781	26	28.0	314	7	US-11-129-143-86	Sequence 86, Appl
782	26	28.0	319	6	US-10-793-626-1040	Sequence 1040, Ap
783	26	28.0	332	7	US-11-113-424-55	Sequence 55, Appl
784	26	28.0	334	7	US-11-055-822-24	Sequence 24, Appl
785	26	28.0	341	7	US-11-069-642-4	Sequence 4, Appli
786	26	28.0	343	7	US-11-000-463-936	Sequence 936, App
788	26	28.0	349	6	US-10-485-517-417	Sequence 417, App
789	26	28.0	353	6	US-10-667-295-113	Sequence 113, App
790	26	28.0	354	7	US-11-064-769-4	Sequence 4, Appli
791	26	28.0	354	7	US-11-064-774A-119	Sequence 119, App
792	26	28.0	354	7	US-11-090-439-60	Sequence 60, Appl
793	26	28.0	354	7	US-11-090-439-62	Sequence 62, Appl
794	26	28.0	356	7	US-11-012-762-46	Sequence 46, Appl
795	26	28.0	358	6	US-10-793-626-2136	Sequence 2136, Ap
796	26	28.0	365	6	US-10-793-626-470	Sequence 470, App
797	26	28.0	368	7	US-11-053-185-12	Sequence 12, Appl
798	26	28.0	369	7	US-11-055-822-116	Sequence 116, App
799	26	28.0	369	7	US-11-055-822-486	Sequence 486, App
800	26	28.0	373	7	US-11-149-349-2	Sequence 2, Appli
801	26	28.0	376	7	US-11-055-822-152	Sequence 152, App
802	26	28.0	380	6	US-10-793-626-1402	Sequence 1402, Ap
803	26	28.0	386	7	US-11-012-762-44	Sequence 44, Appl
804	26	28.0	387	7	US-11-060-008-10	Sequence 10, Appl
805	26	28.0	389	6	US-10-979-821-2	Sequence 2, Appli
806	26	28.0	389	7	US-11-012-762-72	Sequence 72, Appl
807	26	28.0	391	6	US-10-821-234-1487	Sequence 1487, Ap
808	26	28.0	391	7	US-11-105-172-4	Sequence 4, Appli
809	26	28.0	394	6	US-10-793-626-552	Sequence 552, App
810	26	28.0	394	6	US-10-873-528-41	Sequence 41, Appl
811	26	28.0	401	6	US-10-793-626-836	Sequence 836, App
812	26	28.0	404	6	US-10-667-295-112	Sequence 112, App
813	26	28.0	413	6	US-10-967-648A-8	Sequence 8, Appli
814	26	28.0	421	7	US-11-082-389-70	Sequence 70, Appl
815	26	28.0	422	7	US-10-821-234-1313	Sequence 1313, Ap
816	26	28.0	422	7	US-11-186-284-75	Sequence 75, Appl
817	26	28.0	423	7	US-11-074-176-4	Sequence 4, Appli
818	26	28.0	428	7	US-11-055-822-606	Sequence 606, App
819	26	28.0	430	7	US-11-055-822-412	Sequence 412, App
820	26	28.0	431	6	US-10-467-657-202	Sequence 202, App
821	26	28.0	431	6	US-10-467-657-6310	Sequence 6310, Ap
822	26	28.0	437	7	US-11-088-634A-4	Sequence 4, Appli
823	26	28.0	440	6	US-10-606-302-9	Sequence 9, Appli
824	26	28.0	442	7	US-11-055-822-402	Sequence 402, App
825	26	28.0	445	6	US-10-873-528-30	Sequence 30, Appl
826	26	28.0	446	6	US-10-667-295-111	Sequence 111, App
827	26	28.0	448	6	US-10-467-657-4416	Sequence 4416, Ap
828	26	28.0	449	7	US-11-071-062-1	Sequence 1, Appli
829	26	28.0	449	7	US-11-196-459-1	Sequence 1, Appli
830	26	28.0	449	7	US-11-196-459-2	Sequence 2, Appli
831	26	28.0	450	7	US-11-074-176-212	Sequence 212, App
832	26	28.0	461	7	US-11-054-385-6	Sequence 6, Appli
833	26	28.0	464	6	US-10-763-712A-46	Sequence 46, Appl
834	26	28.0	468	6	US-10-763-712A-3	Sequence 3, Appli
835	26	28.0	481	7	US-11-090-439-16	Sequence 16, Appl
836	26	28.0	482	6	US-10-878-556A-30	Sequence 30, Appl
837	26	28.0	482	6	US-10-878-556A-139	Sequence 139, App
838	26	28.0	487	7	US-11-113-424-56	Sequence 56, Appl
839	26	28.0	487	7	US-11-113-424-57	Sequence 57, Appl
840	26	28.0	491	7	US-11-053-185-22	Sequence 22, Appl
841	26	28.0	492	6	US-10-148-606-1	Sequence 1, Appli
842	26	28.0	500	6	US-10-467-657-48	Sequence 48, Appl
843	26	28.0	500	7	US-11-087-100-24	Sequence 24, Appl
844	26	28.0	500	7	US-11-087-084-24	Sequence 24, Appl
845	26	28.0	500	7	US-11-087-085-24	Sequence 24, Appl

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847	26	28.0	509	6	US-10-508-263-18	Sequence 18, Appl	923	26	28.0	1145	6	US-10-793-626-1432	Sequence 1432, Ap
849	26	28.0	513	7	US-11-102-240-124	Sequence 124, App	924	26	28.0	1163	7	US-11-044-899-2	Sequence 2, Appli
850	26	28.0	530	7	US-11-088-634A-2	Sequence 2, Appli	925	26	28.0	1163	7	US-11-044-899-30	Sequence 30, Appl
851	26	28.0	537	6	US-10-719-311-10	Sequence 10, Appl	926	26	28.0	1167	7	US-11-097-125-2	Sequence 2, Appli
852	26	28.0	539	6	US-10-467-657-7736	Sequence 7736, Ap	927	26	28.0	1176	6	US-10-821-234-897	Sequence 897, App
853	26	28.0	544	6	US-10-719-311-18	Sequence 18, Appl	928	26	28.0	1178	7	US-11-044-899-29	Sequence 29, Appl
854	26	28.0	545	7	US-11-102-240-110	Sequence 110, App	929	26	28.0	1179	7	US-11-097-125-1	Sequence 1, Appli
855	26	28.0	548	7	US-11-119-769-3	Sequence 7704, Ap	930	26	28.0	1186	7	US-11-053-100-46	Sequence 46, Appl
856	26	28.0	548	7	US-11-119-769-3	Sequence 3, Appli	931	26	28.0	1196	6	US-10-995-561-921	Sequence 921, App
857	26	28.0	550	6	US-10-467-657-234	Sequence 234, App	932	26	28.0	1234	6	US-10-995-561-870	Sequence 870, App
858	26	28.0	550	6	US-10-467-657-924	Sequence 924, App	933	26	28.0	1236	7	US-10-995-561-870	Sequence 68, Appl
859	26	28.0	593	7	US-11-194-246-317	Sequence 317, App	934	26	28.0	1238	7	US-11-080-991-68	Sequence 21, Appl
860	26	28.0	596	7	US-11-090-878-22	Sequence 22, Appl	935	26	28.0	1255	7	US-11-078-735-21	Sequence 235, App
861	26	28.0	598	6	US-10-719-311-16	Sequence 16, Appl	936	26	28.0	1360	7	US-11-023-562-235	Sequence 22, Appl
862	26	28.0	598	7	US-11-090-878-8	Sequence 8, Appli	937	26	28.0	1365	6	US-11-188-743-22	Sequence 867, App
863	26	28.0	598	7	US-11-090-878-10	Sequence 10, Appl	938	26	28.0	1366	6	US-10-995-561-868	Sequence 868, App
864	26	28.0	598	7	US-11-090-878-12	Sequence 12, Appl	939	26	28.0	1400	6	US-10-995-561-868	Sequence 1045, Ap
865	26	28.0	598	7	US-11-055-822-820	Sequence 820, App	940	26	28.0	1402	6	US-10-821-234-1045	Sequence 2, Appli
866	26	28.0	600	6	US-10-467-657-4866	Sequence 4866, Ap	941	26	28.0	1411	6	US-10-971-982-2	Sequence 869, App
867	26	28.0	600	6	US-10-606-302-3	Sequence 3, Appli	942	26	28.0	1663	6	US-10-995-561-869	Sequence 6, Appli
868	26	28.0	616	6	US-10-982-545-5	Sequence 5, Appli	943	26	28.0	1960	7	US-10-982-545-6	Sequence 48, Appl
869	26	28.0	616	7	US-11-090-878-20	Sequence 20, Appl	944	26	28.0	2059	7	US-11-069-834-48	Sequence 4, Appli
870	26	28.0	617	7	US-11-090-878-18	Sequence 18, Appl	945	26	28.0	2059	7	US-11-087-100-4	Sequence 4, Appli
871	26	28.0	621	7	US-11-184-380-26	Sequence 26, Appl	946	26	28.0	2059	7	US-11-087-084-4	Sequence 4, Appli
872	26	28.0	623	6	US-10-719-311-2	Sequence 2, Appli	947	26	28.0	2059	7	US-11-087-085-4	Sequence 28, Appl
873	26	28.0	623	6	US-10-719-311-11	Sequence 11, Appl	948	26	28.0	2087	7	US-11-075-185-28	Sequence 606, App
874	26	28.0	624	7	US-11-090-878-2	Sequence 2, Appli	949	26	28.0	2096	6	US-10-995-561-606	Sequence 827, App
875	26	28.0	624	7	US-11-090-878-4	Sequence 4, Appli	950	26	28.0	2107	6	US-10-995-561-600	Sequence 600, App
876	26	28.0	624	7	US-11-090-878-6	Sequence 6, Appli	951	26	28.0	2261	6	US-10-995-561-608	Sequence 608, App
877	26	28.0	633	7	US-11-063-343-26	Sequence 26, Appl	952	26	28.0	2351	6	US-10-995-561-825	Sequence 825, App
878	26	28.0	637	7	US-11-090-878-24	Sequence 24, Appl	953	26	28.0	2480	6	US-10-995-561-825	Sequence 52, Appl
879	26	28.0	642	6	US-10-467-657-5900	Sequence 5900, Ap	954	26	28.0	2725	7	US-11-113-424-52	Sequence 826, App
881	26	28.0	653	7	US-11-135-855-25	Sequence 25, Appl	955	26	28.0	3116	6	US-10-995-561-826	Sequence 2, Appli
882	26	28.0	657	7	US-11-110-082-37	Sequence 37, Appl	956	25.5	27.4	4374	7	US-11-128-572-2	Sequence 48, Appl
883	26	28.0	659	6	US-10-661-966-14	Sequence 14, Appl	957	25.5	27.4	33	7	US-11-121-301-48	Sequence 30, Appl
885	26	28.0	695	7	US-10-661-966-34	Sequence 34, Appl	958	25.5	27.4	143	6	US-10-995-951A-30	Sequence 30, Appl
886	26	28.0	696	7	US-11-029-003-8	Sequence 8, Appli	959	25.5	27.4	143	7	US-11-067-425A-65	Sequence 65, Appl
887	26	28.0	715	7	US-11-089-551A-47	Sequence 47, Appl	960	25.5	27.4	186	6	US-10-467-657-5598	Sequence 5598, Ap
888	26	28.0	718	7	US-11-074-176-306	Sequence 306, App	961	25.5	27.4	203	6	US-10-467-657-8012	Sequence 8012, Ap
889	26	28.0	723	7	US-11-074-176-18	Sequence 18, Appl	962	25.5	27.4	213	7	US-11-102-621-135	Sequence 135, App
890	26	28.0	732	7	US-11-078-189-14	Sequence 14, Appl	963	25.5	27.4	223	6	US-10-793-626-2824	Sequence 2824, Ap
891	26	28.0	734	6	US-10-719-311-4	Sequence 4, Appli	964	25.5	27.4	236	7	US-11-140-965-4	Sequence 4, Appli
892	26	28.0	736	7	US-11-053-100-45	Sequence 45, Appl	965	25.5	27.4	263	6	US-10-873-528-68	Sequence 68, Appl
893	26	28.0	745	7	US-11-147-109-8	Sequence 8, Appli	966	25.5	27.4	283	7	US-11-080-991-80	Sequence 80, Appl
894	26	28.0	756	7	US-11-113-837-20	Sequence 20, Appl	967	25.5	27.4	321	7	US-11-102-240-10	Sequence 10, Appl
895	26	28.0	762	7	US-11-055-822-912	Sequence 912, App	968	25.5	27.4	332	7	US-11-105-268-59	Sequence 59, Appl
896	26	28.0	767	6	US-10-467-962B-91	Sequence 91, Appl	969	25.5	27.4	364	7	US-11-067-884-2	Sequence 2, Appli
897	26	28.0	779	7	US-11-128-420-12	Sequence 12, Appl	970	25.5	27.4	368	6	US-10-689-742-100	Sequence 100, App
898	26	28.0	786	7	US-11-070-627-9	Sequence 9, Appli	971	25.5	27.4	384	7	US-11-120-543-2	Sequence 2, Appli
899	26	28.0	794	6	US-10-793-626-1050	Sequence 1050, Ap	972	25.5	27.4	384	7	US-11-120-543-4	Sequence 4, Appli
900	26	28.0	803	6	US-10-821-234-1643	Sequence 1643, Ap	973	25.5	27.4	384	7	US-11-120-543-6	Sequence 6, Appli
901	26	28.0	825	6	US-10-995-561-679	Sequence 679, App	974	25.5	27.4	384	7	US-11-120-543-8	Sequence 8, Appli
902	26	28.0	832	7	US-11-108-172-1081	Sequence 1081, Ap	975	25.5	27.4	384	7	US-11-120-543-14	Sequence 14, Appl
903	26	28.0	843	6	US-10-645-441-8	Sequence 8, Appli	976	25.5	27.4	396	7	US-11-120-543-22	Sequence 22, Appl
904	26	28.0	849	6	US-10-467-962B-53	Sequence 53, Appl	977	25.5	27.4	400	7	US-11-120-543-12	Sequence 12, Appl
905	26	28.0	852	7	US-11-104-923A-5	Sequence 5, Appli	978	25.5	27.4	416	6	US-10-467-657-5284	Sequence 5284, Ap
906	26	28.0	879	7	US-11-022-562-340	Sequence 340, App	979	25.5	27.4	421	7	US-11-120-543-16	Sequence 16, Appl
907	26	28.0	902	7	US-11-057-058-64	Sequence 64, Appl	980	25.5	27.4	422	7	US-11-120-543-20	Sequence 20, Appl
908	26	28.0	943	6	US-10-475-204-34	Sequence 34, Appl	981	25.5	27.4	441	6	US-10-821-234-1668	Sequence 1668, Ap
909	26	28.0	958	7	US-11-108-172-1087	Sequence 1087, Ap	983	25.5	27.4	477	6	US-10-763-712A-57	Sequence 57, Appl
910	26	28.0	963	6	US-10-467-962B-2	Sequence 2, Appli	985	25.5	27.4	512	6	US-10-467-657-4870	Sequence 4870, Ap
911	26	28.0	977	7	US-11-093-274-39	Sequence 39, Appl	986	25.5	27.4	521	7	US-11-109-156-34	Sequence 34, Appl
912	26	28.0	1005	7	US-11-113-424-63	Sequence 63, Appl	987	25.5	27.4	521	7	US-11-105-268-58	Sequence 58, Appl
913	26	28.0	1023	6	US-10-995-561-968	Sequence 968, App	988	25.5	27.4	532	6	US-10-857-780-18	Sequence 18, Appl
914	26	28.0	1032	6	US-10-835-475-1	Sequence 1, Appli	989	25.5	27.4	532	6	US-10-995-561-897	Sequence 897, App
915	26	28.0	1032	7	US-11-014-367-1	Sequence 1, Appli	990	25.5	27.4	532	7	US-11-104-812-2	Sequence 2, Appli
916	26	28.0	1062	7	US-11-137-465-43	Sequence 43, Appl	991	25.5	27.4	532	7	US-11-105-279-2	Sequence 2, Appli
917	26	28.0	1075	7	US-11-089-551A-23	Sequence 23, Appl	992	25.5	27.4	532	7	US-11-107-028-22	Sequence 22, Appl
918	26	28.0	1076	6	US-10-467-657-5708	Sequence 5708, Ap	993	25.5	27.4	546	6	US-10-661-966-18	Sequence 18, Appl
919	26	28.0	1087	7	US-11-117-169-10	Sequence 10, Appl	994	25.5	27.4	712	6	US-10-995-561-984	Sequence 984, App
920	26	28.0	1092	6	US-10-821-234-999	Sequence 999, App	995	25.5	27.4	752	6	US-10-793-626-1036	Sequence 1036, Ap
921	26	28.0	1124	7	US-11-195-197-9	Sequence 9, Appli	996	25.5	27.4	769	6	US-10-995-561-985	Sequence 985, App

997	25.5	27.4	769	6	US-10-995-561-986	Sequence 986, App	1070	25	26.9	168	6	US-10-467-657-268	Sequence 268, App
998	25.5	27.4	769	7	US-11-107-028-5	Sequence 5, Appli	1071	25	26.9	168	6	US-10-467-657-3658	Sequence 3658, Ap
999	25.5	27.4	858	6	US-10-878-556A-113	Sequence 113, App	1072	25	26.9	173	6	US-10-984-376-13	Sequence 13, Appl
1000	25.5	27.4	1206	6	US-10-995-561-709	Sequence 709, App	1073	25	26.9	174	6	US-10-984-376-14	Sequence 14, Appl
1001	25.5	27.4	1907	7	US-11-039-398-25	Sequence 25, Appl	1074	25	26.9	177	6	US-10-980-388-94	Sequence 94, Appl
1002	25.5	27.4	7968	7	US-11-143-980-49	Sequence 49, Appl	1075	25	26.9	181	6	US-10-467-657-278	Sequence 278, App
1003	25	26.9	14	7	US-11-054-515-2506	Sequence 2506, Ap	1076	25	26.9	181	6	US-10-467-657-4306	Sequence 4306, Ap
1004	25	26.9	15	7	US-11-045-024-13379	Sequence 13379, A	1077	25	26.9	181	6	US-10-746-959C-10	Sequence 10, Appl
1005	25	26.9	19	6	US-10-503-575-155	Sequence 155, App	1078	25	26.9	182	6	US-10-467-657-2626	Sequence 2626, Ap
1006	25	26.9	25	6	US-10-986-501-238	Sequence 238, App	1079	25	26.9	189	6	US-10-467-657-2688	Sequence 2688, Ap
1007	25	26.9	27	6	US-10-723-207-66	Sequence 66, Appl	1080	25	26.9	190	7	US-11-055-822-538	Sequence 538, App
1008	25	26.9	42	6	US-10-467-657-1670	Sequence 1670, Ap	1081	25	26.9	192	6	US-10-821-234-1299	Sequence 1299, Ap
1009	25	26.9	42	6	US-10-656-894-7	Sequence 7, Appli	1082	25	26.9	197	7	US-11-013-247A-10	Sequence 10, Appl
1010	25	26.9	42	6	US-10-656-894-8	Sequence 8, Appli	1083	25	26.9	199	6	US-10-647-072-2	Sequence 2, Appli
1011	25	26.9	42	6	US-10-656-894-9	Sequence 9, Appli	1084	25	26.9	206	7	US-11-036-797-34	Sequence 34, Appl
1012	25	26.9	42	6	US-10-656-894-10	Sequence 10, Appl	1085	25	26.9	206	7	US-10-467-657-3098	Sequence 3098, Ap
1013	25	26.9	42	6	US-10-656-894-11	Sequence 11, Appl	1086	25	26.9	210	6	US-10-454-437-302	Sequence 302, App
1014	25	26.9	42	6	US-10-656-894-12	Sequence 12, Appl	1087	25	26.9	210	7	US-11-055-822-1026	Sequence 1026, Ap
1015	25	26.9	42	6	US-10-656-894-13	Sequence 13, Appl	1088	25	26.9	219	6	US-10-793-626-22	Sequence 22, Appl
1016	25	26.9	42	6	US-10-656-894-14	Sequence 14, Appl	1089	25	26.9	223	6	US-10-793-626-2884	Sequence 2884, Ap
1017	25	26.9	48	6	US-10-467-657-8368	Sequence 8368, Ap	1091	25	26.9	225	6	US-10-485-517-143	Sequence 143, App
1018	25	26.9	53	6	US-10-656-894-21	Sequence 21, Appl	1092	25	26.9	227	6	US-10-948-429A-6	Sequence 6, Appli
1019	25	26.9	54	6	US-10-656-894-17	Sequence 17, Appl	1093	25	26.9	227	7	US-11-000-463-301	Sequence 301, App
1020	25	26.9	64	6	US-10-467-657-3224	Sequence 3224, Ap	1094	25	26.9	232	6	US-10-793-626-2194	Sequence 2194, Ap
1021	25	26.9	65	6	US-10-467-657-5106	Sequence 5106, Ap	1095	25	26.9	239	7	US-11-170-653-40	Sequence 40, Appl
1022	25	26.9	67	6	US-10-467-657-8858	Sequence 8858, Ap	1096	25	26.9	241	6	US-10-987-663-8	Sequence 8, Appli
1023	25	26.9	75	6	US-10-667-295-53	Sequence 53, Appl	1097	25	26.9	244	6	US-10-467-657-3662	Sequence 3662, Ap
1024	25	26.9	79	6	US-10-467-657-1888	Sequence 1888, Ap	1098	25	26.9	244	6	US-10-467-657-6684	Sequence 6684, Ap
1025	25	26.9	80	6	US-10-952-535A-27	Sequence 27, Appl	1099	25	26.9	247	7	US-11-054-515-2124	Sequence 2124, Ap
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1027	25	26.9	83	6	US-10-746-959C-2	Sequence 2, Appli	1101	25	26.9	249	7	US-11-054-515-632	Sequence 632, App
1028	25	26.9	84	6	US-10-467-657-1844	Sequence 1844, Ap	1102	25	26.9	250	6	US-10-793-626-2310	Sequence 2310, Ap
1029	25	26.9	91	7	US-11-126-126-10	Sequence 10, Appl	1103	25	26.9	250	6	US-10-467-657-3132	Sequence 3132, Ap
1030	25	26.9	92	7	US-11-102-476-15	Sequence 15, Appl	1104	25	26.9	261	6	US-10-617-034A-12	Sequence 12, Appl
1031	25	26.9	94	7	US-11-126-126-14	Sequence 14, Appl	1105	25	26.9	264	6	US-10-793-626-1112	Sequence 1112, Ap
1032	25	26.9	98	6	US-10-928-446A-140	Sequence 140, App	1106	25	26.9	264	6	US-10-821-234-1660	Sequence 1660, Ap
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1034	25	26.9	102	6	US-10-467-657-5146	Sequence 5146, Ap	1108	25	26.9	270	6	US-10-821-234-1348	Sequence 1348, Ap
1035	25	26.9	103	7	US-11-053-076-109	Sequence 109, App	1109	25	26.9	277	6	US-10-878-556A-4	Sequence 4, Appli
1036	25	26.9	104	7	US-11-000-463-939	Sequence 939, App	1110	25	26.9	286	7	US-11-089-551A-27	Sequence 27, Appl
1037	25	26.9	106	7	US-11-126-126-4	Sequence 4, Appli	1111	25	26.9	287	6	US-10-793-626-468	Sequence 468, App
1038	25	26.9	106	7	US-11-126-126-8	Sequence 8, Appli	1112	25	26.9	289	6	US-10-987-663-2	Sequence 2, Appli
1039	25	26.9	106	7	US-11-000-463-467	Sequence 467, App	1113	25	26.9	290	6	US-10-793-626-214	Sequence 214, App
1040	25	26.9	109	7	US-11-126-126-6	Sequence 6, Appli	1114	25	26.9	290	6	US-10-793-626-758	Sequence 758, App
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1042	25	26.9	123	6	US-10-467-657-4920	Sequence 4920, Ap	1116	25	26.9	295	6	US-10-987-663-10	Sequence 10, Appl
1043	25	26.9	125	6	US-10-986-501-198	Sequence 198, App	1117	25	26.9	296	7	US-11-074-176-166	Sequence 166, App
1044	25	26.9	125	7	US-11-194-246-395	Sequence 395, App	1118	25	26.9	300	7	US-11-179-977-4	Sequence 4, Appli
1045	25	26.9	126	6	US-10-821-234-1318	Sequence 1318, Ap	1119	25	26.9	301	6	US-10-793-626-1826	Sequence 1826, Ap
1046	25	26.9	126	7	US-11-084-508-25	Sequence 25, Appl	1120	25	26.9	301	7	US-11-147-047-37	Sequence 37, Appl
1047	25	26.9	127	6	US-10-467-657-1320	Sequence 1320, Ap	1121	25	26.9	302	6	US-10-878-556A-61	Sequence 61, Appl
1048	25	26.9	127	6	US-10-467-657-5548	Sequence 5548, Ap	1122	25	26.9	303	7	US-11-186-284-193	Sequence 193, App
1049	25	26.9	127	6	US-10-467-657-5606	Sequence 5606, Ap	1123	25	26.9	306	6	US-10-467-657-4304	Sequence 4304, Ap
1050	25	26.9	127	6	US-10-467-657-7500	Sequence 7500, Ap	1124	25	26.9	309	6	US-10-793-626-936	Sequence 936, App
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1052	25	26.9	127	6	US-10-467-657-8312	Sequence 8312, Ap	1126	25	26.9	310	7	US-11-092-168-9	Sequence 9, Appli
1053	25	26.9	132	6	US-10-793-626-1058	Sequence 1058, Ap	1127	25	26.9	311	7	US-11-000-463-345	Sequence 345, App
1054	25	26.9	137	6	US-10-821-234-1242	Sequence 1242, Ap	1128	25	26.9	311	7	US-11-000-463-829	Sequence 829, App
1055	25	26.9	139	6	US-10-878-556A-117	Sequence 117, App	1129	25	26.9	312	6	US-10-793-626-3104	Sequence 3104, Ap
1056	25	26.9	141	6	US-10-467-657-4110	Sequence 4110, Ap	1130	25	26.9	313	6	US-10-723-207-4	Sequence 4, Appli
1057	25	26.9	144	7	US-11-174-398-10	Sequence 10, Appl	1131	25	26.9	314	7	US-11-143-980-56	Sequence 56, Appl
1058	25	26.9	146	7	US-11-034-569-14	Sequence 14, Appl	1132	25	26.9	317	7	US-11-129-143-85	Sequence 85, Appl
1059	25	26.9	148	6	US-10-467-657-5478	Sequence 5478, Ap	1133	25	26.9	318	6	US-10-793-626-1600	Sequence 1600, Ap
1060	25	26.9	149	6	US-10-986-501-231	Sequence 231, App	1134	25	26.9	318	7	US-11-000-463-432	Sequence 432, App
1061	25	26.9	151	6	US-10-467-657-244	Sequence 244, App	1135	25	26.9	318	7	US-11-000-463-904	Sequence 904, App
1062	25	26.9	152	7	US-11-069-642-7	Sequence 7, Appli	1136	25	26.9	321	6	US-10-485-517-133	Sequence 133, App
1063	25	26.9	158	6	US-10-821-234-1294	Sequence 1294, Ap	1137	25	26.9	326	7	US-11-102-621-33	Sequence 33, Appl
1064	25	26.9	161	6	US-10-467-657-1786	Sequence 1786, Ap	1138	25	26.9	326	7	US-10-485-517-268	Sequence 268, App
1065	25	26.9	161	7	US-11-126-126-2	Sequence 2, Appli	1139	25	26.9	333	6	US-10-467-657-6450	Sequence 6450, Ap
1066	25	26.9	162	7	US-11-069-642-6	Sequence 6, Appli	1140	25	26.9	333	6	US-10-467-657-2662	Sequence 2662, Ap
1067	25	26.9	163	6	US-10-467-657-2662	Sequence 2662, Ap	1141	25	26.9	333	7	US-11-074-176-32	Sequence 32, Appl
1068	25	26.9	164	6	US-10-467-657-232	Sequence 232, App	1142	25	26.9	333	7	US-11-050-440-2	Sequence 2, Appli
1069	25	26.9	164	6	US-10-467-657-664	Sequence 664, App	1143	25	26.9	334	6	US-10-793-626-10	Sequence 10, Appl

1144	25	26.9	334	7	US-11-140-417-8	Sequence 8, Appli	1218	25	26.9	457	6	US-10-763-712A-61	Sequence 61, Appli
1145	25	26.9	335	6	US-10-995-561-704	Sequence 704, App	1219	25	26.9	458	6	US-10-618-320A-1	Sequence 1, Appli
1146	25	26.9	335	7	US-11-141-947-2	Sequence 2, Appli	1220	25	26.9	462	7	US-11-132-142-10	Sequence 10, Appl
1147	25	26.9	337	6	US-10-980-388-115	Sequence 115, App	1221	25	26.9	463	6	US-10-467-657-6352	Sequence 6352, Ap
1148	25	26.9	341	6	US-10-467-657-62	Sequence 62, Appl	1222	25	26.9	463	6	US-10-467-657-7604	Sequence 7604, Ap
1149	25	26.9	341	6	US-10-467-657-2166	Sequence 2166, Ap	1223	25	26.9	465	7	US-11-186-284-197	Sequence 197, App
1150	25	26.9	341	7	US-11-092-168-4	Sequence 4, Appli	1224	25	26.9	468	6	US-10-957-569-28	Sequence 28, Appl
1151	25	26.9	343	7	US-11-080-991-86	Sequence 86, Appl	1225	25	26.9	468	7	US-11-167-273-1	Sequence 1, Appli
1152	25	26.9	343	7	US-11-092-168-3	Sequence 3, Appli	1226	25	26.9	469	7	US-11-186-284-119	Sequence 119, App
1153	25	26.9	344	6	US-10-467-657-6546	Sequence 6546, Ap	1227	25	26.9	484	7	US-11-051-568-13	Sequence 13, Appl
1154	25	26.9	344	7	US-11-102-240-42	Sequence 42, Appl	1228	25	26.9	489	6	US-10-467-657-6158	Sequence 6158, Ap
1155	25	26.9	350	6	US-10-497-767-4	Sequence 4, Appli	1229	25	26.9	490	7	US-11-069-642-23	Sequence 23, Appl
1156	25	26.9	350	6	US-10-878-556A-66	Sequence 66, Appl	1230	25	26.9	494	7	US-11-165-697-48	Sequence 48, Appl
1157	25	26.9	350	6	US-10-873-528-89	Sequence 89, Appl	1231	25	26.9	494	7	US-11-165-697-49	Sequence 49, Appl
1158	25	26.9	351	7	US-11-132-142-13	Sequence 13, Appl	1232	25	26.9	497	6	US-10-984-376-3	Sequence 3, Appli
1159	25	26.9	351	7	US-11-132-142-14	Sequence 14, Appl	1233	25	26.9	501	7	US-11-013-247A-2	Sequence 2, Appli
1160	25	26.9	352	6	US-10-926-709-18	Sequence 18, Appl	1234	25	26.9	502	6	US-10-821-234-1554	Sequence 1554, Ap
1161	25	26.9	353	7	US-11-132-142-11	Sequence 11, Appl	1235	25	26.9	509	6	US-10-793-626-98	Sequence 98, Appl
1162	25	26.9	360	6	US-10-467-657-2796	Sequence 2796, Ap	1236	25	26.9	511	6	US-10-510-947-3	Sequence 3, Appli
1163	25	26.9	362	7	US-11-013-247A-7	Sequence 7, Appli	1237	25	26.9	513	7	US-11-055-822-348	Sequence 348, App
1164	25	26.9	363	6	US-10-793-626-302	Sequence 302, App	1238	25	26.9	513	7	US-11-149-349-6	Sequence 6, Appli
1165	25	26.9	364	6	US-10-510-947-2	Sequence 2, Appli	1239	25	26.9	515	6	US-10-821-234-1411	Sequence 1411, Ap
1166	25	26.9	364	7	US-11-013-247A-6	Sequence 6, Appli	1240	25	26.9	519	6	US-10-485-517-220	Sequence 220, App
1167	25	26.9	365	6	US-10-467-657-3846	Sequence 3846, Ap	1241	25	26.9	522	6	US-10-467-657-7238	Sequence 7238, Ap
1168	25	26.9	366	7	US-11-000-463-457	Sequence 457, App	1242	25	26.9	526	7	US-11-054-168B-19	Sequence 19, Appl
1169	25	26.9	369	6	US-10-467-657-1336	Sequence 1336, Ap	1243	25	26.9	529	7	US-11-013-247A-17	Sequence 17, Appl
1170	25	26.9	371	6	US-10-467-962B-41	Sequence 41, Appl	1244	25	26.9	542	7	US-11-074-176-30	Sequence 30, Appl
1171	25	26.9	371	6	US-10-467-657-1166	Sequence 1166, Ap	1245	25	26.9	543	7	US-11-087-227-16	Sequence 16, Appl
1172	25	26.9	371	7	US-11-137-671-16	Sequence 16, Appl	1246	25	26.9	545	6	US-10-858-730-90	Sequence 90, Appl
1173	25	26.9	372	7	US-11-143-980-37	Sequence 37, Appl	1247	25	26.9	548	6	US-10-858-730-68	Sequence 68, Appl
1174	25	26.9	377	6	US-10-467-657-7508	Sequence 7508, Ap	1248	25	26.9	548	7	US-11-132-142-5	Sequence 5, Appli
1175	25	26.9	379	6	US-10-858-730-24	Sequence 24, Appl	1249	25	26.9	558	6	US-10-467-657-4258	Sequence 4258, Ap
1176	25	26.9	379	6	US-10-858-730-281	Sequence 281, App	1250	25	26.9	572	6	US-10-793-626-2846	Sequence 2846, Ap
1177	25	26.9	379	6	US-10-858-730-285	Sequence 285, App	1251	25	26.9	574	6	US-10-821-234-1624	Sequence 1624, Ap
1178	25	26.9	379	6	US-10-858-730-290	Sequence 290, App	1252	25	26.9	574	7	US-11-102-240-164	Sequence 164, App
1179	25	26.9	385	6	US-10-873-528-144	Sequence 144, App	1253	25	26.9	575	7	US-11-131-212-23	Sequence 23, Appl
1180	25	26.9	388	7	US-11-186-284-169	Sequence 169, App	1254	25	26.9	575	7	US-11-131-212-24	Sequence 24, Appl
1181	25	26.9	389	6	US-10-467-657-4468	Sequence 4468, Ap	1255	25	26.9	585	6	US-10-878-556A-42	Sequence 42, Appl
1182	25	26.9	391	6	US-10-770-726-59	Sequence 59, Appl	1256	25	26.9	588	6	US-10-763-712A-95	Sequence 95, Appl
1183	25	26.9	393	6	US-10-821-234-1043	Sequence 1043, Ap	1257	25	26.9	595	7	US-11-102-476-33	Sequence 33, Appl
1184	25	26.9	394	6	US-10-793-626-58	Sequence 58, Appl	1258	25	26.9	607	7	US-11-096-051-14	Sequence 14, Appl
1185	25	26.9	395	7	US-11-132-142-12	Sequence 12, Appl	1259	25	26.9	612	6	US-10-821-234-1101	Sequence 1101, Ap
1186	25	26.9	395	6	US-10-362-772-4	Sequence 4, Appli	1260	25	26.9	612	6	US-10-467-657-764	Sequence 764, App
1187	25	26.9	402	7	US-11-055-822-778	Sequence 778, App	1261	25	26.9	626	7	US-11-082-389-392	Sequence 392, App
1188	25	26.9	402	7	US-11-055-822-780	Sequence 780, App	1262	25	26.9	628	7	US-11-074-176-244	Sequence 244, App
1189	25	26.9	402	7	US-11-000-463-449	Sequence 449, App	1263	25	26.9	634	7	US-11-082-389-390	Sequence 390, App
1190	25	26.9	406	6	US-10-467-657-1048	Sequence 1048, Ap	1264	25	26.9	636	6	US-10-763-712A-29	Sequence 29, Appl
1191	25	26.9	408	7	US-11-051-568-15	Sequence 15, Appl	1265	25	26.9	636	6	US-10-763-712A-93	Sequence 93, Appl
1192	25	26.9	414	6	US-10-873-528-76	Sequence 76, Appl	1266	25	26.9	648	6	US-10-501-039-6	Sequence 6, Appli
1193	25	26.9	414	7	US-11-089-551A-28	Sequence 28, Appl	1267	25	26.9	649	7	US-11-102-240-132	Sequence 132, App
1194	25	26.9	425	7	US-11-096-276-2	Sequence 2, Appli	1268	25	26.9	654	6	US-10-528-031-1	Sequence 1, Appli
1195	25	26.9	428	7	US-11-000-463-448	Sequence 448, App	1269	25	26.9	654	6	US-10-770-726-82	Sequence 82, Appl
1196	25	26.9	430	6	US-10-821-234-1437	Sequence 1437, Ap	1270	25	26.9	656	6	US-10-821-234-1121	Sequence 1121, Ap
1197	25	26.9	430	6	US-10-650-326B-19	Sequence 19, Appl	1272	25	26.9	664	6	US-10-878-556A-44	Sequence 44, Appl
1198	25	26.9	430	7	US-11-051-568-25	Sequence 25, Appl	1273	25	26.9	669	6	US-10-997-201A-30	Sequence 30, Appl
1199	25	26.9	431	6	US-10-816-768-39	Sequence 39, Appl	1274	25	26.9	673	7	US-11-102-240-16	Sequence 16, Appl
1200	25	26.9	431	6	US-10-650-326B-3	Sequence 3, Appli	1275	25	26.9	674	6	US-10-501-039-10	Sequence 10, Appl
1201	25	26.9	431	7	US-11-051-568-2	Sequence 2, Appli	1276	25	26.9	676	6	US-10-510-947-1	Sequence 1, Appli
1202	25	26.9	431	7	US-11-186-284-10	Sequence 10, Appl	1277	25	26.9	693	6	US-10-873-528-185	Sequence 185, App
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1204	25	26.9	432	6	US-10-467-657-6128	Sequence 6128, Ap	1280	25	26.9	716	7	US-11-147-047-52	Sequence 52, Appl
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23	62.5	13.9	270	2	US-09-270-767-46312
24	62.5	13.9	416	2	US-09-949-016-7087
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27	62	13.8	341	2	US-09-248-796A-20844

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52	58.5	13.0	208	2	US-09-992-598-416	Sequence 416, App
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132	56.5	12.6	811	2	US-09-605-703B-1116	Sequence 1116, Ap	206	55	12.2	213	2	US-09-996-265-231	Sequence 231, App
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146	56	12.5	269	1	US-08-484-905-116	Sequence 116, App	220	55	12.2	214	2	US-09-996-265-249	Sequence 249, App
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252	55	12.2	2973	2	US-09-136-605-7	Sequence 7, Appli	325	53	11.8	43	1	US-08-332-562A-26	Sequence 26, Appl
253	54.5	12.1	108	2	US-09-281-760E-37	Sequence 37, Appl	326	53	11.8	73	2	US-09-621-976-6146	Sequence 6146, Ap
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262	54.5	12.1	2523	2	US-09-121-457-3	Sequence 3, Appli	335	53	11.8	170	2	US-09-245-764-10	Sequence 10, Appl
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266	54	12.0	226	1	US-08-505-058-6	Sequence 26, Appl	339	53	11.8	171	2	US-09-245-764-14	Sequence 14, Appl
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269	54	12.0	226	1	US-08-465-078-26	Sequence 26, Appl	342	53	11.8	213	2	US-09-996-265-211	Sequence 211, App
270	54	12.0	226	1	US-08-725-776-26	Sequence 26, Appl	343	53	11.8	214	1	US-08-458-516-12	Sequence 12, Appl
271	54	12.0	226	1	US-08-488-062-26	Sequence 26, Appl	344	53	11.8	231	2	US-09-252-991A-26289	Sequence 26289, A
272	54	12.0	243	1	US-07-958-140-2	Sequence 2, Appli	345	53	11.8	237	2	US-08-908-469-100	Sequence 100, App
273	54	12.0	243	4	PCT-US93-09166-2	Sequence 2, Appli	346	53	11.8	262	2	US-09-248-796A-15819	Sequence 15819, A
274	54	12.0	299	1	US-08-872-437-2	Sequence 2, Appli	347	53	11.8	281	2	US-10-027-736A-67	Sequence 67, Appl
275	54	12.0	299	2	US-08-651-136C-12	Sequence 12, Appl	348	53	11.8	291	2	US-10-027-736A-19	Sequence 19, Appl
276	54	12.0	299	2	US-09-229-911A-12	Sequence 12, Appl	349	53	11.8	307	1	US-08-332-562A-83	Sequence 83, Appl
277	54	12.0	299	2	US-10-007-521-12	Sequence 12, Appl	350	53	11.8	315	2	US-09-949-016-7014	Sequence 7014, Ap
278	54	12.0	488	1	US-08-554-659-2	Sequence 2, Appli	351	53	11.8	315	2	US-09-949-016-11121	Sequence 11121, A
279	54	12.0	488	1	US-08-554-659-4	Sequence 4, Appli	352	53	11.8	315	2	US-09-949-016-11122	Sequence 11122, A
280	54	12.0	621	2	US-09-949-016-11557	Sequence 11557, A	353	53	11.8	316	2	US-10-027-736A-17	Sequence 17, Appl
281	54	12.0	984	1	US-08-257-073-3	Sequence 3, Appli	354	53	11.8	317	2	US-10-027-736A-16	Sequence 16, Appl
282	54	12.0	984	1	US-08-184-009-120	Sequence 120, App	355	53	11.8	345	1	US-08-220-151-19	Sequence 19, Appl
283	54	12.0	984	1	US-08-458-356-120	Sequence 120, App	356	53	11.8	345	1	US-08-413-118-20	Sequence 20, Appl
284	54	12.0	984	2	US-08-460-736-120	Sequence 120, App	357	53	11.8	345	1	US-08-413-118-19	Sequence 19, Appl
285	54	12.0	984	2	US-09-535-370-120	Sequence 120, App	358	53	11.8	345	1	US-08-413-118-20	Sequence 20, Appl
286	54	12.0	984	2	US-09-663-667-120	Sequence 120, App	359	53	11.8	345	1	US-08-413-118-128	Sequence 128, App
287	54	12.0	989	2	US-08-213-419B-2	Sequence 2, Appli	360	53	11.8	345	1	US-08-680-726A-54	Sequence 54, Appl
288	54	12.0	989	2	US-08-213-419B-4	Sequence 4, Appli	361	53	11.8	345	1	US-08-332-562A-132	Sequence 132, App
289	53.5	11.9	113	2	US-09-232-290-25	Sequence 25, Appl	362	53	11.8	345	2	US-08-473-446-19	Sequence 19, Appl
290	53.5	11.9	141	2	US-09-248-796A-20650	Sequence 20650, A	363	53	11.8	345	2	US-08-473-446-20	Sequence 20, Appl
291	53.5	11.9	148	2	US-09-621-976-4783	Sequence 4783, Ap	364	53	11.8	345	2	US-08-473-446-128	Sequence 128, App
292	53.5	11.9	226	2	US-09-456-090A-72	Sequence 72, Appl	365	53	11.8	345	2	US-09-092-409-54	Sequence 54, Appl
293	53.5	11.9	226	2	US-09-453-234-72	Sequence 6, Appli	366	53	11.8	379	2	US-09-949-016-10257	Sequence 10257, A
294	53.5	11.9	235	2	US-08-781-420-6	Sequence 6, Appli	367	53	11.8	467	2	US-09-002-361-3	Sequence 3, Appli
295	53.5	11.9	235	2	US-08-874-102-6	Sequence 6, Appli	368	53	11.8	481	4	PCT-US91-02166-13	Sequence 13, Appl
296	53.5	11.9	235	2	US-08-984-919A-6	Sequence 6, Appli	369	53	11.8	491	2	US-10-011-125A-2	Sequence 2, Appli
297	53.5	11.9	235	2	US-09-006-595A-6	Sequence 6, Appli	370	53	11.8	496	2	US-09-002-361-2	Sequence 2, Appli
298	53.5	11.9	268	2	US-09-647-224A-20	Sequence 20, Appl	371	53	11.8	686	2	US-09-248-796A-18636	Sequence 18636, A
299	53.5	11.9	297	2	US-09-252-991A-18764	Sequence 18764, A	372	53	11.8	742	2	US-09-107-532A-6890	Sequence 6890, Ap
300	53.5	11.9	342	2	US-10-104-047-2985	Sequence 2985, Ap	373	53	11.8	754	2	US-09-214-564A-2	Sequence 2, Appli
301	53.5	11.9	359	2	US-09-270-767-43751	Sequence 43751, A	374	53	11.8	808	2	US-10-104-047-3401	Sequence 3401, Ap
302	53.5	11.9	366	2	US-08-984-919A-11	Sequence 11, Appl	375	53	11.8	858	2	US-07-956-483-17	Sequence 17, Appl
303	53.5	11.9	368	2	US-09-000-092-2	Sequence 2, Appli	376	53	11.8	858	2	US-09-206-551-18	Sequence 18, Appl
304	53.5	11.9	368	2	US-09-000-092-4	Sequence 4, Appli	377	53	11.8	1337	2	US-08-854-585-2	Sequence 2, Appli
305	53.5	11.9	368	2	US-09-000-092-8	Sequence 8, Appli	378	53	11.8	1337	2	US-09-447-533-2	Sequence 2, Appli
306	53.5	11.9	368	2	US-09-000-092-10	Sequence 10, Appl	379	53	11.8	1337	4	PCT-US95-05512-2	Sequence 2, Appli
307	53.5	11.9	368	2	US-08-781-420-11	Sequence 11, Appl	380	52.5	11.7	99	2	US-09-073-009-141	Sequence 141, App
308	53.5	11.9	368	2	US-08-874-102-11	Sequence 11, Appl	381	52.5	11.7	99	2	US-09-073-010-141	Sequence 141, App
309	53.5	11.9	368	2	US-09-006-595A-11	Sequence 11, Appl	382	52.5	11.7	116	2	US-09-270-767-33915	Sequence 33915, A
310	53.5	11.9	466	2	US-08-984-919A-33	Sequence 33, Appl	383	52.5	11.7	116	2	US-09-270-767-49132	Sequence 49132, A
311	53.5	11.9	468	2	US-08-874-102-33	Sequence 33, Appl	384	52.5	11.7	172	2	US-09-270-767-37433	Sequence 37433, A
312	53.5	11.9	470	2	US-08-984-919A-55	Sequence 55, Appl	385	52.5	11.7	172	2	US-09-270-767-52650	Sequence 52650, A
313	53.5	11.9	472	2	US-08-874-102-55	Sequence 55, Appl	386	52.5	11.7	232	1	US-08-704-744-80	Sequence 80, Appl
314	53.5	11.9	482	2	US-09-252-991A-21327	Sequence 21327, A	387	52.5	11.7	237	1	US-08-469-537A-85	Sequence 85, Appl
315	53.5	11.9	495	2	US-08-984-919A-47	Sequence 47, Appl	388	52.5	11.7	251	4	PCT-US96-01314-59	Sequence 59, Appl
316	53.5	11.9	497	2	US-08-874-102-47	Sequence 47, Appl	389	52.5	11.7	288	2	US-09-818-247-22	Sequence 22, Appl
317	53.5	11.9	519	2	US-09-270-767-57156	Sequence 57156, A	390	52.5	11.7	290	2	US-09-643-596B-144	Sequence 144, App
318	53.5	11.9	615	1	US-08-752-307B-9	Sequence 9, Appli	391	52.5	11.7	305	2	US-09-270-767-59446	Sequence 59446, A
319	53.5	11.9	615	2	US-09-707-802-9	Sequence 9, Appli	392	52.5	11.7	318	1	US-07-704-288C-9	Sequence 9, Appli

393	52.5	11.7	318	1	US-08-379-259-9	Sequence 9, Appli	466	52	11.6	259	2	US-09-911-513-6	Sequence 6, Appli
394	52.5	11.7	319	2	US-09-270-767-44038	Sequence 44038, A	467	52	11.6	272	2	US-09-583-110-5240	Sequence 5240, Ap
395	52.5	11.7	328	2	US-07-791-931-7	Sequence 7, Appli	468	52	11.6	282	2	US-09-117-853-8	Sequence 8, Appli
396	52.5	11.7	370	2	US-08-857-076-107	Sequence 107, App	469	52	11.6	282	2	US-09-911-154-8	Sequence 8, Appli
397	52.5	11.7	370	2	US-09-205-658-107	Sequence 107, App	470	52	11.6	282	2	US-09-911-514-8	Sequence 8, Appli
398	52.5	11.7	387	2	US-09-563-269-2	Sequence 2, Appli	471	52	11.6	282	2	US-09-911-513-8	Sequence 8, Appli
399	52.5	11.7	387	2	US-09-643-596B-136	Sequence 136, App	472	52	11.6	287	2	US-09-107-433-5100	Sequence 5100, Ap
400	52.5	11.7	460	1	US-08-933-821-17	Sequence 17, Appl	473	52	11.6	317	1	US-08-619-362A-8	Sequence 8, Appli
401	52.5	11.7	460	2	US-08-934-494-6	Sequence 6, Appli	474	52	11.6	318	1	US-08-960-022-4	Sequence 4, Appli
402	52.5	11.7	460	2	US-08-960-507-17	Sequence 17, Appl	475	52	11.6	334	2	US-09-248-796A-16418	Sequence 16418, A
403	52.5	11.7	460	2	US-08-143-068-6	Sequence 6, Appli	476	52	11.6	418	2	US-09-019-095A-10	Sequence 10, Appl
404	52.5	11.7	460	2	US-09-143-707-6	Sequence 6, Appli	477	52	11.6	471	2	US-09-071-709-4	Sequence 4, Appli
405	52.5	11.7	460	2	US-09-202-089-6	Sequence 6, Appli	478	52	11.6	471	2	US-09-160-494-2	Sequence 2, Appli
406	52.5	11.7	460	2	US-09-136-828-17	Sequence 17, Appl	479	52	11.6	471	2	US-09-713-669-4	Sequence 4, Appli
407	52.5	11.7	460	2	US-09-332-928A-17	Sequence 17, Appl	480	52	11.6	491	2	US-09-710-279-2808	Sequence 2808, Ap
408	52.5	11.7	460	2	US-09-511-133-6	Sequence 6, Appli	481	52	11.6	494	2	US-09-477-962-104	Sequence 104, App
409	52.5	11.7	460	2	US-09-136-801-17	Sequence 17, Appl	482	52	11.6	517	2	US-09-487-558B-100	Sequence 100, App
410	52.5	11.7	460	2	US-09-332-929-17	Sequence 17, Appl	483	52	11.6	532	2	US-09-117-853-2	Sequence 2, Appli
411	52.5	11.7	460	2	US-09-690-169-6	Sequence 6, Appli	484	52	11.6	532	2	US-09-911-154-2	Sequence 2, Appli
412	52.5	11.7	460	2	US-09-511-631-6	Sequence 6, Appli	485	52	11.6	532	2	US-09-485-529-2	Sequence 2, Appli
413	52.5	11.7	460	2	US-09-333-075-17	Sequence 17, Appl	486	52	11.6	532	2	US-09-911-514-2	Sequence 2, Appli
414	52.5	11.7	460	2	US-09-690-189-6	Sequence 6, Appli	487	52	11.6	532	2	US-09-911-513-2	Sequence 2, Appli
415	52.5	11.7	460	2	US-09-202-088A-17	Sequence 17, Appl	488	52	11.6	534	2	US-09-248-796A-19568	Sequence 19568, A
416	52.5	11.7	460	2	US-09-333-077-17	Sequence 17, Appl	489	52	11.6	681	2	US-08-760-615-4	Sequence 4, Appli
417	52.5	11.7	475	2	US-09-949-016-7940	Sequence 7940, Ap	490	52	11.6	681	2	US-09-336-910A-2	Sequence 2, Appli
418	52.5	11.7	613	2	US-09-949-016-7353	Sequence 7353, Ap	491	52	11.6	2496	2	US-09-125-028-2	Sequence 2, Appli
419	52.5	11.7	651	2	US-09-949-016-8426	Sequence 8426, Ap	492	52	11.6	2958	2	US-08-894-344C-2	Sequence 2, Appli
420	52.5	11.7	798	1	US-07-728-215-30	Sequence 30, Appl	493	52	11.6	2958	2	US-09-678-023A-2	Sequence 2, Appli
421	52.5	11.7	798	2	US-08-938-085A-30	Sequence 30, Appl	494	52	11.6	3460	2	US-09-334-220-1	Sequence 1, Appli
422	52.5	11.7	798	2	US-10-072-844-30	Sequence 30, Appl	495	51.5	11.5	79	2	US-09-248-796A-21029	Sequence 21029, A
423	52.5	11.7	798	2	US-10-072-838-30	Sequence 30, Appl	496	51.5	11.5	91	2	US-09-248-796A-22642	Sequence 22642, A
424	52.5	11.7	798	2	US-10-072-841A-30	Sequence 30, Appl	497	51.5	11.5	101	2	US-09-461-325-214	Sequence 214, App
425	52.5	11.7	798	2	US-10-219-631A-30	Sequence 30, Appl	498	51.5	11.5	101	2	US-10-012-542-214	Sequence 214, App
426	52.5	11.7	798	2	US-09-949-016-6193	Sequence 6193, Ap	499	51.5	11.5	101	2	US-10-115-123-214	Sequence 214, App
427	52.5	11.7	886	2	US-08-956-171E-5235	Sequence 5235, Ap	500	51.5	11.5	106	2	US-08-397-411-8	Sequence 8, Appli
428	52.5	11.7	886	2	US-08-781-986A-5235	Sequence 5235, Ap	501	51.5	11.5	107	2	US-09-438-954-1	Sequence 1, Appli
429	52.5	11.7	909	2	US-10-172-502-6	Sequence 6, Appli	502	51.5	11.5	142	2	US-09-380-882-9	Sequence 9, Appli
430	52.5	11.7	1041	1	US-08-494-714-2	Sequence 2, Appli	503	51.5	11.5	158	2	US-09-270-767-38728	Sequence 38728, A
431	52.5	11.7	1041	4	PCT-US96-10782-2	Sequence 2, Appli	504	51.5	11.5	158	2	US-09-270-767-53945	Sequence 53945, A
432	52.5	11.7	1367	1	US-08-249-687C-2	Sequence 2, Appli	505	51.5	11.5	163	2	US-09-252-991A-17451	Sequence 17451, A
433	52.5	11.7	1367	1	US-08-625-819-2	Sequence 2, Appli	506	51.5	11.5	171	2	US-09-248-796A-25024	Sequence 25024, A
434	52.5	11.7	1367	2	US-08-746-559A-2	Sequence 2, Appli	507	51.5	11.5	183	2	US-09-328-352-5634	Sequence 5634, Ap
435	52.5	11.7	1367	2	US-08-864-641B-18	Sequence 18, Appl	508	51.5	11.5	197	2	US-09-252-991A-28579	Sequence 28579, A
436	52.5	11.7	1367	2	US-09-343-551-2	Sequence 2, Appli	509	51.5	11.5	213	2	US-10-104-047-2722	Sequence 2722, Ap
437	52.5	11.7	1367	2	US-09-949-001-18	Sequence 18, Appl	510	51.5	11.5	226	2	US-09-456-090A-38	Sequence 38, Appl
438	52.5	11.7	1377	2	US-09-949-001-21	Sequence 21, Appl	511	51.5	11.5	226	2	US-09-456-090A-74	Sequence 74, Appl
439	52.5	11.7	3788	2	US-09-336-447A-76	Sequence 76, Appl	512	51.5	11.5	226	2	US-09-453-234-38	Sequence 38, Appl
440	52.5	11.7	3788	2	US-09-952-267B-76	Sequence 76, Appl	513	51.5	11.5	226	2	US-09-453-234-74	Sequence 74, Appl
441	52	11.6	76	2	US-09-252-991A-25030	Sequence 25030, A	514	51.5	11.5	258	2	US-09-248-796A-23723	Sequence 23723, A
442	52	11.6	83	2	US-09-270-767-38732	Sequence 38732, A	515	51.5	11.5	277	2	US-09-354-151-3	Sequence 3, Appli
443	52	11.6	83	2	US-09-270-767-53949	Sequence 53949, A	516	51.5	11.5	310	2	US-09-907-794A-423	Sequence 423, App
444	52	11.6	141	2	US-09-472-087-88	Sequence 88, Appl	517	51.5	11.5	310	2	US-09-905-125A-423	Sequence 423, App
445	52	11.6	144	2	US-09-949-016-11102	Sequence 11102, A	518	51.5	11.5	310	2	US-09-902-775A-423	Sequence 423, App
446	52	11.6	167	1	US-08-627-610-6	Sequence 6, Appli	519	51.5	11.5	310	2	US-09-906-700-423	Sequence 423, App
447	52	11.6	168	1	US-08-508-735-46	Sequence 46, Appl	520	51.5	11.5	310	2	US-09-903-603A-423	Sequence 423, App
448	52	11.6	168	2	US-09-201-139-46	Sequence 46, Appl	521	51.5	11.5	310	2	US-09-904-920A-423	Sequence 423, App
449	52	11.6	218	4	PCT-US96-13152-2	Sequence 2, Appli	522	51.5	11.5	310	2	US-09-909-064-423	Sequence 423, App
450	52	11.6	221	2	US-09-117-853-4	Sequence 4, Appli	523	51.5	11.5	310	2	US-09-905-381A-423	Sequence 423, App
451	52	11.6	221	2	US-09-911-154-4	Sequence 4, Appli	524	51.5	11.5	310	2	US-09-906-618-423	Sequence 423, App
452	52	11.6	221	2	US-09-911-514-4	Sequence 4, Appli	525	51.5	11.5	310	2	US-09-906-646-423	Sequence 423, App
453	52	11.6	221	2	US-09-911-513-4	Sequence 4, Appli	526	51.5	11.5	310	2	US-09-904-462-423	Sequence 423, App
454	52	11.6	233	1	US-08-792-824-6	Sequence 6, Appli	527	51.5	11.5	310	2	US-09-902-736A-423	Sequence 423, App
455	52	11.6	233	2	US-09-216-393B-110	Sequence 110, App	528	51.5	11.5	310	2	US-10-033-301-20	Sequence 20, Appl
456	52	11.6	235	2	US-09-472-087-14	Sequence 14, Appl	529	51.5	11.5	310	2	US-09-906-722A-423	Sequence 423, App
457	52	11.6	235	2	US-09-472-087-65	Sequence 65, Appl	530	51.5	11.5	376	2	US-09-404-296B-32	Sequence 32, Appl
458	52	11.6	236	1	US-08-792-824-3	Sequence 3, Appli	531	51.5	11.5	436	2	US-10-169-048-50	Sequence 50, Appl
459	52	11.6	236	1	US-08-792-824-9	Sequence 9, Appli	532	51.5	11.5	448	2	US-09-717-364A-7	Sequence 7, Appli
460	52	11.6	236	1	US-08-792-824-12	Sequence 12, Appl	533	51.5	11.5	511	2	US-08-646-695-5	Sequence 5, Appli
461	52	11.6	236	2	US-09-726-219A-188	Sequence 188, App	534	51.5	11.5	511	4	PCT-US96-06053-5	Sequence 5, Appli
462	52	11.6	236	2	US-09-196-522-188	Sequence 188, App	535	51.5	11.5	668	2	US-09-248-796A-19350	Sequence 19350, A
463	52	11.6	259	2	US-09-117-853-6	Sequence 6, Appli	536	51.5	11.5	1676	2	US-09-949-016-7610	Sequence 7610, Ap
464	52	11.6	259	2	US-09-911-154-6	Sequence 6, Appli	537	51.5	11.5	3635	2	US-09-845-583A-2	Sequence 2, Appli
465	52	11.6	259	2	US-09-911-514-6	Sequence 6, Appli	538	51.5	11.5	3635	2	US-10-037-417-47	Sequence 47, Appl

539	51.5	11.5	3635	2	US-10-037-182-4	Sequence 4, Appli	612	50.5	11.2	254	1	US-08-047-413-9	Sequence 9, Appli
540	51.5	11.5	3852	2	US-10-025-225-4	Sequence 4, Appli	613	50.5	11.2	254	2	US-08-229-050-9	Sequence 9, Appli
541	51.5	11.5	4585	2	US-10-025-225-6	Sequence 6, Appli	614	50.5	11.2	254	2	US-08-801-563-9	Sequence 9, Appli
542	51.5	11.5	4588	2	US-10-025-225-8	Sequence 8, Appli	615	50.5	11.2	281	2	US-09-270-767-58184	Sequence 58184, A
543	51.5	11.5	4589	2	US-10-025-225-2	Sequence 2, Appli	616	50.5	11.2	289	2	US-09-489-039A-12627	Sequence 12627, A
544	51	11.4	88	2	US-09-248-796A-18363	Sequence 18363, A	617	50.5	11.2	294	2	US-09-328-352-7430	Sequence 7430, Ap
545	51	11.4	96	2	US-09-270-767-48032	Sequence 48032, A	618	50.5	11.2	338	2	US-09-489-039A-12787	Sequence 12787, A
546	51	11.4	148	2	US-09-270-767-31975	Sequence 31975, A	619	50.5	11.2	361	2	US-09-032-372-12	Sequence 12, Appl
547	51	11.4	148	2	US-09-270-767-47192	Sequence 47192, A	620	50.5	11.2	377	2	US-09-489-039A-9429	Sequence 9429, Ap
548	51	11.4	151	1	US-08-387-942C-50	Sequence 50, Appl	621	50.5	11.2	418	2	US-09-328-352-4525	Sequence 4525, Ap
549	51	11.4	161	2	US-09-252-991A-18142	Sequence 18142, A	622	50.5	11.2	454	2	US-09-470-512A-8	Sequence 8, Appli
550	51	11.4	195	2	US-09-134-001C-5045	Sequence 5045, Ap	623	50.5	11.2	486	2	US-09-270-767-42864	Sequence 42864, A
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556	51	11.4	224	2	US-09-453-234-46	Sequence 46, Appl	629	50.5	11.2	607	2	US-08-685-467-6	Sequence 6, Appli
557	51	11.4	234	4	PCT-US94-07659-4	Sequence 4, Appli	630	50.5	11.2	607	2	US-08-913-942-6	Sequence 6, Appli
558	51	11.4	252	2	US-09-270-767-40634	Sequence 40634, A	631	50.5	11.2	607	2	US-09-684-707-6	Sequence 6, Appli
559	51	11.4	252	2	US-09-270-767-55850	Sequence 55850, A	632	50.5	11.2	722	2	US-09-198-452A-513	Sequence 513, App
560	51	11.4	260	2	US-08-081-929-10	Sequence 10, Appl	633	50.5	11.2	722	2	US-09-438-185A-477	Sequence 477, App
561	51	11.4	260	2	US-10-000-954-10	Sequence 10, Appl	634	50.5	11.2	790	2	US-09-270-767-45954	Sequence 45954, A
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572	51	11.4	550	2	US-09-107-433-3858	Sequence 3858, Ap	645	50.5	11.2	1752	2	US-09-949-002-294	Sequence 294, App
573	51	11.4	627	2	US-10-246-658-4	Sequence 4, Appli	646	50.5	11.2	1917	2	US-09-949-002-485	Sequence 485, App
574	51	11.4	627	2	US-10-843-131-4	Sequence 4, Appli	647	50.5	11.2	2167	2	US-09-487-558B-56	Sequence 56, Appl
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584	51	11.4	1097	1	US-07-943-843-6	Sequence 6, Appli	657	50	11.1	196	2	US-10-012-231A-216	Sequence 216, App
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586	51	11.4	1097	2	US-09-949-016-6209	Sequence 6209, Ap	659	50	11.1	196	2	US-10-006-768A-216	Sequence 216, App
587	51	11.4	1119	2	US-09-949-016-10081	Sequence 10081, A	660	50	11.1	196	2	US-10-015-671A-216	Sequence 216, App
588	51	11.4	1148	2	US-09-949-016-8328	Sequence 8328, Ap	661	50	11.1	196	2	US-10-015-393A-216	Sequence 216, App
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591	51	11.4	1187	1	US-09-003-289-8	Sequence 8, Appli	664	50	11.1	196	2	US-10-012-064A-216	Sequence 216, App
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593	51	11.4	1187	2	US-08-946-994-13	Sequence 13, Appl	666	50	11.1	221	1	US-08-480-229C-29	Sequence 29, Appl
594	51	11.4	1187	2	US-08-946-994-13	Sequence 13, Appl	667	50	11.1	221	1	US-08-659-235C-29	Sequence 29, Appl
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596	51	11.4	1302	2	US-09-949-016-10852	Sequence 10852, A	669	50	11.1	230	2	US-09-333-809-221	Sequence 221, App
597	51	11.4	1402	2	US-09-125-635-12	Sequence 12, Appl	670	50	11.1	230	2	US-09-333-809-222	Sequence 222, App
598	51	11.4	1402	2	US-09-445-353E-2	Sequence 2, Appli	671	50	11.1	230	2	US-09-333-809-223	Sequence 223, App
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606	50.5	11.2	108	2	US-09-848-798-41	Sequence 41, Appl	679	50	11.1	230	2	US-09-746-311B-373	Sequence 373, App
607	50.5	11.2	183	2	US-09-270-767-45510	Sequence 45510, A	680	50	11.1	230	2	US-09-746-311B-374	Sequence 374, App
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610	50.5	11.2	248	2	US-09-248-796A-20545	Sequence 20545, A	683	50	11.1	230	2	US-09-746-311B-377	Sequence 377, App
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689	50	11.1	330	2	US-09-248-796A-16751	Sequence 16751, A	762	50	11.1	1523	2	US-10-015-389A-198	Sequence 198, App
690	50	11.1	349	2	US-08-462-467B-18	Sequence 18, Appl	763	50	11.1	1523	2	US-10-006-768A-198	Sequence 198, App
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692	50	11.1	430	2	US-09-270-767-43174	Sequence 43174, A	765	50	11.1	1523	2	US-10-015-393A-198	Sequence 198, App
693	50	11.1	430	2	US-09-964-956-76	Sequence 76, Appl	766	50	11.1	1523	2	US-10-011-833A-198	Sequence 198, App
694	50	11.1	436	2	US-08-709-974A-2	Sequence 2, Appli	767	50	11.1	1523	2	US-10-006-041A-198	Sequence 198, App
695	50	11.1	446	2	US-09-902-540-12677	Sequence 12677, A	768	50	11.1	1523	2	US-10-012-064A-198	Sequence 198, App
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702	50	11.1	554	2	US-08-462-467B-22	Sequence 22, Appl	775	49.5	11.0	111	2	US-09-823-746-12	Sequence 12, Appl
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705	50	11.1	592	1	US-08-217-327-8	Sequence 8, Appli	778	49.5	11.0	135	2	US-09-270-767-34805	Sequence 34805, A
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711	50	11.1	652	6	5258288-4	Patent No. 5258288	784	49.5	11.0	204	2	US-09-252-991A-29026	Sequence 29026, A
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726	50	11.1	829	2	US-10-055-364-46	Sequence 46, Appl	799	49.5	11.0	259	2	US-08-481-985B-117	Sequence 117, App
727	50	11.1	854	2	US-09-350-841A-1589	Sequence 1589, Ap	800	49.5	11.0	259	2	US-08-370-476-117	Sequence 117, App
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737	50	11.1	856	2	US-08-485-546A-103	Sequence 103, App	810	49.5	11.0	425	2	US-09-274-570-3	Sequence 3, Appli
738	50	11.1	856	2	US-08-487-266A-103	Sequence 103, App	811	49.5	11.0	431	2	US-09-479-614-14	Sequence 14, Appl
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741	50	11.1	857	1	US-08-413-118-10	Sequence 10, Appl	814	49.5	11.0	496	2	US-09-479-614-29	Sequence 29, Appl
742	50	11.1	857	2	US-08-804-439A-18	Sequence 18, Appl	815	49.5	11.0	496	2	US-09-479-614-29	Sequence 29, Appl
743	50	11.1	857	2	US-08-360-107A-113	Sequence 113, App	816	49.5	11.0	539	2	US-09-719-402A-2	Sequence 2, Appli
744	50	11.1	857	2	US-08-473-446-10	Sequence 10, Appl	817	49.5	11.0	593	2	US-09-489-039A-8609	Sequence 8609, Ap
745	50	11.1	857	2	US-08-720-229-18	Sequence 18, Appl	818	49.5	11.0	633	2	US-09-041-991A-10	Sequence 10, Appl
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753	50	11.1	1065	2	US-09-949-016-11618	Sequence 11618, A	826	49.5	11.0	790	1	US-08-286-846A-9	Sequence 9, Appli
754	50	11.1	1280	2	US-09-377-285B-18	Sequence 18, Appl	827	49.5	11.0	790	1	US-08-457-880A-9	Sequence 9, Appli
755	50	11.1	1280	2	US-10-192-381-18	Sequence 18, Appl	828	49.5	11.0	790	2	US-08-444-622A-9	Sequence 9, Appli
756	50	11.1	1323	1	US-08-026-138E-4	Sequence 4, Appli	829	49.5	11.0	790	2	US-08-942-562-9	Sequence 9, Appli
757	50	11.1	1345	2	US-09-949-016-11209	Sequence 11209, A	830	49.5	11.0	790	2	US-09-156-923-9	Sequence 9, Appli

831	49.5	11.0	814	1	US-08-286-305A-3	Sequence 3, Appli	904	49	10.9	886	2	US-09-631-603-14	Sequence 14, Appl
832	49.5	11.0	814	1	US-08-441-104A-3	Sequence 3, Appli	905	49	10.9	906	2	US-09-252-991A-31458	Sequence 31458, A
833	49.5	11.0	814	1	US-08-440-816A-3	Sequence 3, Appli	906	49	10.9	1031	2	US-09-914-259-24	Sequence 24, Appl
834	49.5	11.0	814	2	US-09-417-381A-3	Sequence 3, Appli	907	49	10.9	1456	2	US-09-976-594-168	Sequence 168, App
835	49.5	11.0	877	2	US-09-619-353-2	Sequence 2, Appli	908	48.5	10.8	70	2	US-09-621-976-6026	Sequence 6026, Ap
836	49.5	11.0	877	2	US-09-206-551-20	Sequence 20, Appl	909	48.5	10.8	91	2	US-09-621-976-6959	Sequence 6959, Ap
837	49.5	11.0	970	2	US-09-248-796A-16191	Sequence 16191, A	910	48.5	10.8	107	2	US-09-438-954-3	Sequence 3, Appli
838	49.5	11.0	1137	1	US-08-365-043-2	Sequence 2, Appli	911	48.5	10.8	108	2	US-09-240-274-32	Sequence 32, Appl
839	49.5	11.0	1175	2	US-09-252-991A-25044	Sequence 25044, A	912	48.5	10.8	108	2	US-09-240-274-43	Sequence 43, Appl
840	49.5	11.0	1193	1	US-08-400-159-10	Sequence 10, Appl	913	48.5	10.8	108	2	US-09-240-274-167	Sequence 167, App
841	49.5	11.0	1193	2	US-08-611-729A-10	Sequence 10, Appl	914	48.5	10.8	108	2	US-09-848-798-32	Sequence 32, Appl
842	49.5	11.0	1193	2	US-09-195-524-10	Sequence 10, Appl	915	48.5	10.8	108	2	US-09-848-798-43	Sequence 43, Appl
843	49.5	11.0	1193	2	US-09-310-685-8	Sequence 8, Appli	916	48.5	10.8	108	2	US-09-848-798-167	Sequence 167, App
844	49.5	11.0	1237	1	US-08-241-853-2	Sequence 2, Appli	917	48.5	10.8	110	2	US-09-025-769B-30	Sequence 30, Appl
845	49.5	11.0	1237	1	US-08-850-917-2	Sequence 2, Appli	918	48.5	10.8	110	2	US-09-025-769B-47	Sequence 47, Appl
846	49.5	11.0	1377	2	US-09-711-164-467	Sequence 467, App	919	48.5	10.8	110	2	US-09-490-070A-30	Sequence 30, Appl
847	49	10.9	61	2	US-09-674-973A-243	Sequence 243, App	920	48.5	10.8	110	2	US-09-490-070A-47	Sequence 47, Appl
848	49	10.9	64	2	US-09-300-008B-44	Sequence 44, Appl	921	48.5	10.8	110	2	US-09-490-153-30	Sequence 30, Appl
849	49	10.9	71	2	US-09-248-796A-26023	Sequence 26023, A	922	48.5	10.8	110	2	US-09-490-153-47	Sequence 47, Appl
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851	49	10.9	104	2	US-09-178-881-5	Sequence 5, Appli	924	48.5	10.8	110	2	US-09-490-324-47	Sequence 47, Appl
852	49	10.9	104	2	US-09-621-976-4800	Sequence 4800, Ap	925	48.5	10.8	112	2	US-09-252-991A-17063	Sequence 17063, A
853	49	10.9	142	2	US-09-472-087-19	Sequence 19, Appl	926	48.5	10.8	126	1	US-08-656-586-6	Sequence 6, Appli
854	49	10.9	142	2	US-09-472-087-92	Sequence 92, Appl	927	48.5	10.8	139	2	US-09-252-991A-18862	Sequence 18862, A
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856	49	10.9	187	2	US-09-270-767-49927	Sequence 34710, A	929	48.5	10.8	168	2	US-09-270-767-46658	Sequence 46658, A
857	49	10.9	187	2	US-09-270-767-49927	Sequence 49927, A	930	48.5	10.8	179	2	US-09-252-991A-22072	Sequence 22072, A
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860	49	10.9	212	2	US-09-270-767-48657	Sequence 48657, A	933	48.5	10.8	226	2	US-09-134-001C-3578	Sequence 3578, Ap
861	49	10.9	241	2	US-09-489-039A-12829	Sequence 12829, A	934	48.5	10.8	233	2	US-09-252-991A-18455	Sequence 18455, A
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865	49	10.9	292	2	US-09-248-796A-16215	Sequence 16215, A	938	48.5	10.8	264	1	US-08-484-905-120	Sequence 120, App
866	49	10.9	315	2	US-09-248-796A-18003	Sequence 18003, A	939	48.5	10.8	264	2	US-08-481-985B-120	Sequence 120, App
867	49	10.9	333	2	US-09-540-236-2769	Sequence 2769, Ap	940	48.5	10.8	264	2	US-08-969-644-16	Sequence 16, Appl
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870	49	10.9	386	2	US-09-130-491-6	Sequence 6, Appli	943	48.5	10.8	264	2	US-08-468-544-16	Sequence 16, Appl
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872	49	10.9	386	2	US-09-769-402-2	Sequence 2, Appli	945	48.5	10.8	276	1	US-08-183-213-2	Sequence 2, Appli
873	49	10.9	386	2	US-09-949-002-357	Sequence 357, App	946	48.5	10.8	338	1	US-08-359-850-2	Sequence 15, Appl
874	49	10.9	399	2	US-09-949-002-437	Sequence 437, App	947	48.5	10.8	343	2	US-09-922-501-15	Sequence 2, Appli
875	49	10.9	401	2	US-09-270-767-42828	Sequence 42828, A	948	48.5	10.8	344	2	US-09-392-772-2	Sequence 2, Appli
876	49	10.9	453	2	US-09-134-001C-3749	Sequence 3749, Ap	949	48.5	10.8	352	2	US-09-270-767-42197	Sequence 2624, Ap
877	49	10.9	515	2	US-09-489-039A-10635	Sequence 10635, A	950	48.5	10.8	415	2	US-10-104-047-2624	Sequence 11, Appl
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881	49	10.9	614	2	US-09-388-743-18	Sequence 18, Appl	954	48.5	10.8	491	4	PCT-US92-10511-2	Patent No. 5378464
882	49	10.9	614	2	US-10-044-543-18	Sequence 18, Appl	955	48.5	10.8	574	6	5378464-3	Sequence 10, Appl
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884	49	10.9	640	2	US-09-252-991A-20343	Sequence 20343, A	957	48.5	10.8	590	1	US-08-756-317-12	Sequence 216, App
885	49	10.9	689	2	US-09-949-016-8258	Sequence 8258, Ap	958	48.5	10.8	613	2	US-09-170-496D-216	Sequence 218, App
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887	49	10.9	713	2	US-08-477-346-63	Sequence 63, Appl	960	48.5	10.8	624	2	US-09-248-796A-24363	Sequence 15, Appl
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889	49	10.9	713	2	US-08-487-072A-63	Sequence 63, Appl	962	48.5	10.8	625	2	US-08-995-659-15	Sequence 15, Appl
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891	49	10.9	713	2	US-09-487-558B-408	Sequence 408, App	964	48.5	10.8	625	2	US-09-577-780-15	Sequence 15, Appl
892	49	10.9	721	2	US-08-872-855-7	Sequence 7, Appli	965	48.5	10.8	625	2	US-09-577-800-15	Sequence 15, Appl
893	49	10.9	721	2	US-08-901-392-5	Sequence 5, Appli	966	48.5	10.8	625	2	US-09-466-496-15	Sequence 15, Appl
894	49	10.9	721	2	US-09-908-322-5	Sequence 5, Appli	967	48.5	10.8	625	2	US-09-871-856-15	Sequence 15, Appl
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897	49	10.9	747	2	US-09-583-110-3066	Sequence 3066, Ap	970	48.5	10.8	625	2	US-09-865-363-15	Sequence 15, Appl
898	49	10.9	751	2	US-09-107-433-3375	Sequence 3375, Ap	971	48.5	10.8	625	2	US-09-688-459-15	Sequence 15, Appl
899	49	10.9	815	2	US-09-914-259-18	Sequence 18, Appl	972	48.5	10.8	625	2	US-09-957-944-4	Sequence 4, Appli
900	49	10.9	848	2	US-09-538-092-33	Sequence 33, Appl	973	48.5	10.8	644	2	US-09-248-796A-17325	Sequence 17325, A
901	49	10.9	849	1	US-08-162-809-6	Sequence 6, Appli	974	48.5	10.8	661	2	US-09-198-452A-36	Sequence 36, Appl
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978	48.5	10.8	830	1	US-08-110-158-4	Sequence 4, Appli	1051	48	10.7	318	1	US-08-619-362A-9	Sequence 9, Appli
979	48.5	10.8	842	4	PCT-US96-02331-15	Sequence 15, Appl	1052	48	10.7	318	2	US-09-058-368-3	Sequence 3, Appli
980	48.5	10.8	843	2	US-09-543-681A-7176	Sequence 7176, Ap	1053	48	10.7	318	2	US-09-930-026-3	Sequence 3, Appli
981	48.5	10.8	849	2	US-09-949-016-10271	Sequence 10271, A	1054	48	10.7	325	2	US-09-701-623C-1	Sequence 1, Appli
982	48.5	10.8	992	2	US-09-252-991A-27095	Sequence 27095, A	1055	48	10.7	331	2	US-09-401-636-1	Sequence 1, Appli
983	48.5	10.8	1070	2	US-09-107-532A-3716	Sequence 3716, Ap	1056	48	10.7	332	1	US-08-637-763B-8	Sequence 8, Appli
984	48.5	10.8	1231	2	US-08-714-741-41	Sequence 41, Appl	1057	48	10.7	332	2	US-09-170-354-8	Sequence 8, Appli
985	48.5	10.8	1249	2	US-09-964-899-33	Sequence 33, Appl	1058	48	10.7	379	2	US-09-934-868-50	Sequence 50, Appl
986	48.5	10.8	1336	1	US-08-551-356-6	Sequence 6, Appli	1059	48	10.7	379	2	US-10-701-200-50	Sequence 50, Appl
987	48.5	10.8	1336	4	PCT-US93-12687-6	Sequence 6, Appli	1060	48	10.7	427	2	US-09-270-767-45426	Sequence 45426, A
988	48.5	10.8	1418	2	US-08-963-825-20	Sequence 20, Appl	1061	48	10.7	440	2	US-09-615-192A-290	Sequence 290, App
989	48.5	10.8	1418	2	US-09-010-999-1	Sequence 1, Appli	1062	48	10.7	448	2	US-09-949-016-10130	Sequence 10130, A
990	48.5	10.8	1418	2	US-09-500-811-20	Sequence 20, Appl	1063	48	10.7	459	1	US-08-087-732-2	Sequence 2, Appli
991	48.5	10.8	1418	2	US-09-570-573-20	Sequence 20, Appl	1064	48	10.7	459	6	5210189-2	Patent No. 5210189
992	48.5	10.8	1418	2	US-09-548-608-20	Sequence 20, Appl	1065	48	10.7	460	2	US-09-248-796A-16750	Sequence 16750, A
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994	48.5	10.8	1971	2	US-09-914-272A-1	Sequence 1, Appli	1067	48	10.7	464	2	US-09-823-038A-47	Sequence 47, Appl
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996	48.5	10.8	1971	2	US-10-747-133A-1	Sequence 1, Appli	1069	48	10.7	513	1	US-08-480-229C-14	Sequence 14, Appl
997	48.5	10.8	2231	1	US-08-153-799-16	Sequence 16, Appl	1070	48	10.7	513	1	US-08-659-235C-14	Sequence 14, Appl
998	48.5	10.8	2324	1	US-08-283-857-1	Sequence 1, Appli	1071	48	10.7	513	2	US-09-071-035-68	Sequence 68, Appl
999	48.5	10.8	2324	4	PCT-US95-09819-1	Sequence 1, Appli	1072	48	10.7	513	2	US-10-206-576-68	Sequence 68, Appl
1000	48.5	10.8	2327	6	5455158-1	Patent No. 5455158	1073	48	10.7	532	2	US-09-071-035-66	Sequence 66, Appl
1001	48.5	10.8	2355	2	US-10-360-101-235	Sequence 235, App	1074	48	10.7	532	2	US-10-206-576-66	Sequence 66, Appl
1002	48.5	10.8	2386	1	US-09-016-366A-12	Sequence 12, Appl	1075	48	10.7	540	2	US-09-513-057C-33	Sequence 33, Appl
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1004	48.5	10.8	2446	1	US-08-551-356-2	Sequence 2, Appli	1077	48	10.7	540	2	US-10-719-885-33	Sequence 33, Appl
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1006	48	10.7	44	6	5177197-48	Patent No. 5177197	1079	48	10.7	554	2	US-08-909-125-6	Sequence 6, Appli
1007	48	10.7	67	2	US-09-513-999C-7447	Sequence 7447, Ap	1080	48	10.7	557	2	US-09-248-796A-18379	Sequence 18379, A
1008	48	10.7	77	1	US-07-689-693B-9	Sequence 9, Appli	1081	48	10.7	600	2	US-09-134-000C-6286	Sequence 6286, Ap
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1011	48	10.7	109	1	US-08-037-579A-2	Sequence 2, Appli	1084	48	10.7	699	2	US-09-248-796A-23200	Sequence 23200, A
1012	48	10.7	109	2	US-08-601-184-2	Sequence 2, Appli	1085	48	10.7	732	2	US-09-949-002-291	Sequence 291, App
1013	48	10.7	110	1	US-08-399-106A-6	Sequence 6, Appli	1086	48	10.7	758	2	US-09-487-558B-224	Sequence 224, App
1014	48	10.7	110	1	US-08-433-105A-6	Sequence 6, Appli	1087	48	10.7	761	2	US-09-328-352-7492	Sequence 7492, Ap
1015	48	10.7	110	1	US-08-434-869A-6	Sequence 6, Appli	1088	48	10.7	765	2	US-09-949-002-419	Sequence 419, App
1016	48	10.7	112	2	US-08-442-001C-66	Sequence 66, Appl	1089	48	10.7	823	2	US-09-107-532A-6343	Sequence 6343, Ap
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1018	48	10.7	125	2	US-09-270-767-54759	Sequence 54759, A	1091	48	10.7	832	2	US-10-015-389A-227	Sequence 227, App
1019	48	10.7	131	2	US-09-252-991A-23278	Sequence 23278, A	1092	48	10.7	832	2	US-10-015-389A-227	Sequence 227, App
1020	48	10.7	138	2	US-09-248-796A-24261	Sequence 24261, A	1093	48	10.7	832	2	US-10-006-768A-227	Sequence 227, App
1021	48	10.7	180	2	US-09-949-016-6478	Sequence 6478, Ap	1094	48	10.7	832	2	US-10-015-671A-227	Sequence 227, App
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1024	48	10.7	199	2	US-09-270-767-42408	Sequence 42408, A	1097	48	10.7	832	2	US-10-006-041A-227	Sequence 227, App
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1028	48	10.7	214	2	US-09-680-148-1	Sequence 1, Appli	1100	48	10.7	1093	2	US-09-487-558B-392	Sequence 392, App
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1035	48	10.7	236	1	US-08-157-101A-5	Sequence 5, Appli	1107	48	10.7	2004	2	US-09-030-793-9	Sequence 9, Appli
1036	48	10.7	237	1	US-08-463-587A-25	Sequence 25, Appl	1108	48	10.7	2004	2	US-09-231-899-9	Sequence 9, Appli
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1044	48	10.7	289	2	US-09-949-016-10744	Sequence 10744, A	1116	48	10.7	4563	2	US-09-538-092-842	Sequence 842, App
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							1122	47.5	10.6	106	2	US-09-771-415-21	Sequence 21, Appl

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1129	47.5	10.6	108	2	US-09-240-274-177	Sequence 177, App	1202	47.5	10.6	571	2	US-09-460-295B-13	Sequence 13, Appl
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1157	47.5	10.6	282	2	US-09-909-064-127	Sequence 127, App	1230	47.5	10.6	796	2	US-09-765-272A-56	Sequence 56, Appl
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1159	47.5	10.6	282	2	US-09-906-618-127	Sequence 127, App	1232	47.5	10.6	798	2	US-09-964-956-28	Sequence 28, Appl
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1161	47.5	10.6	282	2	US-09-904-462-127	Sequence 127, App	1234	47.5	10.6	809	2	US-09-186-276B-58	Sequence 58, Appl
1162	47.5	10.6	282	2	US-09-902-736A-127	Sequence 127, App	1235	47.5	10.6	809	2	US-08-842-445-58	Sequence 58, Appl
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1166	47.5	10.6	287	1	US-08-433-783-37	Sequence 37, Appl	1239	47.5	10.6	819	2	US-09-468-656A-8	Sequence 8, Appli
1167	47.5	10.6	287	1	US-08-337-358-37	Sequence 37, Appl	1240	47.5	10.6	829	2	US-09-583-110-3851	Sequence 3851, Ap
1168	47.5	10.6	287	4	PCT-US95-07537A-37	Sequence 37, Appl	1241	47.5	10.6	830	4	PCT-US91-05059-2	Sequence 2, Appli
1169	47.5	10.6	287	4	PCT-US95-07537-37	Sequence 37, Appl	1242	47.5	10.6	830	6	5378464-2	Patent No. 5378464
1170	47.5	10.6	292	2	US-09-134-000C-3527	Sequence 3527, Ap	1243	47.5	10.6	837	2	US-09-964-956-5	Sequence 5, Appli
1171	47.5	10.6	318	2	US-09-248-796A-26749	Sequence 26749, A	1244	47.5	10.6	841	2	US-09-935-430-657	Sequence 657, App
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1173	47.5	10.6	321	2	US-09-107-433-2993	Sequence 2993, Ap	1246	47.5	10.6	879	2	US-09-872-733A-16	Sequence 16, Appl
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1175	47.5	10.6	338	2	US-09-252-991A-16820	Sequence 16820, A	1248	47.5	10.6	989	2	US-09-954-987B-171	Sequence 171, App
1176	47.5	10.6	339	2	US-08-444-818-158	Sequence 158, App	1249	47.5	10.6	1036	2	US-10-104-047-2812	Sequence 2812, Ap
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1178	47.5	10.6	345	2	US-09-222-786-2	Sequence 2, Appli	1251	47.5	10.6	1049	2	US-09-954-987B-170	Sequence 170, App
1179	47.5	10.6	365	2	US-09-270-767-58705	Sequence 58705, A	1252	47.5	10.6	1049	2	US-09-954-987B-172	Sequence 172, App
1180	47.5	10.6	366	2	US-09-270-767-35334	Sequence 35334, A	1253	47.5	10.6	1049	2	US-10-020-445A-496	Sequence 496, App
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1188	47.5	10.6	424	1	US-09-165-234-9	Sequence 9, Appli	1261	47.5	10.6	1291	2	US-08-569-214-3	Sequence 3, Appli
1189	47.5	10.6	424	2	US-09-274-570-9	Sequence 9, Appli	1262	47.5	10.6	1291	2	US-08-937-236-2	Sequence 2, Appli
1190	47.5	10.6	424	2	US-09-538-092-1317	Sequence 1317, Ap	1263	47.5	10.6	1295	2	US-08-569-214-2	Sequence 2, Appli
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1194	47.5	10.6	524	2	US-09-171-553B-4	Sequence 4, Appli	1267	47.5	10.6	1639	2	US-09-269-874A-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 258, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 449; DB 2; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.9e-48;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGPLMCNPSNSNANCEPSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPNTSNDTMASGW 60
Db 111 KGPLMCNPSNSNANCEPSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPNTSNDTMASGW 170
QY 61 RASSFHFDSEENKRLIHFS 80
Db 171 RASSFHFDSEENKRLIHFS 190

RESULT 4

US-09-992-598-258
; Sequence 258, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gruney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952

;
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGPLMCNSPNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPSTNSNDTMASGW 60
Db 111 KGPLMCNSPNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPSTNSNDTMASGW 170

Qy 61 RASSPHFEDSEENKRLIHFS 80
Db 171 RASSPHFEDSEENKRLIHFS 190

RESULT 5
US-08-793-273C-2
; Sequence 2, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME
; FILE REFERENCE: BEC0022S
; CURRENT APPLICATION NUMBER: US/08/793,273C
; CURRENT FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: 08/308,359
; PRIOR FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2199
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-793-273C-2

Query Match 15.1%; Score 68; DB 2; Length 2199;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 22 NISDIHPESFNLOWFFND 39
Db 1444 NVSDITPESFNLSWMTD 1461

RESULT 6
PCT-US95-11684-2
; Sequence 2, Application PC/TUS9511684
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
; TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING SAME
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11684
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,359
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: BEC0019P

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-11684-2

Query Match      15.1%; Score 68; DB 4; Length 2199;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      22 NISDIHPESFNLQWFFND 39
Db      1444 NVSDITPESFNLWMATD 1461

RESULT 7
US-09-796-575-2
; Sequence 2, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:
; APPLICANT: Genesegues, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G332.12-0001
; CURRENT APPLICATION NUMBER: US/09/796,575
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-575-2

Query Match      15.1%; Score 68; DB 2; Length 2200;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      22 NISDIHPESFNLQWFFND 39
Db      1444 NVSDITPESFNLWMATD 1461

RESULT 8
US-09-248-796A-26951
; Sequence 26951, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26951
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26951

Query Match      14.9%; Score 67; DB 2; Length 345;
Best Local Similarity 27.5%; Pred. No. 4.2;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Matches 22; Conservative 10; Mismatches 28; Indels 20; Gaps 3;

Qy      17 EFSLKNISDI-HPESFNLQWFFNDSCAPP-----TGFNKPTSNDTMA 58
Db      29 KPSLNQLQDIFHEETTEIKSFVETSPQPKQAPRRKWPYSKSIETTFKKQKQKNTFAS 88

Qy      59 GWRASSFHFDSEENKHLIH 78
Db      89 KHRAA--HTPEEPNSYQGVH 106

RESULT 9
US-09-345-468-12
; Sequence 12, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-12

Query Match      14.9%; Score 67; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 9.3;
Matches 23; Conservative 16; Mismatches 35; Indels 22; Gaps 4;

Qy      3 PLMCNPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPP-----TGF-NKPT-- 51
Db      68 PLDRNPLEPKNKAREPSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFPYKPTLS 127

Qy      52 -----SNDTMASGWRASSFHFD-SEENKHL 76
Db      128 ALPSPVVASGGNMTLRCSQKGYHFFVLMKEGEHQL 163

RESULT 10
US-09-414-453A-12
; Sequence 12, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-12

Query Match      14.9%; Score 67; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 9.3;
Matches 23; Conservative 16; Mismatches 35; Indels 22; Gaps 4;

Qy      3 PLMCNPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPP-----TGF-NKPT-- 51

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Db 68 PLDRNNPLEPKNKARFSPISPMTEHHAGRYRCHYYSAGWSEPSDPLELVMTGFYKPTLS 127
QY 52 -----SNDTMASGWRASSFHFD-SEENKHRL 76
Db 128 ALPSPVVASGNNMTLRCSQKGYHHFVLMKEGEHQL 163

RESULT 11
US-09-248-796A-14877
; Sequence 14877, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14877
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14877

Query Match 14.8%; Score 66.5; DB 2; Length 271;
Best Local Similarity 27.9%; Pred. No. 3.5;
Matches 19; Conservative 11; Mismatches 29; Indels 9; Gaps 2;

QY 2 GPLMCNPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWR 61
Db 1 GRILPASVGEDNNQNESMANIVDAKNYFQIQWYR-----PRDISKTSDSRL----- 51

QY 62 ASSFHFD 69
Db 52 FASMTDS 59

RESULT 12
US-09-902-540-11280
; Sequence 11280, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11280
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11280

Query Match 14.8%; Score 66.5; DB 2; Length 1627;
Best Local Similarity 28.6%; Pred. No. 37;
Matches 16; Conservative 8; Mismatches 27; Indels 5; Gaps 1;

QY 2 GPLMCNPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMA 57
Db 61 GPCMCNGPLILSHWMDHCDLGRYYPFSEFCRWL-----APQHGTVVCRDTVA 111

RESULT 13
US-08-121-713D-60
; Sequence 60, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-60

Query Match 14.6%; Score 65.5; DB 1; Length 650;
Best Local Similarity 31.8%; Pred. No. 15;
Matches 21; Conservative 7; Mismatches 27; Indels 11; Gaps 2;

QY 7 NSPSNS---NANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWRAS 63
Db 202 NTPSNSIPGSAVCAFLQDIADTFEGQFKEQTGINSNWLPPVNNAKVPDP-----RPG 253

QY 64 SFHFD 69
Db 254 SCHNDS 259

RESULT 14
US-08-835-268-60
; Sequence 60, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-835-268-60

Query Match 14.6%; Score 65.5; DB 1; Length 650;
Best Local Similarity 31.8%; Pred. No. 15;
Matches 21; Conservative 7; Mismatches 27; Indels 11; Gaps 2;

Qy 7 NSPSNS---NANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWRAS 63
Db 202 NTPSNSIPGSAVCAFAALQDIADTFEGQFKEQTGINSNWLFPVNNAKVPDP-----RPG 253

Qy 64 SFHFD 69
Db 254 SCHNDS 259

RESULT 15
US-09-060-692-60
; Sequence 60, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
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; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514

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; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
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; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-692-60

Query Match 14.6%; Score 65.5; DB 1; Length 650;
Best Local Similarity 31.8%; Pred. No. 15;
Matches 21; Conservative 7; Mismatches 27; Indels 11; Gaps 2;

Qy 7 NSPSNS---NANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWRAS 63
Db 202 NTPSNSIPGSAVCAFAALQDIADTFEGQFKEQTGINSNWLFPVNNAKVPDP-----RPG 253

Qy 64 SFHFD 69
Db 254 SCHNDS 259

Search completed: December 22, 2005, 03:00:42
Job time : 68.5102 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:42:57 ; Search time 240 Seconds
(without alignments)
235.176 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190

Perfect score: 449

Sequence: 1 KGPLMCNPSNSNANCEPSL.....RASSFHFDSEENKRLIHFS 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	449	100.0	229	2	Q9H5X9	HUMAN Q9h5x9 homo sapien
2	449	100.0	229	2	Q53R12	HUMAN Q53r12 homo sapien
3	449	100.0	229	2	Q6UWS1	HUMAN Q6uws1 homo sapien
4	449	100.0	229	2	Q5U609	HUMAN Q5u609 homo sapien
5	237.5	52.9	226	2	Q9CQY8	MUS Q9cqy8 m mus muscu
6	237.5	52.9	226	2	Q9D3R0	MOUSE Q9d3r0 mus musculus
7	231.5	51.6	226	2	Q9D3Q0	MOUSE Q9d3q0 mus musculus
8	93	20.7	242	2	Q4KL96	XENLA Q4kl96 xenopus lae
9	83.5	18.6	277	2	Q66S52	UROCA Q66s52 oikopleura
10	83	18.5	342	2	Q9PT67	XENLA Q9pt67 xenopus lae
11	82	18.3	142	2	Q695C3	PICMA Q695c3 picea maria
12	82	18.3	148	2	Q65095	PICMA Q65095 picea maria
13	80	17.8	352	2	Q9PRJ8	XENLA Q9prj8 xenopus lae
14	79	17.6	808	2	Q70W02	CIOIN Q70w02 ciona intes
15	78.5	17.5	149	2	Q695B5	PICGL Q695b5 picea glauc
16	78.5	17.5	149	2	Q695B6	PICMA Q695b6 picea maria
17	78.5	17.5	149	2	Q695B7	PICMA Q695b7 picea maria
18	78.5	17.5	149	2	Q695B8	PICAB Q695b8 picea abies
19	78.5	17.5	154	2	Q9SPX7	PICAB Q9spx7 picea abies
20	78.5	17.5	156	2	Q65096	PICMA Q65096 picea maria
21	78.5	17.5	281	2	Q65061	PICMA Q65061 picea maria
22	78	17.4	832	2	Q8IBT8	PLAF7 Q8ibt8 plasmodium
23	77.5	17.3	151	2	Q695B3	PICMA Q695b3 picea maria
24	77.5	17.3	156	2	Q65097	PICMA Q65097 picea maria
25	76.5	17.0	149	2	Q695B0	TSUCA Q695b0 tsuga canad
26	76.5	17.0	149	2	Q695B1	PSEMC Q695b1 pseudotsuga
27	76.5	17.0	149	2	Q695B2	PINCE Q695b2 pinus cembr
28	76.5	17.0	149	2	Q695B4	PICGL Q695b4 picea glauc
29	76.5	17.0	154	2	Q9SPW4	PICGL Q9spw4 picea glauc
30	75	16.7	853	2	O93245	ONCMY O93245 oncorhynch
31	75	16.7	989	2	Q6FP46	CANGA Q6fp46 candida gla

32	74.5	16.6	296	2	Q722C5	LISMF Q722c5 listeria mo
33	73.5	16.4	353	2	Q9PT68	XENLA Q9pt68 xenopus lae
34	73	16.3	145	2	Q695C2	PICAB Q695c2 picea abies
35	73	16.3	150	2	Q9SPX8	PICAB Q9spx8 picea abies
36	73	16.3	412	1	AATC_MOUSE	P05201 mus musculus
37	72	16.0	854	2	O93244	ONCMY O93244 oncorhynch
38	72	16.0	1443	2	Q5A450	CANAL Q5a450 candida alb
39	71	15.8	352	2	Q5WM45	XENTR Q5wm45 xenopus tro
40	71	15.8	852	2	Q6CLB3	KLULA Q6clb3 kluyveromyc
41	70.5	15.7	146	2	Q695B9	PICGL Q695b9 picea glauc
42	70.5	15.7	146	2	Q695C0	PICGL Q695c0 picea glauc
43	70.5	15.7	146	2	Q695C1	PICAB Q695c1 picea abies
44	70.5	15.7	151	2	Q9SPW5	PICGL Q9spw5 picea glauc
45	70.5	15.7	151	2	Q9SPX9	PICAB Q9spx9 picea abies
46	70.5	15.7	527	2	Q8BYW9	MOUSE Q8byw9 mus musculu
47	70	15.6	490	1	MOT3_YEAST	P54785 saccharomyc
48	70	15.6	814	2	Q9VNP2	DROME Q9vnp2 drosophila
49	70	15.6	1011	2	Q24273	DROME Q24273 drosophila
50	68.5	15.3	710	2	Q5CRR2	CRYPV Q5crr2 cryptospori
51	68.5	15.3	710	2	Q5CN99	CRYHO Q5cn99 cryptospori
52	68.5	15.3	890	2	Q54YH9	DICDI Q54yh9 dictyosteli
53	68	15.1	293	2	Q692Q7	GCLOS Q692q7 citrus tris
54	68	15.1	2201	1	TENA_HUMAN	P24821 homo sapien
55	68	15.1	2201	2	Q5T7S3	HUMAN Q5t7s3 homo sapien
56	68	15.1	2233	2	Q4LE33	HUMAN Q4le33 homo sapien
57	67.5	15.0	351	2	Q4WIU3	ASPFU Q4wiu3 aspergillus
58	67.5	15.0	527	2	Q5NDL0	RAT Q5ndl0 rattus norv
59	67.5	15.0	623	2	Q8JNB7	WSSV Q8jnb7 white spot
60	67.5	15.0	623	2	Q91LN4	WSSV Q91ln4 white spot
61	67.5	15.0	1282	2	Q6FRR1	CANGA Q6frr1 candida gla
62	67	14.9	296	2	Q8Y8V0	LISMO Q8y8v0 listeria mo
63	67	14.9	322	2	Q52G15	MAGGR Q52g15 magnaporthe
64	67	14.9	369	2	Q54B59	DICDI Q54b59 dictyosteli
65	67	14.9	619	2	Q62701	RAT Q62701 rattus norv
66	66.5	14.8	126	2	Q4I7X6	GIBZE Q4i7x6 gibberella
67	66.5	14.8	296	2	Q4YK5	PLABE Q4ygk5 plasmodium
68	66.5	14.8	375	2	Q6LYB9	METMP Q6lyb9 methanococc
69	66.5	14.8	926	2	Q6ZU11	HUMAN Q6zul1 homo sapien
70	66	14.7	575	2	Q62657	RAT Q62657 rattus norv
71	66	14.7	1131	2	Q54K42	DICDI Q54k42 dictyosteli
72	66	14.7	1217	2	Q5W9G9	HUMAN Q5w9g9 homo sapien
73	66	14.7	1324	2	Q8JKQ9	9VIRU Q8jkq9 heliothis z
74	66	14.7	1425	2	Q5KHV2	CRYNE Q5khv2 cryptococcu
75	66	14.7	1538	2	Q55UJ3	CRYNE Q55uj3 cryptococcu
76	66	14.7	1538	2	Q5KHV3	CRYNE Q5khv3 cryptococcu
77	65.5	14.6	413	2	Q4R5L1	MACFA Q4r5l1 macaca faec
78	65.5	14.6	620	2	Q9LXX4	ARATH Q9lxx4 arabidopsis
79	65.5	14.6	760	2	Q4IDC6	GIBZE Q4idc6 gibberella
80	65.5	14.6	850	1	SEM1A_DROME	Q24322 drosophila
81	65.5	14.6	1043	2	Q55DW9	DICDI Q55dw9 dictyosteli
82	65.5	14.6	1073	2	Q9W1T8	DROME Q9w1t8 drosophila
83	65.5	14.6	1173	2	Q6NR54	DROME Q6nr54 drosophila
84	65.5	14.6	1278	2	Q4Z391	PLABE Q4z391 plasmodium
85	65.5	14.6	2525	2	Q4Q184	LEIMA Q4q184 leishmania
86	65	14.5	144	2	Q9J6E7	9HIV1 Q9j6e7 human immun
87	65	14.5	193	2	Q6PI73	HUMAN Q6pi73 homo sapien
88	65	14.5	389	2	Q4PEM5	USTMA Q4p5m5 ustilago ma
89	65	14.5	493	2	Q65XF7	ORYSA Q65xf7 oryza sativ
90	65	14.5	652	2	Q97MJ1	CLOAB Q97mj1 clostridium
91	65	14.5	1612	2	Q5BFT6	EMENI Q5bft6 aspergillus
92	64.5	14.4	343	2	Q54EK7	DICDI Q54ek7 dictyosteli
93	64.5	14.4	350	2	Q6BNJ6	DEBHA Q6bnj6 debaryomyce
94	64.5	14.4	387	2	P90905	CABEL P90905 caenorhabdi
95	64.5	14.4	460	2	Q61D03	CABER Q61d03 caenorhabdi
96	64.5	14.4	461	2	P91197	CABEL P91197 caenorhabdi
97	64.5	14.4	468	2	Q52KU4	XENLA Q52ku4 xenopus lae
98	64.5	14.4	475	2	O74315	XSCHO Q74315 schizosacch
99	64.5	14.4	486	2	Q73CW4	BACC1 Q73cw4 bacillus ce
100	64.5	14.4	503	1	YEPA_SCHPO	O14470 schizosacch
101	64.5	14.4	508	2	Q74118	9HIV2 Q74118 human immun
102	64.5	14.4	577	2	Q894E2	CLOTE Q894e2 clostridium
103	64.5	14.4	754	2	Q8IBU4	PLAF7 Q8ibu4 plasmodium
104	64.5	14.4	764	2	O97343	SUBDO O97343 suberites d

105	64.5	14.4	1163	1	LEPR_MACMU	Q9myl0 macaca mula	178	62	13.8	293	2	Q692Q5_9CLOS	Q692q5 citrus tris
106	64	14.3	228	1	IF4E2_CABEL	Q21693 caenorhabdi	179	62	13.8	293	2	Q692Q6_9CLOS	Q692q6 citrus tris
107	64	14.3	252	2	Q6C9E9_YARLI	Q6c9e9 yarrowia li	180	62	13.8	293	2	Q692Q8_9CLOS	Q692q8 citrus tris
108	64	14.3	798	2	Q86HW6_DICDI	Q86hw6 dictyosteli	181	62	13.8	293	2	Q692R0_9CLOS	Q692r0 citrus tris
109	64	14.3	802	2	Q55U46_CRYNE	Q55u46 cryptococcu	182	62	13.8	293	2	Q692R2_9CLOS	Q692r2 citrus tris
110	64	14.3	802	2	Q5KI96_CRYNE	Q5ki96 cryptococcu	183	62	13.8	327	2	Q5DD47_SCHJA	Q5dd47 schistosoma
111	64	14.3	819	2	Q55U47_CRYNE	Q55u47 cryptococcu	184	62	13.8	382	2	Q83E23_COXBU	Q83e23 coxiella bu
112	64	14.3	819	2	Q5KI97_CRYNE	Q5ki97 cryptococcu	185	62	13.8	498	2	Q50MM6_ENTHI	Q50mm6 entamoeba h
113	64	14.3	881	2	Q8XSL4_RALSO	Q8xsl4 ralstonia s	186	62	13.8	508	2	Q74116_9HIV2	Q74116 human immun
114	64	14.3	992	1	PHS2_DICDI	P34114 dictyosteli	187	62	13.8	537	1	ACEA_EMBNI	P28298 emericella
115	64	14.3	993	2	Q54F21_DICDI	Q54f21 dictyosteli	188	62	13.8	592	2	Q5A4E1_CANAL	Q5a4e1 candida alb
116	64	14.3	1500	2	Q42080_9BETA	Q42080 human herpe	189	62	13.8	862	2	Q74113_9HIV2	Q74113 human immun
117	64	14.3	1500	2	Q77Z83_HHV6U	Q77z83 human herpe	190	62	13.8	864	2	Q6CD66_YARLI	Q6cd66 yarrowia li
118	64	14.3	3056	2	Q8I639_PLAF7	Q8i639 plasmodium	191	62	13.8	868	2	Q54VT5_DICDI	Q54vt5 dictyosteli
119	64	14.3	5864	2	Q869L3_DICDI	Q869l3 d similar t	192	62	13.8	917	2	Q593T3_RAT	Q593t3 rattus norv
120	63.5	14.1	341	2	Q5ACM8_CANAL	Q5acm8 candida alb	193	62	13.8	924	2	Q9FIC2_ARATH	Q9fic2 arabidopsis
121	63.5	14.1	415	2	Q6INN9_XENLA	Q6inn9 xenopus lae	194	62	13.8	971	1	SEC5_YEAST	P89102 saccharomyc
122	63.5	14.1	450	2	Q55DH3_DICDI	Q55dh3 dictyosteli	195	62	13.8	1011	2	Q7RD67_PLAYO	Q7rd67 plasmodium
123	63.5	14.1	485	2	Q81HD7_BACCR	Q81hd7 bacillus ce	196	62	13.8	1466	2	Q8BB47_9BETA	Q8bb47 human herpe
124	63.5	14.1	654	2	Q7TLW5_NPVCF	Q7tlw5 choristoneu	197	62	13.8	1604	2	Q4UNE0_RICFE	Q4une0 rickettsia
125	63.5	14.1	864	2	Q6BGY9_DEBHA	Q6bgy9 debaryomyce	198	62	13.8	1921	2	Q5X4P0_LEGPA	Q5x4p0 legionella
126	63.5	14.1	886	2	Q622L7_CAEBR	Q622l7 caenorhabdi	199	62	13.8	2179	2	Q7PDL7_PLAYO	Q7pdl7 plasmodium
127	63.5	14.1	906	2	Q93XS1_PRUPE	Q93xs1 prunus pers	200	62	13.8	2266	2	Q8WYP5_HUMAN	Q8wyp5 homo sapien
128	63	14.0	231	2	Q5BWA1_SCHJA	Q5bwa1 schistosoma	201	62	13.8	3115	2	Q9IFX0_9CLOS	Q9ifx0 citrus tris
129	63	14.0	231	2	Q8VRH7_AERHY	Q8vrh7 aeromonas h	202	61.5	13.7	411	2	Q6NX26_XENTR	Q6nx26 xenopus tro
130	63	14.0	299	2	Q6FD33_ACIAD	Q6fd33 acinetobact	203	61.5	13.7	417	2	Q8YY26_ANASP	Q8yy26 anabaena sp
131	63	14.0	418	1	NAC9_ARATH	Q6vdh0 arabidopsis	204	61.5	13.7	422	2	Q4HQ78_CAMUP	Q4hq78 campylobact
132	63	14.0	467	2	Q660K0_BORGA	Q660k0 borrelia ga	205	61.5	13.7	442	2	Q5CFX3_CRYHO	Q5cfx3 cryptospori
133	63	14.0	577	2	Q9AUH9_PINTA	Q9auh9 pinus taeda	206	61.5	13.7	473	2	Q5GU60_XANOR	Q5gu60 xanthomonas
134	63	14.0	617	2	Q4YHS1_PLABE	Q4yhs1 plasmodium	207	61.5	13.7	487	2	Q9P6E4_NEUCR	Q9p6e4 neuropsora
135	63	14.0	684	1	CDC4_CANAL	P53699 candida alb	208	61.5	13.7	492	2	Q51IW5_MAGGR	Q51iw5 magnaporthe
136	63	14.0	737	2	Q6J3P9_SIVCZ	Q6j3p9 chimpanzee	209	61.5	13.7	493	2	Q4MWI7_BACCE	Q4mwi7 bacillus ce
137	63	14.0	742	2	Q55ZA4_CRYNE	Q55za4 cryptococcu	210	61.5	13.7	512	2	Q6BH61_DEBHA	Q6bh61 debaryomyce
138	63	14.0	742	2	Q5KNL9_CRYNE	Q5knl9 cryptococcu	211	61.5	13.7	519	2	Q50ZA0_ENTHI	Q50za0 entamoeba h
139	63	14.0	768	2	Q5A9A6_CANAL	Q5a9a6 candida alb	212	61.5	13.7	544	2	Q4H3K1_CIOIN	Q4h3k1 ciona intes
140	63	14.0	830	2	Q69565_9BETA	Q69565 human herpe	213	61.5	13.7	556	2	Q6DEK7_BRARB	Q6dek7 brachydanio
141	63	14.0	1080	2	Q6R7G6_9HERP	Q6r7g6 ostreid her	214	61.5	13.7	647	2	Q99077_USTHO	Q99077 ustilago ho
142	63	14.0	1081	2	Q4P8L6_USTMA	Q4p8l6 ustilago ma	215	61.5	13.7	686	2	Q4WKV2_ASPPFU	Q4wkv2 aspergillus
143	63	14.0	1165	1	CHS3_YEAST	P29465 saccharomyc	216	61.5	13.7	825	2	Q9FK21_ARATH	Q9fk21 arabidopsis
144	63	14.0	1198	2	Q55E26_DICDI	Q55e26 dictyosteli	217	61.5	13.7	889	2	Q6ZHH7_ORYSA	Q6zhh7 oryza sativ
145	63	14.0	1295	2	Q69471_9BETA	Q69471 human herpe	218	61.5	13.7	1034	1	ULP2_YEAST	P40537 saccharomyc
146	63	14.0	1447	2	Q6FLG8_CANGA	Q6flg8 candida gla	219	61.5	13.7	1282	2	Q7Z8J6_USTMA	Q7z8j6 ustilago ma
147	63	14.0	1570	2	Q9U0H8_PLAF7	Q9u0h8 plasmodium	220	61.5	13.7	1351	2	Q4RQD6_TETNG	Q4rqd6 tetraodon n
148	63	14.0	1740	2	Q8IJK9_PLAF7	Q8ijk9 plasmodium	221	61.5	13.7	1413	2	Q9NBD3_CABEL	Q9nbd3 caenorhabdi
149	63	14.0	1931	2	Q7YXK9_CRYPV	Q7yyk9 cryptospori	222	61.5	13.7	1439	2	Q5CQG9_CRYPV	Q5cqq9 cryptospori
150	63	14.0	2051	2	Q96682_DROME	Q96682 drosophila	223	61.5	13.7	1493	2	Q9N5D3_CABEL	Q9n5d3 caenorhabdi
151	63	14.0	2051	2	Q9V4A7_DROME	Q9v4a7 drosophila	224	61.5	13.7	1873	2	Q83044_9CLOS	Q83044 lettuce inf
152	62.5	13.9	177	2	Q4Y2N4_PLACH	Q4y2n4 plasmodium	225	61.5	13.7	3023	2	Q4P701_USTMA	Q4p701 ustilago ma
153	62.5	13.9	180	2	Q7RK89_PLAYO	Q7rk89 plasmodium	226	61.5	13.7	3462	1	RELN_RAT	P58751 rattus norv
154	62.5	13.9	201	2	Q5AYF3_EMENI	Q5ayf3 aspergillus	227	61	13.6	192	2	Q49390_MYCGE	Q49390 mycoplasma
155	62.5	13.9	210	2	Q4IR16_GIBZE	Q4ir16 gibberella	228	61	13.6	204	1	RPC8_HUMAN	Q9y535 homo sapien
156	62.5	13.9	296	2	Q92DM8_LISIN	Q92dm8 listeria in	229	61	13.6	204	1	RPC8_MOUSE	Q9d2c6 mus musculu
157	62.5	13.9	318	2	Q4WX16_ASPPFU	Q4wx16 aspergillus	230	61	13.6	204	2	Q5M7Y8_HUMAN	Q5m7y8 homo sapien
158	62.5	13.9	368	2	Q5JZR1_SOYBN	Q5jzr1 glycine max	231	61	13.6	212	2	Q4Y2P3_PLACH	Q4y2p3 plasmodium
159	62.5	13.9	412	1	AATC_HUMAN	P17174 homo sapien	232	61	13.6	241	2	Q8AI21_9HIV1	Q8ai21 human immun
160	62.5	13.9	413	2	Q5VW80_HUMAN	Q5vw80 homo sapien	233	61	13.6	326	2	Q23659_ARATH	O23659 arabidopsis
161	62.5	13.9	561	2	Q8LM20_ORYSA	Q8lm20 oryza sativ	234	61	13.6	326	2	Q8H1N3_ARATH	Q8hin3 arabidopsis
162	62.5	13.9	646	2	Q99071_USTHO	Q99071 ustilago ho	235	61	13.6	375	2	Q55S52_CRYNE	Q55s52 cryptococcu
163	62.5	13.9	702	2	Q7XF64_ORYSA	Q7xf64 oryza sativ	236	61	13.6	375	2	Q5KKG4_CRYNE	Q5kgk4 cryptococcu
164	62.5	13.9	702	2	Q8SB54_ORYSA	Q8sb54 oryza sativ	237	61	13.6	406	2	Q6ZC71_ORYSA	Q6zc71 oryza sativ
165	62.5	13.9	826	2	Q8SX11_DROME	Q8sx11 drosophila	238	61	13.6	412	1	AATC_RAT	P13221 rattus norv
166	62.5	13.9	826	2	Q9VHN9_DROME	Q9vhn9 drosophila	239	61	13.6	413	2	Q6P721_RAT	Q6p721 rattus norv
167	62.5	13.9	851	2	Q4Y4G6_PLACH	Q4y4g6 plasmodium	240	61	13.6	419	2	Q86M56_DROME	Q86m56 drosophila
168	62.5	13.9	911	2	Q7RJ02_PLAYO	Q7rj02 plasmodium	241	61	13.6	493	2	P94128_AERPU	P94128 aeromonas p
169	62.5	13.9	932	2	Q7VJK1_HELHP	Q7vjk1 helicobacte	242	61	13.6	574	2	Q8EC75_SHEON	Q8ec75 shewanella
170	62.5	13.9	1014	2	Q52F11_MAGGR	Q52f11 magnaporthe	243	61	13.6	642	2	Q75JG6_DICDI	Q75jg6 dictyosteli
171	62.5	13.9	1071	2	Q4HZT1_GIBZE	Q4hzt1 gibberella	244	61	13.6	681	2	Q552J1_DICDI	Q552j1 dictyosteli
172	62.5	13.9	1215	2	Q600C2_MYCHV	Q600c2 mycoplasma	245	61	13.6	687	2	Q8W3M2_CITUN	Q8w3m2 citrus unsh
173	62.5	13.9	1445	2	Q5CPT3_CRYPV	Q5cpt3 cryptospori	246	61	13.6	715	2	Q59K73_CANAL	Q59k73 candida alb
174	62.5	13.9	1630	2	Q6PCS0_MOUSE	Q6pcso mus musculu	247	61	13.6	725	2	Q8T124_DICDI	Q8t124 dictyosteli
175	62.5	13.9	1811	2	Q36184_9VIRU	Q36184 plautia sta	248	61	13.6	729	2	Q59K69_CANAL	Q59k69 candida alb
176	62.5	13.9	2222	2	Q4RY92_TETNG	Q4ry92 tetraodon n	249	61	13.6	771	2	Q8I5E1_PLAP7	Q8i5e1 plasmodium
177	62.5	13.9	3446	2	Q86AC8_DICDI	Q86ac8 dictyosteli	250	61	13.6	788	2	Q9W4N2_DROME	Q9w4n2 drosophila

251	61	13.6	852	2	Q89607_9HIV2	Q89607 human immun	324	60	13.4	691	2	Q9NJZ4_DROHE	Q9njz4 drosophila
252	61	13.6	889	2	Q6ZC72_ORYSA	Q6zc72 oryza sativ	325	60	13.4	698	2	Q9NJZ3_DROHE	Q9njz3 drosophila
253	61	13.6	905	2	Q4XEP1_PLACH	Q4xef1 plasmodium	326	60	13.4	701	2	Q4RNN8_TETNG	Q4rnn8 tetraodon n
254	61	13.6	915	2	Q43042_PETHY	Q43042 petunia hyb	327	60	13.4	777	2	Q5R600_PONPY	Q5r600 pongo pygma
255	61	13.6	1023	2	Q5CUV4_CRYPV	Q5cuv4 cryptospori	328	60	13.4	841	2	Q9NJY9_DROHE	Q9njy9 drosophila
256	61	13.6	1109	2	Q6BWG1_DEBHA	Q6bwg1 debaryomyce	329	60	13.4	841	2	Q9NJY5_DROSHLA	Q9njy5 drosophila
257	61	13.6	1203	2	Q55B98_DICDI	Q55b98 dictyosteli	330	60	13.4	841	2	Q9NJZ6_DROHE	Q9njz6 drosophila
258	61	13.6	1469	2	Q4P4A6_USTWA	Q4p4a6 ustilago ma	331	60	13.4	938	2	Q7N2M7_PHOLL	Q7n2m7 photorhabdu
259	61	13.6	1550	2	Q55601_9VIRU	Q55601 garlic viru	332	60	13.4	947	2	Q4S557_TETNG	Q4s557 tetraodon n
260	61	13.6	1668	2	Q4RUS6_TETNG	Q4rus6 tetraodon n	333	60	13.4	955	2	Q54V91_DICDI	Q54v91 dictyosteli
261	61	13.6	1714	2	Q90995_CHICK	Q90995 gallus gall	334	60	13.4	1016	2	Q5ATD1_EMENI	Q5atd1 aspergillus
262	61	13.6	1808	1	TENA_CHICK	P10039 gallus gall	335	60	13.4	1148	1	AT8A2_MOUSE	P98200 mus musculu
263	61	13.6	1810	2	Q90824_CHICK	Q90824 gallus gall	336	60	13.4	1321	2	Q6A7F3_PROAC	Q6a7f3 propionibac
264	61	13.6	2019	2	Q80YX2_MOUSE	Q80yx2 mus musculu	337	60	13.4	1336	2	Q6UK63_DICDI	Q6uk63 dictyosteli
265	61	13.6	2019	2	Q64706_MOUSE	Q64706 mus musculu	338	60	13.4	1946	2	Q97291_PLAF7	O97291 plasmodium
266	61	13.6	2110	2	Q80YX1_MOUSE	Q80yx1 mus musculu	339	60	13.4	2504	2	Q54PL8_DICDI	Q54pl8 dictyosteli
267	61	13.6	4293	2	O08852_MOUSE	O08852 mus musculu	340	60	13.4	3574	2	Q8IDA8_PLAF7	Q8ida8 plasmodium
268	60.5	13.5	127	2	O18855_SHEEP	O18855 ovis aries	341	60	13.4	4540	2	Q55EG2_DICDI	Q55eg2 dictyosteli
269	60.5	13.5	135	2	O18TSF8_ANOGA	Q5tsf8 anopheles g	342	59.5	13.3	126	2	Q7S979_NEUCR	Q7s979 neurospora
270	60.5	13.5	139	2	Q8LRP9_CRAMN	Q8lrp9 crataegus m	343	59.5	13.3	187	2	Q4UKA1_RICPE	Q4uka1 rickettsia
271	60.5	13.5	241	2	Q8A144_9HIV1	Q8a144 human immun	344	59.5	13.3	208	2	Q60RG6_CAEBR	Q60rg6 caenorhabdi
272	60.5	13.5	267	2	Q84HS5_RHIEP	Q84hs5 rhizobium e	345	59.5	13.3	255	2	Q689Z6_9HYME	Q689z6 cotesia glo
273	60.5	13.5	343	2	Q7TU21_PROMP	Q7tu21 prochloroco	346	59.5	13.3	297	2	Q6H970_ANTMA	Q6h970 antirrhinum
274	60.5	13.5	382	2	Q60U30_CAEBR	Q60u30 caenorhabdi	347	59.5	13.3	321	2	Q83AR3_COXBU	Q83ar3 coxiella bu
275	60.5	13.5	402	2	Q4V9H4_BRARE	Q4v9h4 brachydanio	348	59.5	13.3	368	2	Q5NVH2_PONPY	Q5nvh2 pongo pygma
276	60.5	13.5	444	2	Q97HP3_CLOAB	Q97hp3 clostridium	349	59.5	13.3	379	2	Q8BH91_MOUSE	Q8bh91 m mus muscu
277	60.5	13.5	468	2	Q9XY08_BOMMO	Q9xy08 bombyx mori	350	59.5	13.3	395	2	O69347_9VIBR	Q69347 vibrio sp.
278	60.5	13.5	502	2	Q6BKP6_DEBHA	Q6bkp6 debaryomyce	351	59.5	13.3	398	2	Q66LE0_9HIV1	Q66le0 human immun
279	60.5	13.5	602	2	Q6MY96_ASPPU	Q6my96 aspergillus	352	59.5	13.3	413	2	Q5R524_PONPY	Q5r524 pongo pygma
280	60.5	13.5	602	2	Q4WS52_ASPPU	Q4ws52 aspergillus	353	59.5	13.3	413	2	Q5R691_PONPY	Q5r691 pongo pygma
281	60.5	13.5	604	2	Q51X20_MAGGR	Q51x20 magnaporthe	354	59.5	13.3	420	2	Q68VY9_RICTY	Q68vy9 rickettsia
282	60.5	13.5	612	2	Q7RGB3_PLAYO	Q7rgb3 plasmodium	355	59.5	13.3	428	2	Q5CVC4_CRYPV	Q5cvc4 cryptospori
283	60.5	13.5	661	1	INVB DAUCA	P80065 daucus caro	356	59.5	13.3	460	2	Q9M4V1_ELAGV	Q9m4v1 elaeis guin
284	60.5	13.5	668	2	Q6BYI7_DEBHA	Q6byi7 debaryomyce	357	59.5	13.3	515	2	Q4PD21_USTMA	Q4pd21 ustilago ma
285	60.5	13.5	740	2	Q5RD05_PONPY	Q5rd05 pongo pygma	358	59.5	13.3	530	2	Q4YWN6_PLABE	Q4ywn6 plasmodium
286	60.5	13.5	747	2	Q9DSJ3_9HIV2	Q9dsj3 human immun	359	59.5	13.3	555	2	Q9AUI0_PINTA	Q9auio pinus taeda
287	60.5	13.5	764	2	Q6BJR8_DEBHA	Q6bjr8 debaryomyce	360	59.5	13.3	557	2	P94622_CLOCL	P94622 clostridium
288	60.5	13.5	780	2	Q5AWV0_EMENI	Q5awv0 aspergillus	361	59.5	13.3	562	2	Q51ZT1_MAGGR	Q51zt1 magnaporthe
289	60.5	13.5	785	2	Q54CE0_DICDI	Q54ce0 dictyosteli	362	59.5	13.3	627	2	Q8BXM6_MOUSE	Q8bxm6 mus musculu
290	60.5	13.5	913	2	Q6BIQ9_DEBHA	Q6biq9 debaryomyce	363	59.5	13.3	628	2	Q8D349_WIGBR	Q8d349 wiggleswort
291	60.5	13.5	937	1	NUP98 RAT	P49793 rattus norv	364	59.5	13.3	637	2	Q86B13_DICDI	Q86b13 dictyosteli
292	60.5	13.5	941	2	Q6BZ13_DEBHA	Q6bz13 debaryomyce	365	59.5	13.3	639	2	Q4WR68_ASPPU	Q4wr68 aspergillus
293	60.5	13.5	992	1	VPS41 YEAST	P38959 saccharomyc	366	59.5	13.3	657	2	Q558W6_DICDI	Q558w6 dictyosteli
294	60.5	13.5	1042	2	Q9NAL5_CAEEL	Q9nal5 caenorhabdi	367	59.5	13.3	740	2	Q86IH1_DICDI	Q86ih1 dictyosteli
295	60.5	13.5	1125	2	Q54H49_DICDI	Q54h49 dictyosteli	368	59.5	13.3	821	2	P87237_SCHPO	P87237 schizosacch
296	60.5	13.5	1168	2	Q5VH52_CIOIN	Q5vh52 ciona intes	369	59.5	13.3	832	2	Q6ZGDI_ORYSA	Q6zgd1 oryza sativ
297	60.5	13.5	1313	2	Q93UN0_HELPY	Q93un0 helicobacte	370	59.5	13.3	862	2	Q76606_9HIV2	Q76606 human immun
298	60.5	13.5	1335	2	Q4P846_USTWA	Q4p846 ustilago ma	371	59.5	13.3	862	2	Q9WLD7_9HIV2	Q9wld7 human immun
299	60.5	13.5	1471	2	Q5CKX5_CRYHO	Q5ckx5 cryptospori	372	59.5	13.3	901	2	Q6H972_ANTMA	Q6h972 antirrhinum
300	60.5	13.5	1736	2	Q95PH7_DICDI	Q95ph7 dictyosteli	373	59.5	13.3	902	2	Q4N4B5_THEPA	Q4n4b5 theileria p
301	60.5	13.5	1736	2	Q86AT9_DICDI	Q86at9 dictyosteli	374	59.5	13.3	905	2	Q88A43_PSESM	Q88a43 pseudomonas
302	60.5	13.5	4816	2	Q8T103_BOMMO	Q8t103 bombyx mori	375	59.5	13.3	1317	2	Q7RN19_PLAYO	Q7rn19 plasmodium
303	60	13.4	162	2	Q91M77_9CLOS	Q91m77 citrus tris	376	59.5	13.3	1330	2	Q9SXX5_9STRA	Q9sxx5 heterosigma
304	60	13.4	162	2	Q91M85_9CLOS	Q91m85 citrus tris	377	59.5	13.3	1357	2	Q81KL1_PLAF7	Q81kl1 plasmodium
305	60	13.4	182	2	Q4YF21_PLABE	Q4yfy21 plasmodium	378	59.5	13.3	1358	2	Q4RWU3_TETNG	Q4rwu3 tetraodon n
306	60	13.4	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien	379	59.5	13.3	1361	2	Q7REY0_PLAYO	Q7rey0 plasmodium
307	60	13.4	266	2	Q18362_CAEEL	Q18362 caenorhabdi	380	59.5	13.3	1421	2	Q5CH19_CRYHO	Q5chl9 cryptospori
308	60	13.4	349	2	Q6LJ09_PHOPR	Q6lj09 photobacter	381	59.5	13.3	1962	1	TNR6A_HUMAN	Q8ndv7 homo sapien
309	60	13.4	350	2	Q59WV1_CANAL	Q59wv1 candida alb	382	59.5	13.3	4261	2	Q8IFP4_PLAF7	Q8ifp4 plasmodium
310	60	13.4	350	2	Q59XQ6_CANAL	Q59xq6 candida alb	383	59.5	13.3	7716	2	Q7UWZ8_RHOBA	Q7uwz8 rhodopirell
311	60	13.4	362	2	Q9CNG0_PASMU	Q9cng0 pasteurella	384	59	13.1	119	2	Q84NA0_9PABA	Q84na0 anthyllis h
312	60	13.4	365	2	Q4Z2P3_PLABE	Q4z2p3 plasmodium	385	59	13.1	120	2	Q7RB16_PLAYO	Q7rb16 plasmodium
313	60	13.4	372	2	Q61SF0_CAEBR	Q61sf0 caenorhabdi	386	59	13.1	145	2	Q6HNB8_BACHK	Q6hnb8 bacillus th
314	60	13.4	466	2	Q6CF22_YARLI	Q6cf22 yarrowia li	387	59	13.1	145	2	Q63F08_BACCZ	Q63fu8 bacillus ce
315	60	13.4	482	2	Q4ZJM7_MOUSE	Q4zjm7 mus musculu	388	59	13.1	146	1	CYB5M_HUMAN	O43169 homo sapien
316	60	13.4	489	2	Q5L5H1_CHLAB	Q5l5h1 chlamydophi	389	59	13.1	159	2	Q9JER3_9HIV1	Q9jer3 human immun
317	60	13.4	507	2	Q74115_9HIV2	Q74115 human immun	390	59	13.1	159	2	Q9JER6_9HIV1	Q9jer6 human immun
318	60	13.4	514	1	G6PD BOSIN	Q7ys17 bos indicus	391	59	13.1	183	2	O46871_HUMAN	O46871 homo sapien
319	60	13.4	518	2	Q9NJZ5_DROHE	Q9njz5 drosophila	392	59	13.1	188	2	Q95466_HUMAN	Q95466 homo sapien
320	60	13.4	577	2	O17165_CAEEL	O17165 caenorhabdi	393	59	13.1	198	2	Q8GLI3_ABRHY	Q8gli3 aeromonas h
321	60	13.4	613	2	Q60VC0_CAEBR	Q60vc0 caenorhabdi	394	59	13.1	201	2	Q519E5_ENTHI	Q519e5 entamoeba h
322	60	13.4	667	2	Q7RLG1_PLAYO	Q7rlg1 plasmodium	395	59	13.1	227	2	Q5SQ91_HUMAN	Q5sq91 homo sapien
323	60	13.4	682	2	Q81I15_PLAF7	Q81i15 plasmodium	396	59	13.1	231	2	Q8MGQ8_HUMAN	Q8mgq8 homo sapien

397	59	13.1	231	2	Q8VL68_AERHY	Q8VL68 aeromonas h
398	59	13.1	231	2	Q8VRH4_AERHY	Q8VRH4 aeromonas h
399	59	13.1	231	2	Q8VRH5_AERHY	Q8VRH5 aeromonas h
400	59	13.1	254	2	Q5DFB4_SCHJA	Q5DFB4 schistosoma
401	59	13.1	256	2	Q5SQ92_HUMAN	Q5SQ92 homo sapien
402	59	13.1	260	2	Q5JPL8_HUMAN	Q5JPL8 homo sapien
403	59	13.1	264	2	Q5SQ93_HUMAN	Q5SQ93 homo sapien
404	59	13.1	272	2	Q7P0X1_CHRVO	Q7P0X1 chromobacte
405	59	13.1	275	2	Q5SQ90_HUMAN	Q5SQ90 homo sapien
406	59	13.1	280	2	Q8IIK6_PLAF7	Q8IIK6 plasmodium
407	59	13.1	284	2	Q65499_ARATH	Q65499 arabidopsis
408	59	13.1	289	2	Q4L968_STAHL	Q4L968 staphylococ
409	59	13.1	295	1	METF_BUCBP	Q89BI3 buchnera ap
410	59	13.1	324	2	Q4IG36_GIBZE	Q4IG36 gibberella
411	59	13.1	330	2	Q6GP91_XENLA	Q6GP91 xenopus lae
412	59	13.1	334	2	Q8RN80_AERHY	Q8RN80 aeromonas h
413	59	13.1	337	2	Q8RN84_AERHY	Q8RN84 aeromonas h
414	59	13.1	337	2	Q8RN87_AERHY	Q8RN87 aeromonas h
415	59	13.1	338	2	Q8RN88_AERHY	Q8RN88 aeromonas h
416	59	13.1	343	2	Q8RN78_AERHY	Q8RN78 aeromonas h
417	59	13.1	348	2	Q5LBM6_BACFN	Q5LBM6 bacteroides
418	59	13.1	366	2	Q8RN82_AERHY	Q8RN82 aeromonas h
419	59	13.1	367	2	Q8RN86_AERHY	Q8RN86 aeromonas h
420	59	13.1	369	2	Q8RN83_AERHY	Q8RN83 aeromonas h
421	59	13.1	369	2	Q8RN85_AERHY	Q8RN85 aeromonas h
422	59	13.1	371	2	Q8RJH3_AERHY	Q8RJH3 aeromonas h
423	59	13.1	375	2	Q7RIV1_PLAYO	Q7RIV1 plasmodium
424	59	13.1	380	2	Q8RN77_AERHY	Q8RN77 aeromonas h
425	59	13.1	382	2	Q95QW1_CAEEL	Q95QW1 caenorhabdi
426	59	13.1	393	2	Q54R14_DICDI	Q54R14 dictyosteli
427	59	13.1	394	2	Q34835_KLULA	Q34835 kluyveromyc
428	59	13.1	396	2	Q6DN58_KLULA	Q6DN58 kluyveromyc
429	59	13.1	409	2	Q4YQC9_PLABE	Q4YQC9 plasmodium
430	59	13.1	410	2	Q7ZUW8_BRARE	Q7ZUW8 brachydanio
431	59	13.1	412	1	AATC_HORSE	P08906 equus cabal
432	59	13.1	429	2	Q4QR59_XENLA	Q4QR59 xenopus lae
433	59	13.1	431	2	Q6DCR0_XENLA	Q6DCR0 xenopus lae
434	59	13.1	493	2	Q8GN63_AERHY	Q8GN63 aeromonas h
435	59	13.1	493	2	Q44063_AERHY	Q44063 aeromonas h
436	59	13.1	493	2	Q9S5D4_AERHY	Q9S5D4 aeromonas h
437	59	13.1	517	2	Q559D0_DICDI	Q559D0 dictyosteli
438	59	13.1	518	2	Q9NJZ1_DROSL	Q9NJZ1 drosophila
439	59	13.1	554	2	Q9VDD5_DROME	Q9VDD5 drosophila
440	59	13.1	554	2	Q9LG03_ARATH	Q9LG03 arabidopsis
441	59	13.1	557	2	Q54IT7_DICDI	Q54IT7 dictyosteli
442	59	13.1	575	2	Q4S208_TETNG	Q4S208 tetraodon n
443	59	13.1	605	2	Q6BK98_DEBHA	Q6BK98 debaryomyce
444	59	13.1	616	2	Q7SE17_NEUCR	Q7SE17 neurospora
445	59	13.1	663	2	Q51JY6_MAGGR	Q51JY6 magnaporthe
446	59	13.1	677	2	Q7JFT7_RABIT	Q7JFT7 oryctolagus
447	59	13.1	695	2	Q9NJZ2_DROSL	Q9NJZ2 drosophila
448	59	13.1	709	2	Q8TNF1_METAC	Q8TNF1 methanosarc
449	59	13.1	741	1	HOK1_HALRO	P28468 halocynthia
450	59	13.1	769	2	Q86IH4_DICDI	Q86IH4 dictyosteli
451	59	13.1	819	2	Q8I435_PLAF7	Q8I435 plasmodium
452	59	13.1	820	2	Q6CWX7_KLULA	Q6CWX7 kluyveromyc
453	59	13.1	838	2	Q9TXM3_CAEEL	Q9TXM3 caenorhabdi
454	59	13.1	840	2	Q8I5X4_PLAF7	Q8I5X4 plasmodium
455	59	13.1	841	2	Q9NJZ0_DROSL	Q9NJZ0 drosophila
456	59	13.1	905	2	Q75AU7_ASHGO	Q75AU7 ashbya gos
457	59	13.1	922	2	Q54H00_DICDI	Q54H00 dictyosteli
458	59	13.1	988	2	Q4P446_USTMA	Q4P446 ustilago ma
459	59	13.1	1006	2	Q74458_SCHPO	Q74458 schizosacch
460	59	13.1	1074	2	Q503K3_BRARE	Q503K3 brachydanio
461	59	13.1	1095	2	Q4XZ33_PLACH	Q4XZ33 plasmodium
462	59	13.1	1515	2	Q95XK2_CAEEL	Q95XK2 caenorhabdi
463	59	13.1	1540	2	Q4XL97_PLACH	Q4XL97 plasmodium
464	59	13.1	1781	2	Q5SBL9_LACRE	Q5SBL9 lactobacill
465	59	13.1	1818	2	Q8EVF1_MYCPE	Q8EVF1 mycoplasma
466	59	13.1	2352	1	MOK12_SCHPO	Q9UUL4 schizosacch
467	59	13.1	2413	2	Q4S3T8_TETNG	Q4S3T8 tetraodon n
468	59	13.1	3001	2	Q8II08_PLAF7	Q8II08 plasmodium
469	58.5	13.0	140	2	Q801D0_LATME	Q801D0 latimeria m

470	177	13.0	2	Q6NI13_CORDI	Q6NI13 corynebacte
471	179	13.0	2	Q6TGI5_PYRGO	Q6TGI5 pyrus commu
472	208	13.0	2	Q8IWS2_HUMAN	Q8IWS2 homo sapien
473	208	13.0	2	Q8NI131_HUMAN	Q8NI131 homo sapien
474	241	13.0	2	Q8AI13_9HIV1	Q8AI13 human immu
475	241	13.0	2	Q8AI14_9HIV1	Q8AI14 human immu
476	241	13.0	2	Q8AI18_9HIV1	Q8AI18 human immu
477	241	13.0	2	Q8AI24_9HIV1	Q8AI24 human immu
478	241	13.0	2	Q8AI27_9HIV1	Q8AI27 human immu
479	241	13.0	2	Q8AI28_9HIV1	Q8AI28 human immu
480	241	13.0	2	Q8AI30_9HIV1	Q8AI30 human immu
481	241	13.0	2	Q8AI31_9HIV1	Q8AI31 human immu
482	241	13.0	2	Q8AI32_9HIV1	Q8AI32 human immu
483	241	13.0	2	Q8AI33_9HIV1	Q8AI33 human immu
484	241	13.0	2	Q8AI34_9HIV1	Q8AI34 human immu
485	241	13.0	2	Q8AI36_9HIV1	Q8AI36 human immu
486	241	13.0	2	Q8AI37_9HIV1	Q8AI37 human immu
487	241	13.0	2	Q8AI38_9HIV1	Q8AI38 human immu
488	241	13.0	2	Q8AI39_9HIV1	Q8AI39 human immu
489	241	13.0	2	Q8AI42_9HIV1	Q8AI42 human immu
490	241	13.0	2	Q8AI43_9HIV1	Q8AI43 human immu
491	254	13.0	2	Q4Y1E7_PLACH	Q4Y1E7 plasmodium
492	265	13.0	2	Q7S8J8_NEUCR	Q7S8J8 neurospora
493	272	13.0	2	Q7QIH5_ANOGA	Q7QIH5 anopheles g
494	276	13.0	1	SLBP_DRONE	Q9VAN6 drosophila
495	328	13.0	1	EMB_RAT	Q88775 rattus norv
496	332	13.0	2	Q4PIN4_USTMA	Q4PIN4 ustilago ma
497	362	13.0	2	Q5BI20_EMENI	Q5BI20 aspergillus
498	376	13.0	2	Q95UP2_STYPU	Q95UP2 stylonychia
499	405	13.0	2	Q8BMN8_MOUSE	Q8BMN8 mus musculu
500	421	13.0	2	Q9BIC9_TRISP	Q9BIC9 trichinella
501	431	13.0	2	Q93227_CAEEL	Q93227 caenorhabdi
502	439	13.0	2	Q88928_WASMV	Q88928 watermelon
503	452	13.0	2	Q6GMG6_BRARE	Q6GMG6 brachydanio
504	526	13.0	2	Q517U8_ENTHI	Q517U8 entamoeba h
505	538	13.0	2	Q55JU4_CRYNE	Q55JU4 cryptococcu
506	538	13.0	2	Q5K9Q7_CRYNE	Q5K9Q7 cryptococcu
507	555	13.0	2	Q9ZQW3_POPTR	Q9ZQW3 populus tri
508	555	13.0	2	Q9FSC9_POPTR	Q9FSC9 populus tri
509	561	13.0	2	Q68FR5_RAT	Q68FR5 rattus norv
510	579	13.0	2	Q8T392_DUGJA	Q8T392 dugesia jap
511	588	13.0	2	Q4SGI2_TETNG	Q4SGI2 tetraodon n
512	595	13.0	2	Q4V721_DROME	Q4V721 drosophila
513	610	13.0	2	Q5L9Z2_BACFN	Q5L9Z2 bacteroides
514	610	13.0	2	Q64Q99_BACFR	Q64Q99 bacteroides
515	615	13.0	2	Q8BXX8_MOUSE	Q8BXX8 m mus muscu
516	624	13.0	2	Q9V789_DROME	Q9V789 drosophila
517	640	13.0	1	IGF1R_BOVIN	Q05688 bos taurus
518	647	13.0	2	Q4N9M6_THEPA	Q4N9M6 theileria p
519	762	13.0	2	Q55B06_DICDI	Q55B06 dictyosteli
520	782	13.0	2	Q55C90_DICDI	Q55C90 dictyosteli
521	789	13.0	2	Q8CFX1_MOUSE	Q8CFX1 mus musculu
522	797	13.0	2	Q8BLH1_MOUSE	Q8BLH1 mus musculu
523	826	13.0	2	Q75JF0_DICDI	Q75JF0 dictyosteli
524	837	13.0	2	Q552H0_DICDI	Q552H0 dictyosteli
525	883	13.0	1	LMBL3_MOUSE	Q8BLB7 mus musculu
526	885	13.0	2	Q5CGV6_CRYHO	Q5CGV6 cryptospori
527	932	13.0	2	Q7QB67_ANOGA	Q7QB67 anopheles g
528	961	13.0	2	Q8IC12_PLAF7	Q8IC12 plasmodium
529	966	13.0	2	Q55Y62_CRYNE	Q55Y62 cryptococcu
530	996	13.0	2	Q67V89_ORYSA	Q67V89 oryza sativ
531	999	13.0	2	Q54BN8_DICDI	Q54BN8 dictyosteli
532	1003	13.0	2	Q4UIV2_THEAN	Q4UIV2 theileria a
533	1014	13.0	2	Q6BT63_DEBHA	Q6BT63 debaryomyce
534	1085	13.0	2	Q4XXA1_PLACH	Q4XXA1 plasmodium
535	1256	13.0	2	Q8I575_PLAF7	Q8I575 plasmodium
536	1315	13.0	2	Q8JKP9_9VIRU	Q8JKP9 heliothis z
537	1549	13.0	2	Q6MIW7_BDEBA	Q6MIW7 bdellovibri
538	1615	13.0	1	LRP5_HUMAN	Q75197 homo sapien
539	1615	13.0	2	Q9UES7_HUMAN	Q9UES7 homo sapien
540	1748	13.0	1	POLR_ELV	P35928 erysimum la
541	1748	13.0	2	Q549L0_ELV	Q549L0 erysimum la
542	2251	13.0	2	Q5CJT6_CRYHO	Q5CJT6 cryptospori

543	58.5	13.0	2254	2	Q80N16_9PICO	Q80n16	ljungan vir	616	58	12.9	926	2	Q4ZMG8_PSEBSY	Q4zm98	pseudomonas
544	58.5	13.0	2269	2	Q5CWU1_CRYPV	Q5cwu1	cryptospori	617	58	12.9	985	2	Q617Z9_CAEBR	Q617z9	caenorhabdi
545	58.5	13.0	2335	2	Q7YYR5_CRYPV	Q7yyr5	cryptospori	618	58	12.9	1025	2	Q8NDL1_HUMAN	Q8ndl1	homo sapien
546	58.5	13.0	2522	2	Q7RK50_PLAYO	Q7rk50	plasmodium	619	58	12.9	1039	2	Q86NJ2_CABEL	Q86nj2	caenorhabdi
547	58.5	13.0	2974	2	Q815L7_PLAF7	Q815l7	plasmodium	620	58	12.9	1088	2	Q815S4_PLAF7	Q815s4	plasmodium
548	58.5	13.0	3597	2	Q81LR5_PLAF7	Q81lr5	plasmodium	621	58	12.9	1114	2	Q63HQ7_HUMAN	Q63hq7	homo sapien
549	58	12.9	144	2	Q5C6W5_SCHJA	Q5c6w5	schistosoma	622	58	12.9	1114	2	Q9H0F1_HUMAN	Q9h0f1	homo sapien
550	58	12.9	145	2	Q5UIQ4_BACME	Q5uiq4	bacillus me	623	58	12.9	1177	2	Q5AKV1_CANAL	Q5akv1	candida alb
551	58	12.9	145	2	Q4ML14_BACCB	Q4ml14	bacillus ce	624	58	12.9	1184	2	Q86NJ3_CABEL	Q86nj3	caenorhabdi
552	58	12.9	145	2	Q73DE6_BACCI	Q73de6	bacillus ce	625	58	12.9	1212	2	Q9U0L0_PLAF7	Q9u0l0	plasmodium
553	58	12.9	146	1	CYB5M_FONPY	Q5rdj5	pongo pygma	626	58	12.9	1307	2	Q4YVS2_PLABE	Q4yvs2	plasmodium
554	58	12.9	187	2	Q7URC6_RHORA	Q7urc6	rhodopirell	627	58	12.9	1318	2	Q8IDI3_PLAF7	Q8idi3	plasmodium
555	58	12.9	192	2	Q6UDN3_9HIV1	Q6udn3	human immun	628	58	12.9	1331	2	Q8IBF6_PLAF7	Q8ibf6	plasmodium
556	58	12.9	194	2	Q4XAI8_PLACH	Q4xai8	plasmodium	629	58	12.9	1339	2	Q6NRS1_XENLA	Q6nrs1	xenopus lae
557	58	12.9	209	2	Q7RKE4_PLAYO	Q7rke4	plasmodium	630	58	12.9	1354	2	Q75183_HUMAN	Q75183	homo sapien
558	58	12.9	221	2	Q6VZR4_CNPV	Q6vzr4	canarypox v	631	58	12.9	1411	2	Q8JKS5_9VIRU	Q8jks5	heliothis z
559	58	12.9	229	2	Q30084_HUMAN	Q30084	homo sapien	632	58	12.9	1413	2	Q6YNG7_9VIRU	Q6yng7	botrytis vi
560	58	12.9	229	2	Q29877_HUMAN	Q29877	homo sapien	633	58	12.9	1419	2	Q86NJ4_CABEL	Q86nj4	caenorhabdi
561	58	12.9	232	2	Q4YF69_PLABE	Q4yf69	plasmodium	634	58	12.9	1605	2	Q8AYF1_XENLA	Q8ayf1	xenopus lae
562	58	12.9	241	2	Q8AI20_9HIV1	Q8ai20	human immun	635	58	12.9	1636	2	Q4XZ26_PLACH	Q4xzz6	plasmodium
563	58	12.9	241	2	Q8AI22_9HIV1	Q8ai22	human immun	636	58	12.9	1658	2	Q9BIC1_CABEL	Q9bic1	caenorhabdi
564	58	12.9	241	2	Q8AI23_9HIV1	Q8ai23	human immun	637	58	12.9	1666	2	Q9XY66_CABEL	Q9xy66	caenorhabdi
565	58	12.9	241	2	Q8AI25_9HIV1	Q8ai25	human immun	638	58	12.9	1917	2	Q4X570_PLACH	Q4x570	plasmodium
566	58	12.9	241	2	Q8AI29_9HIV1	Q8ai29	human immun	639	58	12.9	2655	2	Q6H7S8_ORYSA	Q6h7s8	oryza sativ
567	58	12.9	241	2	Q8AI35_9HIV1	Q8ai35	human immun	640	58	12.9	3869	2	Q86PQ3_CRYPV	Q86pq3	cryptospori
568	58	12.9	241	2	Q8AI40_9HIV1	Q8ai40	human immun	641	57.5	12.8	176	2	Q29969_HUMAN	Q29969	homo sapien
569	58	12.9	241	2	Q8AI41_9HIV1	Q8ai41	human immun	642	57.5	12.8	211	2	Q4YJZ8_PLABE	Q4yjz8	plasmodium
570	58	12.9	241	2	Q8AI45_9HIV1	Q8ai45	human immun	643	57.5	12.8	221	2	Q7ZMF2_9HIV1	Q7zmf2	human immun
571	58	12.9	250	2	Q19764_HUMAN	O19764	homo sapien	644	57.5	12.8	229	2	Q30081_HUMAN	Q30081	homo sapien
572	58	12.9	252	2	Q8WLZ6_BOVIN	Q8wlz6	bos taurus	645	57.5	12.8	237	2	Q30098_HUMAN	Q30098	homo sapien
573	58	12.9	261	1	KSGA_WIGBR	Q8d3i1	w dimethyla	646	57.5	12.8	255	2	O19506_HUMAN	O19506	homo sapien
574	58	12.9	261	2	Q29884_HUMAN	Q29884	homo sapien	647	57.5	12.8	261	2	Q5Y7B2_HUMAN	Q5y7b2	homo sapien
575	58	12.9	261	2	Q30093_HUMAN	Q30093	homo sapien	648	57.5	12.8	264	2	Q29970_HUMAN	Q29970	homo sapien
576	58	12.9	261	2	Q5Y7B5_HUMAN	Q5y7b5	homo sapien	649	57.5	12.8	269	2	Q30155_HUMAN	Q30155	homo sapien
577	58	12.9	269	2	Q54NA1_DICDI	Q54na1	dictyosteli	650	57.5	12.8	273	2	Q874V2_PODAN	Q874v2	podospora a
578	58	12.9	278	2	Q4XTE6_PLACH	Q4xte6	plasmodium	651	57.5	12.8	275	1	ICC_ECOLI	P36650	escherichia
579	58	12.9	290	2	Q6LGA0_PHOPR	Q6lga0	photobacter	652	57.5	12.8	275	2	Q8FDI6_ECOL6	Q8fdi6	escherichia
580	58	12.9	299	2	Q5WXQ3_LEGFL	Q5wxq3	legionella	653	57.5	12.8	275	2	Q83Q52_SHIFL	Q83q52	shigella fl
581	58	12.9	321	2	Q9L357_9PSED	Q9l357	pseudomonas	654	57.5	12.8	298	2	Q7R0G3_GIALA	Q7r0g3	giardia lam
582	58	12.9	332	2	Q5BGD5_EMENI	Q5bgd5	aspergillus	655	57.5	12.8	338	2	Q53739_STRCH	Q53739	streptomyce
583	58	12.9	361	2	Q7ZP61_9HIV1	Q7zrp61	human immun	656	57.5	12.8	371	2	Q84U52_9ASPA	Q84u52	dendrobium
584	58	12.9	368	2	Q9YZ35_SIVCZ	Q9yz35	chimpanzee	657	57.5	12.8	371	2	Q87648_SIVCZ	Q87648	chimpanzee
585	58	12.9	375	1	AAT1_METJA	Q60317	methanococ	658	57.5	12.8	383	2	Q753G2_ASHGO	Q753g2	ashbya goss
586	58	12.9	384	2	Q9S5K2_COMTE	Q9s5k2	comamonas t	659	57.5	12.8	392	2	Q6BNJ8_DEBHA	Q6bnj8	debaryomyce
587	58	12.9	405	2	Q9HUU4_PSEAE	Q9huu4	pseudomonas	660	57.5	12.8	400	2	Q4KP34_9MICR	Q4kp34	endoreticul
588	58	12.9	439	1	MYC_MARMO	P22555	marmota mon	661	57.5	12.8	400	2	Q8XKD3_CLOPE	Q8xxd3	clostridium
589	58	12.9	471	2	Q6UZ79_MEDTR	Q6uz79	medicago tr	662	57.5	12.8	413	2	Q01849_PHYCP	Q01849	phytophthor
590	58	12.9	471	2	Q5ZIJ5_CHICK	Q5zlj5	gallus gall	663	57.5	12.8	420	2	Q8I499_CUPSA	Q8i499	cupiennius
591	58	12.9	475	2	Q4R7C6_MACFA	Q4r7c6	macaca fasc	664	57.5	12.8	425	2	Q06513_9HIV2	Q06513	human immun
592	58	12.9	476	2	Q68FX4_RAT	Q68fx4	rattus norv	665	57.5	12.8	442	2	Q5CPH5_CRYPV	Q5cph5	cryptospori
593	58	12.9	479	2	Q4FKF0_9TRYP	Q4fkf0	trypanosoma	666	57.5	12.8	445	2	Q6FX91_CANGA	Q6fx91	candida gla
594	58	12.9	486	1	HCLS1_HUMAN	P14317	homo sapien	667	57.5	12.8	451	2	Q6IKU0_DROME	Q6iku0	drosophila
595	58	12.9	486	1	HCLS1_MOUSE	P49710	mus musculus	668	57.5	12.8	454	2	Q5KU75_GEOKA	Q5ku75	geobacillus
596	58	12.9	486	2	Q53Y93_HUMAN	Q53y93	homo sapien	669	57.5	12.8	458	2	Q7Z9Z5_9HYPO	Q7z9z5	uncultured
597	58	12.9	486	2	Q6IBK9_HUMAN	Q6ibk9	homo sapien	670	57.5	12.8	459	2	Q78672_VICFA	Q78672	vicia faba
598	58	12.9	486	2	Q542G0_MOUSE	Q542g0	mus musculus	671	57.5	12.8	485	2	Q9HEX8_PNECA	Q9hex8	pneumocysti
599	58	12.9	486	2	Q922I8_MOUSE	Q922i8	mus musculus	672	57.5	12.8	495	2	Q6FS46_CANGA	Q6fs46	candida gla
600	58	12.9	497	1	G6PI_LEGPN	Q9rdy2	legionella	673	57.5	12.8	498	2	Q6KHT1_MYCMO	Q6kht1	mycoplasma
601	58	12.9	499	1	G6PI_LEGPA	Q5x6y8	legionella	674	57.5	12.8	509	2	Q6JAH5_SORBI	Q6jah5	sorghum bic
602	58	12.9	499	1	G6PI_LEGPH	Q5zxx2	legionella	675	57.5	12.8	528	2	P91263_CABEL	P91263	caenorhabdi
603	58	12.9	506	2	Q6D5R0_ERWCT	Q6d5r0	erwinia car	676	57.5	12.8	531	2	Q7W8D6_BORPA	Q7w8d6	bordetella
604	58	12.9	520	2	Q61SJ3_CAEBR	Q61sj3	caenorhabdi	677	57.5	12.8	531	2	Q7WLZ5_BORBR	Q7wlz5	bordetella
605	58	12.9	522	2	Q7SB58_NEUCR	P53940	neurospora	678	57.5	12.8	559	2	Q8JR34_9CORO	Q8jr34	avian infec
606	58	12.9	528	1	YNH7_YEAST	Q4y555	saccharomyc	679	57.5	12.8	574	2	Q8Y3W3_LISMO	Q8y3w3	listeria mo
607	58	12.9	529	2	Q4Y555_PLACH	Q4y555	plasmodium	680	57.5	12.8	577	2	Q59RB2_CANAL	Q59rb2	candida alb
608	58	12.9	540	2	Q9S147_COMTE	Q9s147	comamonas t	681	57.5	12.8	590	2	Q6TBR0_CRYPV	Q6tbr0	cryptospori
609	58	12.9	573	2	Q4QHF2_LEIMA	Q4qhf2	leishmania	682	57.5	12.8	637	2	Q5CY08_CRYPV	Q5cy08	cryptospori
610	58	12.9	620	1	SYT_FUSNN	Q8rf86	fusobacteri	683	57.5	12.8	640	2	Q4WZB4_ASPFU	Q4wzb4	aspergillus
611	58	12.9	628	2	Q41604_TULGE	Q41604	tulipa gesn	684	57.5	12.8	640	2	Q84WB1_ARATH	Q84wb1	arabidopsis
612	58	12.9	628	2	Q41605_TULGE	Q41605	tulipa gesn	685	57.5	12.8	640	2	Q7XJW8_ARATH	Q7xjw8	arabidopsis
613	58	12.9	758	2	Q96037_CIOSA	O96037	ciona savig	686	57.5	12.8	655	2	Q815P8_PLAF7	Q815p8	plasmodium
614	58	12.9	795	2	O85889_SPHAR	O85889	sphingomona	687	57.5	12.8	657	2	Q94H30_ORYSA	Q94h30	oryza sativ
615	58	12.9	858	2	Q74114_9HIV2	Q74114	human immun	688	57.5	12.8	659	2	Q4GL38_HUMAN	Q4gl38	homo sapien

689	57.5	12.8	664	2	Q9UVV2_ASPTU	Q9uvv2 aspergillus	762	57	12.7	162	2	Q9J486_9CLOS	Q9j486 citrus tris
690	57.5	12.8	667	2	Q6C222_YARLI	Q6c222 yarrowia li	763	57	12.7	178	2	Q9QRN3_9HIV1	Q9qrn3 human immun
691	57.5	12.8	667	2	Q6AQN1_DESPS	Q6aqn1 desulfotale	764	57	12.7	201	2	Q4Z445_PLABE	Q4z445 plasmodium
692	57.5	12.8	670	2	Q9DSI9_9HIV2	Q9dsi9 human immun	765	57	12.7	205	2	Q70QR2_9HIV1	Q70qr2 human immun
693	57.5	12.8	716	2	Q4JLB5_LACRE	Q4jlb5 lactobacill	766	57	12.7	249	2	Q84V06_ARATH	Q84v06 arabidopsis
694	57.5	12.8	722	1	DYRK2_DROME	Q9v3d5 drosophila	767	57	12.7	275	2	Q7RHB0_PLAYO	Q7rhb0 plasmodium
695	57.5	12.8	722	1	LYAM3_SHEEP	P98i09 ovis aries	768	57	12.7	275	2	Q4YU78_PLABE	Q4yu78 plasmodium
696	57.5	12.8	777	2	Q8IBA1_PLAF7	Q8iba1 plasmodium	769	57	12.7	278	2	Q64N94_BACFR	Q64n94 bacteroides
697	57.5	12.8	783	2	Q5ZC02_ORYSA	Q5zc02 oryza sativ	770	57	12.7	281	2	Q4XDG0_PLACH	Q4xdg0 plasmodium
698	57.5	12.8	785	2	Q6SLA6_GIBMO	Q6sla6 gibberella	771	57	12.7	301	2	Q8EYV9_MYCPE	Q8evy9 mycoplasma
699	57.5	12.8	795	2	Q7QW20_GIALA	Q7qw20 giardia lam	772	57	12.7	307	2	Q03632_PLAPA	Q03632 plasmodium
700	57.5	12.8	808	2	Q4P4V0_USTMA	Q4p4v0 ustilago ma	773	57	12.7	307	2	Q90Y79_BRARE	Q90y79 brachydanio
701	57.5	12.8	850	2	Q4WGA4_ASPTU	Q4wga4 aspergillus	774	57	12.7	307	2	Q90Z46_BRARE	Q90z46 brachydanio
702	57.5	12.8	852	2	Q6CMX0_KLUJLA	Q6cmx0 kluyveromyc	775	57	12.7	314	2	Q73WZ5_MYCPA	Q73wz5 mycobacteri
703	57.5	12.8	873	2	Q4JLK4_LACRE	Q4jlk4 lactobacill	776	57	12.7	334	2	Q4XJT9_PLACH	Q4xjt9 plasmodium
704	57.5	12.8	877	2	Q83LZ9_SHIFL	Q83lz9 shigella fl	777	57	12.7	345	2	Q6CRH4_KLUJLA	Q6crh4 kluyveromyc
705	57.5	12.8	878	2	Q8C6Q7_MOUSE	Q8c6q7 mus musculu	778	57	12.7	351	2	Q9FN76_ARATH	Q9fn76 arabidopsis
706	57.5	12.8	886	2	Q90DC6_SIVCZ	Q90dc6 chimpanzee	779	57	12.7	387	2	Q9RM35_ENTFC	Q9rm35 enterococcu
707	57.5	12.8	895	2	Q5ZC03_ORYSA	Q5zc03 oryza sativ	780	57	12.7	399	2	Q5HZM7_XENLA	Q5hzm7 xenopus lae
708	57.5	12.8	902	2	Q91RC7_ADEO7	Q91rc7 ovine adeno	781	57	12.7	403	2	Q8C214_MOUSE	Q8c214 mus musculu
709	57.5	12.8	902	2	Q9Q3F8_9ADEN	Q9q3f8 goat adenov	782	57	12.7	415	2	Q51XQ9_MAGGR	Q51xq9 magnaportha
710	57.5	12.8	971	1	AREA_GIBFU	P78688 gibberella	783	57	12.7	426	2	Q5XMM5_9HEPC	Q5xmm5 hepatitis c
711	57.5	12.8	1003	2	Q60ZN8_CAEBR	Q60zn8 caenorhabdi	784	57	12.7	438	2	Q8CDY5_MOUSE	Q8cdy5 mus musculu
712	57.5	12.8	1012	2	Q727P3_DESVH	Q727p3 desulfovibr	785	57	12.7	446	2	Q9SKE9_ARATH	Q9ske9 arabidopsis
713	57.5	12.8	1022	2	Q6CFZ0_YARLI	Q6cfz0 yarrowia li	786	57	12.7	453	2	Q80ZM2_MOUSE	Q80zm2 mus musculu
714	57.5	12.8	1049	2	Q4Y187_PLACH	Q4y187 plasmodium	787	57	12.7	454	2	Q58L93_PSEPO	Q58l93 pseudechis
715	57.5	12.8	1051	2	Q6BHJ4_DEBHA	Q6bhj4 debaryomyce	788	57	12.7	458	2	Q4XSJ3_PLACH	Q4xsj3 plasmodium
716	57.5	12.8	1070	2	Q55ZN5_CRYNE	Q55zn5 cryptococcu	789	57	12.7	460	2	Q7UXM5_RHOBA	Q7uxm5 rhodopirell
717	57.5	12.8	1070	2	Q5KNZ9_CRYNE	Q5knz9 cryptococcu	790	57	12.7	471	2	Q8Z0Q8_ANASP	Q8z0q8 anabaena sp
718	57.5	12.8	1123	2	Q4HXT0_GIBZE	Q4hxt0 gibberella	791	57	12.7	485	1	OC90_MOUSE	Q9z0l3 mus musculu
719	57.5	12.8	1151	2	Q612U1_CAEBR	Q612u1 caenorhabdi	792	57	12.7	499	1	G6PI_LEGPL	Q5wye0 legionella
720	57.5	12.8	1165	1	LEPR_HUMAN	P48357 homo sapien	793	57	12.7	560	2	Q80WQ3_MOUSE	Q80wq3 mus musculu
721	57.5	12.8	1173	2	Q7RAF3_PLAYO	Q7rap3 plasmodium	794	57	12.7	561	2	Q8BP02_MOUSE	Q8bp02 mus musculu
722	57.5	12.8	1272	2	O10243_CYVV	O10243 clover yell	795	57	12.7	561	2	Q8BRG8_MOUSE	Q8brg8 mus musculu
723	57.5	12.8	1291	1	CD45_MOUSE	P06800 mus musculu	796	57	12.7	577	2	Q7RSE4_PLAYO	Q7rse4 plasmodium
724	57.5	12.8	1298	2	Q5CSI8_CRYPV	Q5csi8 cryptospori	797	57	12.7	583	1	API_KLUJLA	P56095 kluyveromyc
725	57.5	12.8	1317	2	Q5CQQ4_CRYPV	Q5cqg4 cryptospori	798	57	12.7	599	2	Q4IJM7_GIBZE	Q4ijm7 gibberella
726	57.5	12.8	1343	2	Q64730_MOUSE	Q64730 mus musculu	799	57	12.7	619	1	LAC1_NEUCR	P06811 neurospora
727	57.5	12.8	1557	2	Q8QXW5_9VTRU	Q8qxw5 garlic viru	800	57	12.7	619	1	LAC2_NEUCR	P10574 neurospora
728	57.5	12.8	1773	2	Q55170_CRYNE	Q55i70 cryptococcu	801	57	12.7	622	2	Q8C202_MOUSE	Q8c202 mus musculu
729	57.5	12.8	1774	2	Q8IAU8_PLAF7	Q8iauh plasmodium	802	57	12.7	631	2	Q9DSI6_9HIV2	Q9dsi6 human immun
730	57.5	12.8	1807	1	ITB4_RAT	Q64632 rattus norv	803	57	12.7	639	2	Q6FYV9_BARQU	Q6fyv9 bartonella
731	57.5	12.8	1821	2	Q7PSP2_ANOGA	Q7psp2 anopheles g	804	57	12.7	644	2	Q5QLH2_ORYSA	Q5qlh2 oryza sativ
732	57.5	12.8	1841	2	Q5K7Q5_CRYNE	Q5k7q5 cryptococcu	805	57	12.7	646	2	Q54YN7_DICDI	Q54yn7 dictyosteli
733	57.5	12.8	2048	2	Q4YRV4_PLABE	Q4yrv4 plasmodium	806	57	12.7	659	2	Q9DSL3_9HIV2	Q9dsl3 human immun
734	57.5	12.8	2118	2	Q8TI61_METAC	Q8ti61 methanosarc	807	57	12.7	660	2	Q5CSQ8_CRYPV	Q5csq8 cryptospori
735	57.5	12.8	2121	2	Q4KET1_PSEF5	Q4ket1 pseudomonas	808	57	12.7	678	2	Q643S1_CHICK	Q643s1 gallus gall
736	57.5	12.8	2149	2	Q6CSU4_KLUJLA	Q6csu4 kluyveromyc	809	57	12.7	706	2	Q18320_CABEL	Q18320 caenorhabdi
737	57.5	12.8	2280	2	Q8ILT4_PLAF7	Q8ilt4 plasmodium	810	57	12.7	741	2	Q74107_9HIV2	Q74107 human immun
738	57.5	12.8	2424	2	Q7RN73_PLAYO	Q7rn73 plasmodium	811	57	12.7	782	2	Q54XA6_DICDI	Q54xa6 dictyosteli
739	57.5	12.8	3072	2	Q92645_CYVV	Q92645 clover yell	812	57	12.7	789	2	Q651Z3_ORYSA	Q651z3 oryza sativ
740	57.5	12.8	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n	813	57	12.7	800	2	Q6AU80_ORYSA	Q6au80 oryza sativ
741	57.5	12.8	4590	2	Q54GY7_DICDI	Q54gy7 dictyosteli	814	57	12.7	808	2	Q6N5H8_RHOPA	Q6n5h8 rhodopseudo
742	57	12.7	51	2	Q8CKU4_YERPE	Q8cku4 yersinia pe	815	57	12.7	812	2	Q73M73_TREDE	Q73m73 treponema d
743	57	12.7	93	2	Q7TCG1_9HEPC	Q7tcg1 hepatitis c	816	57	12.7	813	1	PMAX_ARATH	Q9t0e0 arabidopsis
744	57	12.7	97	2	Q8UYQ5_9GEMI	Q8uyq5 tomato yell	817	57	12.7	828	2	Q7XMR2_ORYSA	Q7xmr2 oryza sativ
745	57	12.7	99	2	Q6R4D0_9GEMI	Q6r4d0 tomato yell	818	57	12.7	843	2	Q8I383_PLAF7	Q8i383 plasmodium
746	57	12.7	99	2	Q9J3M2_9GEMI	Q9j3m2 tomato yell	819	57	12.7	846	2	Q7PDN1_PLAYO	Q7pdn1 plasmodium
747	57	12.7	111	2	Q54DQ1_DICDI	Q54dq1 dictyosteli	820	57	12.7	875	2	Q5CJ86_CRYHO	Q5cj86 cryptospori
748	57	12.7	130	2	Q6DUM8_FRAAN	Q6dum8 fragaria an	821	57	12.7	887	2	Q7ZBT2_SIVCZ	Q7zbt2 chimpanzee
749	57	12.7	145	2	Q81V07_BACAN	Q81v07 bacillus an	822	57	12.7	924	2	Q6FN63_CANGA	Q6fn63 candida gla
750	57	12.7	155	2	Q9NFW2_HYDAT	Q9nfw2 hydra atten	823	57	12.7	943	2	Q4Z3B3_PLABE	Q4z3b3 plasmodium
751	57	12.7	162	2	Q91M69_9CLOS	Q91m69 citrus tris	824	57	12.7	944	2	Q7RJ52_PLAYO	Q7rj52 plasmodium
752	57	12.7	162	2	Q91M71_9CLOS	Q91m71 citrus tris	825	57	12.7	964	2	Q4I2C4_GIBZE	Q4i2c4 gibberella
753	57	12.7	162	2	Q91M74_9CLOS	Q91m74 citrus tris	826	57	12.7	971	2	Q9VQB6_DROME	Q9vqb6 drosophila
754	57	12.7	162	2	Q91M75_9CLOS	Q91m75 citrus tris	827	57	12.7	1007	2	Q9RIV8_STRCO	Q9riv8 streptomyce
755	57	12.7	162	2	Q91M76_9CLOS	Q91m76 citrus tris	828	57	12.7	1020	2	Q4UH79_DEBHA	Q4uh79 theileria a
756	57	12.7	162	2	Q91M78_9CLOS	Q91m78 citrus tris	829	57	12.7	1026	2	Q6BY54_DBBHA	Q6by54 debaryomyce
757	57	12.7	162	2	Q91M79_9CLOS	Q91m79 citrus tris	830	57	12.7	1042	1	LIN49_CABEL	Q20318 caenorhabdi
758	57	12.7	162	2	Q91M80_9CLOS	Q91m80 citrus tris	831	57	12.7	1076	2	Q8IL74_PLAF7	Q8il74 plasmodium
759	57	12.7	162	2	Q91M82_9CLOS	Q91m82 citrus tris	832	57	12.7	1110	2	Q5CTI7_CRYPV	Q5cti7 cryptospori
760	57	12.7	162	2	Q9J483_9CLOS	Q9j483 citrus tris	833	57	12.7	1133	2	Q7SA96_NEUCR	Q7sa96 neurospora
761	57	12.7	162	2	Q9J484_9CLOS	Q9j484 citrus tris	834	57	12.7				

Q9uvv2 aspergillus	762	57	12.7	162	2	Q9J486_9CLOS	Q9j486 citrus tris
Q6c222 yarrowia li	763	57	12.7	178	2	Q9QRN3_9HIV1	Q9qrn3 human immun
Q6aqn1 desulfotale	764	57	12.7	201	2	Q4Z445_PLABE	Q4z445 plasmodium
Q9dsi9 human immun	765	57	12.7	205	2	Q70QR2_9HIV1	Q70qr2 human immun
Q4jlb5 lactobacill	766	57	12.7	249	2	Q84V06_ARATH	Q84v06 arabidopsis
Q9v3d5 drosophila	767	57	12.7	275	2	Q7RHB0_PLAYO	Q7rhb0 plasmodium
P98i09 ovis aries	768	57	12.7	275	2	Q4YU78_PLABE	Q4yu78 plasmodium
Q8iba1 plasmodium	769	57	12.7	278	2	Q64N94_BACFR	Q64n94 bacteroides
Q5zc02 oryza sativ	770	57	12.7	281	2	Q4XDG0_PLACH	Q4xdg0 plasmodium
Q6sla6 gibberella	771	57	12.7	301	2	Q8EYV9_MYCPE	Q8evy9 mycoplasma
Q7qw20 giardia lam	772	57	12.7	307	2	Q03632_PLAPA	Q03632 plasmodium
Q4p4v0 ustilago ma	773	57	12.7	307	2	Q90Y79_BRARE	Q90y79 brachydanio
Q4wga4 aspergillus	774	57	12.7	307	2	Q90Z46_BRARE	Q90z46 brachydanio
Q6cmx0 kluyveromyc	775	57	12.7	314	2	Q73WZ5_MYCPA	Q73wz5 mycobacteri
Q4jlk4 lactobacill	776	57	12.7	334	2	Q4XJT9_PLACH	Q4xjt9 plasmodium
Q83lz9 shigella fl	777	57	12.7	345	2	Q6CRH4_KLUJLA	Q6crh4 kluyveromyc
Q8c6q7 mus musculu	778	57	12.7	351	2	Q9FN76_ARATH	Q9fn76 arabidopsis
Q90dc6 chimpanzee	779	57	12.7	387	2	Q9RM35_ENTFC	Q9rm35 enterococcu
Q5zc03 oryza sativ	780	57	12.7	399	2	Q5HZM7_XENLA	Q5hzm7 xenopus lae
Q91rc7 ovine adeno	781	57	12.7	403	2	Q8C214_MOUSE	Q8c214 mus musculu
Q9q3f8 goat adenov	782	57	12.7	415	2	Q51XQ9_MAGGR	Q51xq9 magnaportha
P78688 gibberella	783	57	12.7	426	2	Q5XMM5_9HEPC	Q5xmm5 hepatitis c
Q60zn8 caenorhabdi	784	57	12.7	438	2	Q8CDY5_MOUSE	Q8cdy5 mus musculu
Q727p3 desulfovibr	785	57	12.7	446	2	Q9SKE9_ARATH	Q9ske9 arabidopsis
Q6cfz0 yarrowia li	786	57	12.7	453	2	Q80ZM2_MOUSE	Q80zm2 mus musculu
Q4y187 plasmodium	787	57	12.7	454	2	Q58L93_PSEPO	Q58l93 pseudechis
Q6bhj4 debaryomyce	788	57	12.7	458	2	Q4XSJ3_PLACH	Q4xsj3 plasmodium
Q55zn5 cryptococcu	789	57	12.7	460	2	Q7UXM5_RHOBA	Q7uxm

835	57	12.7	1157	2	Q5AX46	EMENI	Q5AX46	aspergillus	908	56.5	12.6	789	2	Q8QRR9	9CORO	Q8QRR9	transmissib
836	57	12.7	1233	1	MUC5A	HUMAN	P98088	homo sapien	909	56.5	12.6	789	2	Q8QRS3	9CORO	Q8QRS3	transmissib
837	57	12.7	1241	2	Q8SWK2	ENCCU	Q8SWK2	encephalito	910	56.5	12.6	790	2	Q8QRS1	9CORO	Q8QRS1	transmissib
838	57	12.7	1260	2	Q6C3I8	YARLI	Q6C3I8	yarrowia li	911	56.5	12.6	790	2	Q8QRS2	9CORO	Q8QRS2	transmissib
839	57	12.7	1316	2	Q8IAS8	PLAF7	Q8IAS8	plasmodium	912	56.5	12.6	803	2	Q8ND63	HUMAN	Q8ND63	homo sapien
840	57	12.7	1336	2	Q5ZIR3	CHICK	Q5ZIR3	gallus gall	913	56.5	12.6	808	2	Q9QRQ0	9CORO	Q9QRQ0	canine coro
841	57	12.7	1404	2	Q55DE9	DICDI	Q55DE9	dictyosteli	914	56.5	12.6	811	2	Q8NSE2	CORGL	Q8NSE2	corynebacte
842	57	12.7	1411	1	ECM5	YEAST	Q03214	saccharomyc	915	56.5	12.6	825	2	Q5AUT1	EMENI	Q5AUT1	aspergillus
843	57	12.7	1428	2	Q4YU61	PLABE	Q4YU61	plasmodium	916	56.5	12.6	838	2	Q54GJ1	DICDI	Q54GJ1	dictyosteli
844	57	12.7	1614	2	Q7RN98	PLAYO	Q7RN98	plasmodium	917	56.5	12.6	852	2	Q6UFH8	9HIV1	Q6UFH8	human immun
845	57	12.7	1662	2	Q6BGS0	DEBHA	Q6BGS0	debaromyce	918	56.5	12.6	856	1	ENV	HV2NZ	P05883	human immun
846	57	12.7	1828	2	Q8IIS4	PLAF7	Q8IIS4	plasmodium	919	56.5	12.6	868	2	Q75KG8	ORYSA	Q75KG8	oryza sativ
847	57	12.7	1884	2	Q7S737	NEUCR	Q7S737	neurospora	920	56.5	12.6	874	2	Q8YQH8	ANASP	Q8YQH8	anabaena sp
848	57	12.7	1921	2	Q5WW30	LEGPL	Q5WW30	legionella	921	56.5	12.6	879	2	Q5UPF8	MIMIV	Q5UPF8	mimivirus
849	57	12.7	1921	2	Q5ZUX7	LEGPH	Q5ZUX7	legionella	922	56.5	12.6	882	2	Q7SKF3	9HIV2	Q7SKF3	human immun
850	57	12.7	2379	2	Q8IJW3	PLAF7	Q8IJW3	plasmodium	923	56.5	12.6	891	1	NIA7	HORVU	P27968	hordeum vul
851	57	12.7	2515	2	Q4S220	TETNG	Q4S220	tetraodon n	924	56.5	12.6	902	2	Q9Q3G0	9ADEN	Q9Q3G0	bovine aden
852	57	12.7	2761	2	Q19522	CAEEL	Q19522	caenorhabdi	925	56.5	12.6	910	2	O71149	ADEB4	O71149	bovine aden
853	57	12.7	3115	2	Q9WID7	9CLOS	Q9WID7	citrus tris	926	56.5	12.6	952	2	Q55M05	CRYNE	Q55M05	cryptococcu
854	57	12.7	3869	2	Q7WRN5	9NOST	Q7WRN5	anabaena ci	927	56.5	12.6	952	2	Q5K8R4	CRYNE	Q5K8R4	cryptococcu
855	56.5	12.6	128	2	Q6S8L5	PLAFA	Q6S8L5	plasmodium	928	56.5	12.6	974	2	Q7QC91	ANOGEA	Q7QC91	anopheles g
856	56.5	12.6	169	2	Q9U2W1	CAEEL	Q9U2W1	caenorhabdi	929	56.5	12.6	986	2	Q4RQJ2	TETNG	Q4RQJ2	tetraodon n
857	56.5	12.6	192	2	Q5PF60	SALPA	Q5PF60	salmonella	930	56.5	12.6	1018	2	O61295	9DIPT	O61295	chymomyza c
858	56.5	12.6	199	2	Q6S303	9HIV1	Q6S303	human immun	931	56.5	12.6	1065	2	Q4UE85	THEAN	Q4UE85	theileria a
859	56.5	12.6	203	2	Q6S317	9HIV1	Q6S317	human immun	932	56.5	12.6	1068	2	Q7QU18	GIALA	Q7QU18	giardia lam
860	56.5	12.6	232	2	Q98J31	RHILO	Q98J31	rhizobium 1	933	56.5	12.6	1117	2	Q652W3	ORYSA	Q652W3	oryza sativ
861	56.5	12.6	235	2	Q76H40	9CAUD	Q76H40	salmonella	934	56.5	12.6	1125	1	TEA3	SCHPO	O14248	schizosacch
862	56.5	12.6	235	2	Q8HAH5	BPST6	Q8HAH5	bacteriopha	935	56.5	12.6	1158	2	Q6KIC5	MYCMO	Q6KIC5	mycoplasma
863	56.5	12.6	243	2	Q4WP42	ASPFU	Q4WP42	aspergillus	936	56.5	12.6	1173	2	Q8IEM5	PLAF7	Q8IEM5	plasmodium
864	56.5	12.6	246	2	Q9BK03	TRICA	Q9BK03	tribolium c	937	56.5	12.6	1201	2	Q9C0W2	SCHPO	Q9C0W2	schizosacch
865	56.5	12.6	251	1	YMV5	CAEEL	P34507	caenorhabdi	938	56.5	12.6	1208	2	Q54WZ1	DICDI	Q54WZ1	dictyosteli
866	56.5	12.6	263	2	Q9SCR3	ARATH	Q9SCR3	arabidopsis	939	56.5	12.6	1241	2	O13617	SCHPO	O13617	schizosacch
867	56.5	12.6	265	2	Q9F5C6	AGRRH	Q9F5C6	agrobacteri	940	56.5	12.6	1263	2	Q4X3J2	PLACH	Q4X3J2	plasmodium
868	56.5	12.6	276	2	Q8RY28	ARATH	Q8RY28	arabidopsis	941	56.5	12.6	1291	2	Q6BZ89	DEBHA	Q6BZ89	debaromyce
869	56.5	12.6	276	2	Q5XPN1	ACICA	Q5XPN1	acinetobact	942	56.5	12.6	1312	2	Q7RNR7	PLAYO	Q7RNR7	plasmodium
870	56.5	12.6	276	2	Q83WC8	ACICA	Q83WC8	acinetobact	943	56.5	12.6	1360	2	Q5VQS0	ORYSA	Q5VQS0	oryza sativ
871	56.5	12.6	291	1	NANK2	ECOL6	Q8Fdu8	escherichia	944	56.5	12.6	1447	1	VGL2	CVPPU	P07946	porcine tra
872	56.5	12.6	291	2	Q6KCZ0	ECOLI	Q6KCZ0	escherichia	945	56.5	12.6	1447	1	VGL2	CVPRT	Q01977	porcine tra
873	56.5	12.6	293	2	Q9GPT0	DICDI	Q9GPT0	dictyosteli	946	56.5	12.6	1447	2	Q8QQW0	9CORO	Q8QQW0	transmissib
874	56.5	12.6	308	2	Q5FWS0	XENTR	Q5FWS0	xenopus tro	947	56.5	12.6	1447	2	Q9IW04	9CORO	Q9IW04	transmissib
875	56.5	12.6	318	2	Q6MM59	BDEBA	Q6MM59	bdellovibri	948	56.5	12.6	1472	2	Q4YAV8	PLABE	Q4YAV8	plasmodium
876	56.5	12.6	324	2	Q4QKL3	HAEI8	Q4QKL3	haemophilus	949	56.5	12.6	1496	2	Q7RJE3	PLAYO	Q7RJE3	plasmodium
877	56.5	12.6	328	2	Q87673	SIVCZ	Q87673	chimpanzee	950	56.5	12.6	1577	2	Q7F2I6	ORYSA	Q7F2I6	oryza sativ
878	56.5	12.6	339	2	Q53QF1	HUMAN	Q53QF1	homo sapien	951	56.5	12.6	1713	2	Q54B29	DICDI	Q54B29	dictyosteli
879	56.5	12.6	340	2	Q6NLV9	ARATH	Q6NLV9	arabidopsis	952	56.5	12.6	1735	2	Q8VIG2	RAT	Q8VIG2	rattus norv
880	56.5	12.6	351	2	Q9W2V8	DROME	Q9W2V8	drosophila	953	56.5	12.6	1748	2	Q54FL9	DICDI	Q54FL9	dictyosteli
881	56.5	12.6	356	2	Q83HE7	TROW8	Q83HE7	tropheryma	954	56.5	12.6	1918	2	Q7RLT6	PLAYO	Q7RLT6	plasmodium
882	56.5	12.6	356	2	Q83FR9	TROWT	Q83FR9	tropheryma	955	56.5	12.6	2122	2	Q54R92	DICDI	Q54R92	dictyosteli
883	56.5	12.6	381	2	Q4P151	USTMA	Q4P151	ustilago ma	956	56.5	12.6	2157	2	Q60T97	CAEBR	Q60T97	caenorhabdi
884	56.5	12.6	396	2	Q78673	9ROSI	Q78673	dictyosteli	957	56.5	12.6	2413	2	P71401	HABIN	P71401	haemophilus
885	56.5	12.6	411	2	Q54RK8	DICDI	Q54RK8	dictyosteli	958	56.5	12.6	2413	2	Q4KTX9	HABIN	Q4KTX9	haemophilus
886	56.5	12.6	432	2	Q4Z345	PLABE	Q4Z345	plasmodium	959	56.5	12.6	3005	1	ZFH2	DROME	P28167	drosophila
887	56.5	12.6	448	2	Q58ED3	BRARE	Q58ED3	brachydanio	960	56.5	12.6	3005	2	Q4SHP3	TETNG	Q4SHP3	tetraodon n
888	56.5	12.6	457	1	PLSB	PEA	P30706	pisum sativ	961	56.5	12.6	3240	2	Q54DT4	DICDI	Q54DT4	dictyosteli
889	56.5	12.6	470	2	Q8S342	CAPAN	Q8S342	capsicum an	962	56.5	12.6	4351	1	FAT2	RAT	Q88277	rattus norv
890	56.5	12.6	481	2	Q84XU5	ELAGV	Q84XU5	elaeis guin	963	56.5	12.6	5138	2	Q9ZW94	ARATH	Q9ZW94	arabidopsis
891	56.5	12.6	516	2	Q4UGS7	THEAN	Q4UGS7	theileria a	964	56	12.5	94	2	Q74HF7	LACJO	Q74HF7	lactobacill
892	56.5	12.6	548	2	Q4Z7R6	PLABE	Q4Z7R6	plasmodium	965	56	12.5	100	2	Q84N94	9FABA	Q84N94	indigofera
893	56.5	12.6	563	2	Q4Z1E3	PLABE	Q4Z1E3	plasmodium	966	56	12.5	131	2	Q5DPK0	9HIV1	Q5DPK0	human immun
894	56.5	12.6	569	2	Q9ZPY2	ARATH	Q9ZPY2	arabidopsis	967	56	12.5	133	2	Q7VBS5	PROMA	Q7VBS5	prochloroco
895	56.5	12.6	571	2	Q4WD61	ASPFU	Q4WD61	aspergillus	968	56	12.5	145	2	Q81HT9	BACCR	Q81HT9	bacillus ce
896	56.5	12.6	572	2	Q4HZG2	GIBZE	Q4HZG2	gibberella	969	56	12.5	162	2	Q91M84	9CLOS	Q91M84	citrus tris
897	56.5	12.6	577	2	Q96756	DUGTI	Q96756	dugesia tig	970	56	12.5	162	2	Q9J482	9CLOS	Q9J482	citrus tris
898	56.5	12.6	605	2	Q00292	ASPTI	Q00292	aspergillus	971	56	12.5	162	2	Q9J487	9CLOS	Q9J487	citrus tris
899	56.5	12.6	616	2	Q524G5	MAGGR	Q524G5	magnaporth	972	56	12.5	162	2	Q9J488	9CLOS	Q9J488	citrus tris
900	56.5	12.6	619	2	Q4X364	PLACH	Q4X364	plasmodium	973	56	12.5	162	2	Q9J489	9CLOS	Q9J489	citrus tris
901	56.5	12.6	629	2	Q8NA79	HUMAN	Q8NA79	homo sapien	974	56	12.5	162	2	Q9J494	9CLOS	Q9J494	citrus tris
902	56.5	12.6	630	2	Q4Z6L0	PLABE	Q4Z6L0	plasmodium	975	56	12.5	164	1	Y461	MYCMS	Q6MTE7	mycoplasma
903	56.5	12.6	649	2	Q502K2	BRARE	Q502K2	brachydanio	976	56	12.5	164	2	Q87KK8	VIBPA	Q87KK8	vibrio para
904	56.5	12.6	682	2	Q5VSN1	HUMAN	Q5VSN1	homo sapien	977	56	12.5	169	2	Q7W864	BORPA	Q7W864	bordetella
905	56.5	12.6	686	2	Q8ND65	HUMAN	Q8ND65	homo sapien	978	56	12.5	169	2	Q7WLL2	BORBR	Q7WLL2	bordetella
906	56.5	12.6	740	2	Q87B20	XYLFT	Q87B20	xylella fas	979	56	12.5	169	2	Q7VX98	BORPE	Q7VX98	bordetella
907	56.5	12.6	740	2	Q9PG63	XYLFA	Q9PG63	xylella fas	980	56	12.5	175	2	Q8WLZ8	BOVIN	Q8WLZ8	bos taurus

908	56.5	12.6	789	2	Q8QRR9	9CORO	Q8QRR9	transmissib	908	56.5	12.6	789	2	Q8QRR9	9CORO	Q8QRR9	transmissib
909	56.5	12.6	789	2	Q8QRS3	9CORO	Q8QRS3	transmissib	909	56.5	12.6	789	2	Q8QRS3	9CORO	Q8QRS3	transmissib
910	56.5	12.6	790	2	Q8QRS1	9CORO	Q8QRS1	transmissib	910	56.5	12.6	790	2	Q8QRS1	9CORO	Q8QRS1	transmissib
911	56.5	12.6	790	2	Q8QRS2	9CORO	Q8QRS2	transmissib	911	56.5	12.6	790	2	Q8QRS2	9CORO	Q8QRS2	transmissib
912	56.5	12.6	803	2	Q8ND63	HUMAN	Q8ND63	homo sapien	912	56.5	12.6	803	2	Q8ND63	HUMAN	Q8ND63	h

981	56	12.5	181	2	Q5Y2L7_9HIV1	Q5Y2L7 human immun
982	56	12.5	191	2	Q9DVE9_9HIV1	Q9dve9 human immun
983	56	12.5	199	2	Q31312_APHCE	Q31312 aphelocoma
984	56	12.5	203	2	Q86S73_CAEBL	Q86s73 caenorhabdi
985	56	12.5	203	2	Q4S9X1_TETNG	Q4s9x1 tetraodon n
986	56	12.5	207	2	Q6S320_9HIV1	Q6s320 human immun
987	56	12.5	207	2	Q6S319_9HIV1	Q6s319 human immun
988	56	12.5	214	2	Q8DB41_VIBVU	Q8db41 vibrio vuln
989	56	12.5	214	2	Q7MIT2_VIBVY	Q7mit2 vibrio vuln
990	56	12.5	220	2	Q4RRZ2_TETNG	Q4rrz2 tetraodon n
991	56	12.5	229	2	Q30080_HUMAN	Q30080 homo sapien
992	56	12.5	231	2	Q8VRH6_AERHY	Q8vrh6 aeromonas h
993	56	12.5	233	2	Q67AJ5_HUMAN	Q67aj5 homo sapien
994	56	12.5	233	2	Q7MZT9_PHOLI	Q7mzt9 photorhabdu
995	56	12.5	234	2	Q67AJ6_HUMAN	Q67aj6 homo sapien
996	56	12.5	237	2	Q30097_HUMAN	Q30097 homo sapien
997	56	12.5	240	2	Q30305_BOVIN	Q30305 bos taurus
998	56	12.5	247	2	Q30310_BOVIN	Q30310 bos taurus
999	56	12.5	248	2	Q5DWG2_CRYJA	Q5dwg2 cryptomeria
1000	56	12.5	250	2	Q19709_HUMAN	Q19709 homo sapien
1001	56	12.5	259	1	YG31_YEAST	P53269 saccharomyc
1002	56	12.5	261	1	HB22_HUMAN	P01919 homo sapien
1003	56	12.5	261	2	Q5Y7D0_HUMAN	Q5y7d0 homo sapien
1004	56	12.5	261	2	Q5Y7F1_HUMAN	Q5y7f1 homo sapien
1005	56	12.5	261	2	Q30266_BOVIN	Q30266 bos taurus
1006	56	12.5	261	2	Q5XWC9_BOVIN	Q5xwc9 bos taurus
1007	56	12.5	270	2	Q24347_SECE	Q24347 secale cere
1008	56	12.5	278	2	Q5L813_BACFN	Q5l813 bacteroides
1009	56	12.5	296	2	Q60ZQ3_CAEBR	Q60zq3 caenorhabdi
1010	56	12.5	302	1	HXC1A_BRARE	Q98sh9 brachydanio
1011	56	12.5	302	2	Q4WIA4_ASPFU	Q4wia4 aspergillus
1012	56	12.5	309	2	Q4XHV1_PLACH	Q4xhv1 plasmodium
1013	56	12.5	331	2	Q5CLY4_CRYHO	Q5cly4 cryptospori
1014	56	12.5	343	2	Q6MK57_BDEBA	Q6mk57 bdellovibri
1015	56	12.5	359	2	Q6PD87_BRARE	Q6pd87 brachydanio
1016	56	12.5	386	2	Q7U9X0_SYNPK	Q7u9x0 synchococc
1017	56	12.5	402	2	Q54PK7_DICDI	Q54pk7 dictyosteli
1018	56	12.5	409	2	Q8A5X6_BACTN	Q8a5x6 bacteroides
1019	56	12.5	411	2	Q45534_CAEBL	Q45534 caenorhabdi
1020	56	12.5	413	2	Q4YTQ8_PLABE	Q4ytq8 plasmodium
1021	56	12.5	447	2	Q9SJK4_ARATH	Q9sjx4 arabidopsis
1022	56	12.5	453	1	TBA1_NEUCR	P38668 neurospora
1023	56	12.5	454	2	Q60AU0_METCA	Q60au0 methylococc
1024	56	12.5	458	2	Q84TK1_ARATH	Q84tk1 arabidopsis
1025	56	12.5	470	2	Q8IIT0_PLAF7	Q8iit0 plasmodium
1026	56	12.5	481	2	Q18471_HELVI	Q18471 heliothis v
1027	56	12.5	484	2	Q7R8T2_PLAYO	Q7r8t2 plasmodium
1028	56	12.5	492	1	AER3_AERHY	Q06305 aeromonas h
1029	56	12.5	492	1	AER4_AERHY	Q06303 aeromonas h
1030	56	12.5	499	2	Q21528_CAEBL	Q21528 caenorhabdi
1031	56	12.5	501	2	Q7XG89_ORYSA	Q7xg89 oryza sativ
1032	56	12.5	501	2	Q8SB08_ORYSA	Q8sb08 oryza sativ
1033	56	12.5	504	2	Q525J6_MAGGR	Q525j6 magnaporthe
1034	56	12.5	512	2	Q7RQG1_PLAYO	Q7rqg1 plasmodium
1035	56	12.5	513	2	Q52572_PSESP	Q52572 pseudomonas
1036	56	12.5	514	2	Q9EZP3_BURCE	Q9ezp3 burkholderi
1037	56	12.5	555	2	Q9I3A5_PSEAE	Q9i3a5 pseudomonas
1038	56	12.5	570	2	Q5ARB0_EMENI	Q5arb0 aspergillus
1039	56	12.5	578	2	Q8RYC7_ARATH	Q8ryc7 arabidopsis
1040	56	12.5	596	2	Q5ATH5_EMENI	Q5ath5 aspergillus
1041	56	12.5	610	2	Q4UG81_THEAN	Q4ug81 theileria a
1042	56	12.5	631	1	LIRB3_HUMAN	Q75022 homo sapien
1043	56	12.5	632	2	Q96KV2_HUMAN	Q96kv2 homo sapien
1044	56	12.5	635	2	Q9Y3H6_HUMAN	Q9y3h6 homo sapien
1045	56	12.5	637	1	SYT_LEGPL	Q5wt82 legionella
1046	56	12.5	648	2	Q9LQV6_ARATH	Q9lqv6 arabidopsis
1047	56	12.5	651	2	Q6ZV26_HUMAN	Q6zv26 homo sapien
1048	56	12.5	657	2	Q8IYS7_HUMAN	Q8iys7 homo sapien
1049	56	12.5	664	2	Q5SLK8_THET8	Q5slk8 thermus the
1050	56	12.5	670	2	Q840Y5_NEIME	Q840y5 neisseria m
1051	56	12.5	674	2	Q7Q378_ANOGA	Q7q378 anopheles g
1052	56	12.5	677	2	Q6LEX4_PLAF7	Q6lex4 plasmodium
1053	56	12.5	695	2	Q6ZNP7_HUMAN	Q6znp7 homo sapien

1054	56	12.5	703	2	Q97DW8_CLOAB	Q97dw8 clostridium
1055	56	12.5	704	2	Q4YCC1_PLABE	Q4ycc1 plasmodium
1056	56	12.5	711	2	Q9KBE8_BACHD	Q9kbe8 bacillus ha
1057	56	12.5	714	1	RGD2_YEAST	P43556 saccharomyc
1058	56	12.5	717	2	Q7PUQ1_ANOGA	Q7puq1 anopheles g
1059	56	12.5	731	1	YJ12_YEAST	P47031 saccharomyc
1060	56	12.5	766	2	Q7RKM1_PLAYO	Q7rkm1 plasmodium
1061	56	12.5	789	2	Q8QRR7_9CORO	Q8qrr7 transmissib
1062	56	12.5	791	2	Q8I299_PLAF7	Q8i299 plasmodium
1063	56	12.5	805	2	Q6DX90_GOSHI	Q6dxs0 gossypium h
1064	56	12.5	846	2	Q52EB6_MAGGR	Q52eb6 magnaporthe
1065	56	12.5	857	2	Q5U897_9HIV1	Q5u897 human immun
1066	56	12.5	904	1	ABRU_DROME	Q24174 drosophila
1067	56	12.5	930	2	Q5CIA6_CRYHO	Q5cia6 cryptospori
1068	56	12.5	932	2	Q5CSP4_CRYPV	Q5csp4 cryptospori
1069	56	12.5	944	2	Q58T20_ARATH	Q58t20 arabidopsis
1070	56	12.5	949	2	Q6CU98_KLUJA	Q6cu98 kluyveromyc
1071	56	12.5	953	1	LUMI_ARATH	Q38796 arabidopsis
1072	56	12.5	955	2	Q20829_CAEBL	Q20829 caenorhabdi
1073	56	12.5	968	2	Q6ZU25_HUMAN	Q6zu25 homo sapien
1074	56	12.5	972	2	Q9VSA5_DROME	Q9vsa5 drosophila
1075	56	12.5	1019	2	Q4YU89_PLAYE	Q4yu89 plasmodium
1076	56	12.5	1022	2	Q6IP11_XENLA	Q6ip11 xenopus lae
1077	56	12.5	1059	2	Q9VVC6_DROME	Q9vvc6 drosophila
1078	56	12.5	1089	2	Q8I605_PLAF7	Q8i605 plasmodium
1079	56	12.5	1125	2	Q54C71_DICDI	Q54c71 dictyosteli
1080	56	12.5	1147	1	DPO3A_BORBU	Q51526 borrelia bu
1081	56	12.5	1148	1	AT8A2_HUMAN	Q9nt12 homo sapien
1082	56	12.5	1155	2	Q8WPH2_BOMMO	Q8wph2 bombyx mori
1083	56	12.5	1188	2	Q6ZSP3_HUMAN	Q6zsp3 homo sapien
1084	56	12.5	1296	2	Q61EL9_CAEBR	Q61el9 caenorhabdi
1085	56	12.5	1297	2	Q759H0_ASHGO	Q759h0 ashbya goss
1086	56	12.5	1308	1	YTX2_XENLA	P14381 xenopus lae
1087	56	12.5	1328	2	Q4RKW3_TETNG	Q4rkw3 tetraodon n
1088	56	12.5	1356	2	Q6LFA0_PLAF7	Q6lfa0 plasmodium
1089	56	12.5	1418	2	Q7PVG3_ANOGA	Q7pvg3 anopheles g
1090	56	12.5	1447	2	Q5CFG8_CRYHO	Q5cfg8 cryptospori
1091	56	12.5	1506	2	Q5CW39_CRYPV	Q5cw39 cryptospori
1092	56	12.5	1527	2	Q54CY2_DICDI	Q54cy2 dictyosteli
1093	56	12.5	1616	2	Q5ZKF9_CHICK	Q5zkf9 gallus gall
1094	56	12.5	1765	2	Q54WL2_DICDI	Q54wl2 dictyosteli
1095	56	12.5	1772	2	Q5SBN0_LACRE	Q5sbn0 lactobacill
1096	56	12.5	1779	2	Q9HCK1_HUMAN	Q9hck1 homo sapien
1097	56	12.5	2147	2	Q54CA8_DICDI	Q54ca8 dictyosteli
1098	56	12.5	2319	2	Q4RT87_TETNG	Q4rt87 tetraodon n
1099	56	12.5	2402	2	Q6LFK0_PLAF7	Q6lfk0 plasmodium
1100	56	12.5	2441	2	Q54F71_DICDI	Q54f71 dictyosteli
1101	56	12.5	2558	2	Q5CWM7_CRYPV	Q5cwm7 cryptospori
1102	56	12.5	2564	2	Q7YZ64_CRYPV	Q7yz64 cryptospori
1103	56	12.5	2603	2	Q5TRL4_ANOGA	Q5trl4 anopheles g
1104	56	12.5	2773	2	Q8IBF4_PLAF7	Q8ibf4 plasmodium
1105	56	12.5	3570	2	Q7Q737_ANOGA	Q7q737 anopheles g
1106	56	12.5	3758	2	Q4QEN3_LEIMA	Q4qen3 leishmania
1107	55.5	12.4	100	2	Q8FGG2_ECOL6	Q8fgg2 escherichia
1108	55.5	12.4	101	2	Q84N77_LUPNA	Q84n77 lupinus nan
1109	55.5	12.4	103	2	Q5XGH4_XENTR	Q5xgh4 xenopus tro
1110	55.5	12.4	109	2	Q6U5M4_KLEPN	Q6u5m4 klebsiella
1111	55.5	12.4	151	2	Q54EC0_DICDI	Q54ec0 dictyosteli
1112	55.5	12.4	160	1	CHLL_POLAC	P36439 polystichum
1113	55.5	12.4	160	2	Q7KR83_DROME	Q7kr83 drosophila
1114	55.5	12.4	161	2	Q28606_SHEEP	Q28606 ovis aries
1115	55.5	12.4	162	2	Q707F0_ECOLI	Q707f0 escherichia
1116	55.5	12.4	208	2	Q6ZTV0_HUMAN	Q6ztv0 homo sapien
1117	55.5	12.4	218	1	CTFA_CLOAB	P33752 clostridium
1118	55.5	12.4	219	2	Q4TYX8_ARATH	Q4tyx8 arabidopsis
1119	55.5	12.4	224	2	Q5D8L0_SCHJA	Q5d8l0 schistosoma
1120	55.5	12.4	226	2	Q59PT7_CANAL	Q59pt7 candida alb
1121	55.5	12.4	226	2	Q5WN15_CAEBR	Q5wn15 caenorhabdi
1122	55.5	12.4	230	2	Q9Y0S2_LYMDI	Q9y0s2 lymantria d
1123	55.5	12.4	243	2	Q9FK29_ARATH	Q9fk29 arabidopsis
1124	55.5	12.4	251	2	Q4ZCW8_9CAUD	Q4zcu8 bacterioph
1125	55.5	12.4	251	2	Q4ZBU8_9CAUD	Q4zbu8 bacterioph
1126	55.5	12.4	261	2	Q4YTC9_PLABE	Q4ytc9 plasmodium

1127	1127	55.5	12.4	267	2	Q93UX0_9RH1Z	Q93ux0 agrobacteri
1128	1128	55.5	12.4	274	2	Q526P9_MAGGR	Q526p9 magnaporthe
1129	1129	55.5	12.4	276	2	Q28774_ARCFU	Q28774 archaeoglob
1130	1130	55.5	12.4	288	2	Q98S12_GUITH	Q98s12 guillardia
1131	1131	55.5	12.4	296	2	Q5PQA4_XENLA	Q5pqa4 xenopus lae
1132	1132	55.5	12.4	300	2	Q5CUS1_CRYPV	Q5cus1 cryptospori
1133	1133	55.5	12.4	301	2	Q7RJR8_PLAYO	Q7rjr8 plasmodium
1134	1134	55.5	12.4	302	2	Q5HQB3_STAEQ	Q5hqb3 staphylococ
1135	1135	55.5	12.4	302	2	Q8CT32_STAEP	Q8ct32 staphylococ
1136	1136	55.5	12.4	304	2	Q5BJ68_XENTR	Q5bj68 xenopus tro
1137	1137	55.5	12.4	306	2	Q7RA21_PLAYO	Q7ra21 plasmodium
1138	1138	55.5	12.4	326	2	Q7X9F6_9FABA	Q7x9f6 galega orie
1139	1139	55.5	12.4	326	2	Q4LTC7_9BURK	Q4lct7 burkholderi
1140	1140	55.5	12.4	337	2	Q8KFB1_CHLTE	Q8kfb1 chlorobium
1141	1141	55.5	12.4	338	2	Q45821_CAEEL	Q45821 caenorhabdi
1142	1142	55.5	12.4	345	2	Q5OUY8_ENTHI	Q5ouy8 entamoeba h
1143	1143	55.5	12.4	350	2	Q4SH30_TETNG	Q4sh30 tetraodon n
1144	1144	55.5	12.4	358	2	Q9V4M3_DROME	Q9v4m3 drosophila
1145	1145	55.5	12.4	359	2	Q71049_9HIV1	Q71049 human immun
1146	1146	55.5	12.4	373	2	Q7R9L3_PLAYO	Q7r9l3 plasmodium
1147	1147	55.5	12.4	379	2	Q7PYJ0_ANOGA	Q7pyj0 anopheles g
1148	1148	55.5	12.4	382	2	Q6ATE2_ORYSA	Q6ate2 oryza sativ
1149	1149	55.5	12.4	393	2	Q5O247_ENTHI	Q5o247 entamoeba h
1150	1150	55.5	12.4	403	2	Q50HW5_LOTJA	Q50hw5 lotus japon
1151	1151	55.5	12.4	417	2	Q97FA3_CLOAB	Q97fa3 clostridium
1152	1152	55.5	12.4	427	2	Q8W3G2_ORYSA	Q8w3g2 oryza sativ
1153	1153	55.5	12.4	427	2	Q8PQY4_XANAC	Q8pgy4 xanthomonas
1154	1154	55.5	12.4	441	1	TBA_ENCCU	Q8sr16 encephalito
1155	1155	55.5	12.4	441	1	VA39_VACCV	P24764 vaccinia vi
1156	1156	55.5	12.4	443	2	Q6P985_HUMAN	Q6p985 homo sapien
1157	1157	55.5	12.4	446	2	Q729L9_COPCI	Q7z9l9 coprinus ci
1158	1158	55.5	12.4	449	1	TBA_GIBZE	Q5i2j3 gibberella
1159	1159	55.5	12.4	449	2	Q4IQ69_GIBZE	Q4iq69 gibberella
1160	1160	55.5	12.4	459	2	Q6MZY0_HUMAN	Q6mzy0 homo sapien
1161	1161	55.5	12.4	462	2	Q683B7_ARATH	Q683b7 arabidopsis
1162	1162	55.5	12.4	470	2	Q76BF8_ORYLA	Q76bf8 oryzias lat
1163	1163	55.5	12.4	477	2	Q683F9_ARATH	Q683f9 arabidopsis
1164	1164	55.5	12.4	486	2	Q87R02_VIBPA	Q87r02 vibrio para
1165	1165	55.5	12.4	488	2	Q67ZA2_ARATH	Q67za2 arabidopsis
1166	1166	55.5	12.4	488	2	Q67X97_ARATH	Q67x97 arabidopsis
1167	1167	55.5	12.4	488	2	Q94CC6_ARATH	Q94cc6 arabidopsis
1168	1168	55.5	12.4	492	2	Q61BF5_CAEBR	Q61bf5 caenorhabdi
1169	1169	55.5	12.4	497	2	Q5XBP8_STRPB	Q5xbp8 streptococc
1170	1170	55.5	12.4	497	2	Q99ZC2_STRPY	Q99zc2 streptococc
1171	1171	55.5	12.4	497	2	Q8P0K6_STRPB	Q8p0k6 streptococc
1172	1172	55.5	12.4	497	2	Q8K751_STRP3	Q8k751 streptococc
1173	1173	55.5	12.4	498	1	ZN271_HUMAN	Q14591 homo sapien
1174	1174	55.5	12.4	501	2	Q43265_MAIZE	Q43265 zea mays (m
1175	1175	55.5	12.4	504	2	Q6TKQ2_HELTI	Q6tkq2 helisoma tr
1176	1176	55.5	12.4	509	2	Q6BYN6_DEBHA	Q6byn6 debaryomyce
1177	1177	55.5	12.4	514	2	Q6CK27_KLULA	Q6ck27 kluyveromyc
1178	1178	55.5	12.4	514	2	Q4G339_9PERO	Q4g339 rhabdosargu
1179	1179	55.5	12.4	516	1	NACH_DROAN	Q61370 drosophila
1180	1180	55.5	12.4	527	2	Q5NDL2_HUMAN	Q5ndl2 homo sapien
1181	1181	55.5	12.4	527	2	Q5NDL1_PANTR	Q5ndl1 pan troglod
1182	1182	55.5	12.4	527	2	Q5NDL9_CANFA	Q5ndl9 canis famil
1183	1183	55.5	12.4	537	2	Q5CS03_CRYPV	Q5cs03 cryptospori
1184	1184	55.5	12.4	544	2	Q97M46_CLOAB	Q97m46 clostridium
1185	1185	55.5	12.4	557	2	Q4Z552_PLABE	Q4z552 plasmodium
1186	1186	55.5	12.4	561	2	Q61K34_CAEBR	Q61k34 caenorhabdi
1187	1187	55.5	12.4	568	1	MMP21_MOUSE	Q8k3f2 mus musculu
1188	1188	55.5	12.4	569	2	Q6ZQ53_MOUSE	Q6zq53 mus musculu
1189	1189	55.5	12.4	578	2	Q4R7H1_MACFA	Q4r7h1 macaca fasc
1190	1190	55.5	12.4	586	2	Q551C4_DICDI	Q551c4 dictyosteli
1191	1191	55.5	12.4	602	2	Q66UC5_9DIPT	Q66uc5 culicoides
1192	1192	55.5	12.4	623	2	Q6FIM0_CANGA	Q6fim0 candida gla
1193	1193	55.5	12.4	643	2	Q6BSN4_DEBHA	Q6bsn4 debaryomyce
1194	1194	55.5	12.4	646	1	LYAM3_BOVIN	P42201 bos taurus
1195	1195	55.5	12.4	649	2	Q28657_RABIT	Q28657 oryctolagus
1196	1196	55.5	12.4	662	2	Q8IAW6_PLAF7	Q8iaw6 plasmodium
1197	1197	55.5	12.4	676	2	Q9H5A7_HUMAN	Q9h5a7 homo sapien
1198	1198	55.5	12.4	683	2	Q36401_9GAMA	Q36401 alcelaphine
1199	1199	55.5	12.4	688	2	Q7S3U0_NEUCR	Q7s3u0 neurospora

1200	55.5	12.4	702	2	Q4SRR8_TETNG	Q4srr8 tetraodon n
1201	55.5	12.4	704	1	MSN2_YEAST	P33748 saccharomyc
1202	55.5	12.4	707	2	Q5CRK5_CRYPV	Q5crk5 cryptospori
1203	55.5	12.4	710	2	Q4RRG6_TETNG	Q4rrg6 tetraodon n
1204	55.5	12.4	718	2	Q8CS09_STAEP	Q8cs09 staphylococ
1205	55.5	12.4	729	2	Q54HB7_DICDI	Q54hb7 dictyosteli
1206	55.5	12.4	789	2	Q8QRS0_9CORO	Q8qrs0 transmissib
1207	55.5	12.4	798	1	ITB1_FELCA	P53713 felis silve
1208	55.5	12.4	798	2	Q8SQC0_BOVIN	Q8sqc0 bos taurus
1209	55.5	12.4	805	2	Q6DXT4_GOSHI	Q6dxt4 gossypium h
1210	55.5	12.4	841	2	Q4ICM6_GIBZE	Q4icm6 gibberella
1211	55.5	12.4	858	1	CYAG_DICDI	Q03101 dictyosteli
1212	55.5	12.4	858	2	Q86A89_DICDI	Q86a89 dictyosteli
1213	55.5	12.4	860	1	ENV_HV2BE	P18094 human immun
1214	55.5	12.4	861	2	Q9IUZ4_9HIV1	Q9iuz4 human immun
1215	55.5	12.4	875	2	Q48930_SOYBN	Q48930 glycine max
1216	55.5	12.4	875	2	Q5H1L0_XANOR	Q5h1l0 xanthomonas
1217	55.5	12.4	877	2	Q8PMQ7_XANAC	Q8pmq7 xanthomonas
1218	55.5	12.4	879	2	Q88028_SIVCZ	Q88028 chimpanzee
1219	55.5	12.4	886	1	NIA1_SOYBN	P54233 glycine max
1220	55.5	12.4	890	1	NIA2_SOYBN	P39870 glycine max
1221	55.5	12.4	890	2	Q9SYR0_SOYBN	Q9syro glycine max
1222	55.5	12.4	911	2	Q83905_ADEO7	Q83905 ovine adeno
1223	55.5	12.4	912	1	NIA2_HORVU	P27969 hordeum vul
1224	55.5	12.4	915	1	NIA1_HORVU	P27967 hordeum vul
1225	55.5	12.4	916	2	Q60BP0_METCA	Q60bp0 methylococc
1226	55.5	12.4	917	2	Q873D8_NEUCR	Q873d8 neurospora
1227	55.5	12.4	987	2	Q5QF51_9CAUD	Q5qf51 pseudomonas
1228	55.5	12.4	992	2	Q4Z6U8_PLABE	Q4z6u8 plasmodium
1229	55.5	12.4	992	2	Q7TT14_MOUSE	Q7tt14 mus musculu
1230	55.5	12.4	1002	1	RBM12_MOUSE	Q8r4x3 mus musculu
1231	55.5	12.4	1004	2	Q8IBA4_PLAF7	Q8iba4 plasmodium
1232	55.5	12.4	1016	2	Q61296_9DIPT	Q61296 chymomyza c
1233	55.5	12.4	1060	2	Q86T73_HUMAN	Q86t73 homo sapien
1234	55.5	12.4	1074	2	Q4XPJ3_PLACH	Q4xpj3 plasmodium
1235	55.5	12.4	1099	2	Q9U9K8_DICDI	Q9u9k8 dictyosteli
1236	55.5	12.4	1130	2	Q6R7G2_9HERP	Q6r7g2 ostreid her
1237	55.5	12.4	1157	2	Q54U88_DICDI	Q54u88 dictyosteli
1238	55.5	12.4	1187	2	Q6PFD9_MOUSE	Q6pfd9 mus musculu
1239	55.5	12.4	1225	2	Q4L4Y3_STAHL	Q4l4y3 staphylococ
1240	55.5	12.4	1245	2	Q5CKS9_CRYHO	Q5cks9 cryptospori
1241	55.5	12.4	1352	2	Q55T02_CRYNE	Q55t02 cryptococcu
1242	55.5	12.4	1439	2	Q5CPF4_CRYPV	Q5cpf4 cryptospori
1243	55.5	12.4	1501	2	Q75J89_DICDI	Q75j89 dictyosteli
1244	55.5	12.4	1540	2	Q559R8_DICDI	Q559r8 dictyosteli
1245	55.5	12.4	1582	2	Q6OST0_CAEBR	Q6ost0 caenorhabdi
1246	55.5	12.4	1608	2	Q54VR7_DICDI	Q54vr7 dictyosteli
1247	55.5	12.4	1710	2	Q54YG2_DICDI	Q54yg2 dictyosteli
1248	55.5	12.4	1729	1	NUP98_HUMAN	P52948 homo sapien
1249	55.5	12.4	1848	2	Q4S113_TETNG	Q4s113 tetraodon n
1250	55.5	12.4	1873	2	Q6S003_DICDI	Q6s003 dictyosteli
1251	55.5	12.4	1874	1	POLR_KYMUJ	P36304 kennedy a ye
1252	55.5	12.4	1946	2	Q4N6K9_THERPA	Q4n6k9 theileria p
1253	55.5	12.4	5432	2	Q7RPX5_PLAYO	Q7rpx5 plasmodium
1254	55.5	12.4	8647	2	Q7KQP5_DROME	Q7kqp5 drosophila
1255	55.5	12.4	8648	2	Q7KQP6_DROME	Q7kqp6 drosophila
1256	55.5	12.4	8930	2	Q7KQP7_DROME	Q7kqp7 drosophila
1257	55.5	12.4	8943	2	Q9V4F7_DROME	Q9v4f7 drosophila
1258	55.5	12.4	9341	2	Q8I3N9_PLAF7	Q8i3n9 plasmodium
1259	55	12.2	89	2	Q4XAV4_PLACH	Q4xav4 plasmodium
1260	55	12.2	95	2	Q4XC10_PLACH	Q4xc10 plasmodium
1261	55	12.2	96	2	O07160_MYCLE	O07160 mycobacteri
1262	55	12.2	97	2	Q6R4D6_9GEMI	Q6r4d6 tomato yell
1263	55	12.2	102	2	Q7TAS6_9GEMI	Q7tas6 sri lankan
1264	55	12.2	132	2	Q4RTY3_TETNG	Q4rty3 tetraodon n
1265	55	12.2	136	2	Q6NG01_CORDI	Q6ng01 corynebacte
1266	55	12.2	140	2	Q6CAM9_YARLI	Q6cam9 yarrowia li
1267	55	12.2	148	2	Q6ZNP2_HUMAN	Q6znp2 homo sapien
1268	55	12.2	150	2	Q84FW6_ECOLI	Q84fw6 escherichia
1269	55	12.2	155	2	Q54CV7_DICDI	Q54cv7 dictyosteli
1270	55	12.2	162	2	Q91M68_9CLOS	Q91m68 citrurus tris
1271	55	12.2	165	2	Q8WYU1_HUMAN	Q8wyu1 homo sapien
1272	55	12.2	165	2	Q6DVP0_SHISO	Q6dvp0 shigella so

Q4srr8	tetraodon n
P33748	saccharomyc
Q5crk5	cryptospori
Q4rrg6	tetraodon n
Q8cs09	staphylococ
Q54hb7	dictyosteli
Q8qrs0	transmissib
P53713	felis silve
Q8sqc0	bos taurus
Q6dxt4	gossypium h
Q4icm6	gibberella
Q03101	dictyosteli
Q86a89	dictyosteli
P18094	human immun
Q9iuz4	human immun
Q48930	glycine max
Q5h1l0	xanthomonas
Q8pmq7	xanthomonas
Q88028	chimpanzee
P54233	glycine max
P39870	glycine max
Q9syro	glycine max
Q83905	ovine adeno
P27969	hordeum vul
P27967	hordeum vul
Q60bp0	methylococc
Q873d8	neurospora
Q5qf51	pseudomonas
Q4z6u8	plasmodium
Q7tt14	mus musculus
Q8r4x3	mus musculus
Q8iba4	plasmodium
Q61296	chymomyza c
Q86t73	homo sapien
Q4xpj3	plasmodium
Q9u9k8	dictyosteli
Q6r7g2	ostreid her
Q54u88	dictyosteli
Q6pfd9	mus musculus
Q4l4y3	staphylococ
Q5cks9	cryptospori
Q55t02	cryptococcu
Q5cpf4	cryptospori
Q75j89	dictyosteli
Q559r8	dictyosteli
Q608t0	caenorhabdi
Q54vr7	dictyosteli
Q54yg2	dictyosteli
P52948	homo sapien
Q48l13	tetraodon n
Q68003	dictyosteli
P36304	kennedy a ye
Q4n6k9	theileria p
Q7rpx5	plasmodium
Q7rkp5	drosophila
Q7rkqp6	drosophila
Q7rkqp7	drosophila
Q9v4f7	drosophila
Q8l3n9	plasmodium
Q4xav4	plasmodium
Q4xcio	plasmodium
Q07160	mycobacteri
Q6r4d6	tomato yell
Q7tas6	sri lankan
Q4rty3	tetraodon n
Q6ng01	corynebacte
Q6cam9	yarrowia li
Q6znp2	homo sapien
Q84fw6	escherichia
Q54cv7	dictyosteli
Q91m68	citrus tris
Q8wyl1	homo sapien
Q6dvp0	shigella so

1273	55	12.2	165	2	Q32551_ECOLI	Q32551 escherichia
1274	55	12.2	175	2	Q8WLZ7_BOVIN	Q8WLZ7 bos taurus
1275	55	12.2	176	2	Q7OR01_9HIV1	Q7OR01 human immun
1276	55	12.2	179	2	Q7XJ29_PYRGO	Q7XJ29 pyrus commu
1277	55	12.2	183	2	Q19715_HUMAN	Q19715 homo sapien
1278	55	12.2	183	2	Q29922_HUMAN	Q29922 homo sapien
1279	55	12.2	183	2	Q30102_HUMAN	Q30102 homo sapien
1280	55	12.2	183	2	Q30090_HUMAN	Q30090 homo sapien
1281	55	12.2	183	2	Q7YP69_HUMAN	Q7YP69 homo sapien
1282	55	12.2	186	2	Q7PQY2_ANOGA	Q7PQY2 anopheles g
1283	55	12.2	188	2	Q5ZB19_ORYSA	Q5ZB19 oryza sativ
1284	55	12.2	205	2	Q4YOH4_PLACH	Q4YOH4 plasmodium
1285	55	12.2	208	2	Q4NWB5_9DELT	Q4NWB5 anaeromyxob
1286	55	12.2	218	1	RPE_TREPA	Q66107 treponema p
1287	55	12.2	218	2	Q9N490_CABEL	Q9N490 caenorhabdi
1288	55	12.2	220	2	Q67AK0_HUMAN	Q67AK0 homo sapien
1289	55	12.2	224	2	Q29967_HUMAN	Q29967 homo sapien
1290	55	12.2	224	2	Q5SP12_HUMAN	Q5SP12 homo sapien
1291	55	12.2	224	2	Q8SZB7_DROME	Q8SZB7 drosophila
1292	55	12.2	227	2	Q67AJ9_HUMAN	Q67AJ9 homo sapien
1293	55	12.2	228	2	P79526_HUMAN	P79526 homo sapien
1294	55	12.2	229	2	Q19712_HUMAN	Q19712 homo sapien
1295	55	12.2	229	2	Q30075_HUMAN	Q30075 homo sapien
1296	55	12.2	229	2	Q19707_HUMAN	Q19707 homo sapien
1297	55	12.2	229	2	Q30078_HUMAN	Q30078 homo sapien
1298	55	12.2	229	2	Q30076_HUMAN	Q30076 homo sapien
1299	55	12.2	229	2	Q30MY2_HUMAN	Q30MY2 homo sapien
1300	55	12.2	229	2	Q30079_HUMAN	Q30079 homo sapien
1301	55	12.2	229	2	Q30077_HUMAN	Q30077 homo sapien
1302	55	12.2	230	2	Q30132_HUMAN	Q30132 homo sapien
1303	55	12.2	230	2	Q4YVZ6_PLABE	Q4YVZ6 plasmodium
1304	55	12.2	230	2	Q9LJG5_ARATH	Q9LJG5 arabidopsis
1305	55	12.2	233	2	Q67AK5_HUMAN	Q67AK5 homo sapien
1306	55	12.2	233	2	Q67AK4_HUMAN	Q67AK4 homo sapien
1307	55	12.2	233	2	Q67AK3_HUMAN	Q67AK3 homo sapien
1308	55	12.2	233	2	Q9I607_PSEAE	Q9I607 pseudomonas
1309	55	12.2	234	2	Q67AL8_HUMAN	Q67AL8 homo sapien
1310	55	12.2	234	2	Q67AL5_HUMAN	Q67AL5 homo sapien
1311	55	12.2	234	2	Q67AL4_HUMAN	Q67AL4 homo sapien
1312	55	12.2	234	2	Q67AL3_HUMAN	Q67AL3 homo sapien
1313	55	12.2	234	2	Q67AL2_HUMAN	Q67AL2 homo sapien
1314	55	12.2	234	2	Q67AL1_HUMAN	Q67AL1 homo sapien
1315	55	12.2	234	2	Q67AL0_HUMAN	Q67AL0 homo sapien
1316	55	12.2	234	2	Q67AK9_HUMAN	Q67AK9 homo sapien
1317	55	12.2	234	2	Q67AK8_HUMAN	Q67AK8 homo sapien
1318	55	12.2	234	2	Q67AK7_HUMAN	Q67AK7 homo sapien
1319	55	12.2	234	2	Q67AK6_HUMAN	Q67AK6 homo sapien
1320	55	12.2	234	2	Q67AK2_HUMAN	Q67AK2 homo sapien
1321	55	12.2	234	2	Q67AK1_HUMAN	Q67AK1 homo sapien
1322	55	12.2	234	2	Q67AJ8_HUMAN	Q67AJ8 homo sapien
1323	55	12.2	234	2	Q67AJ7_HUMAN	Q67AJ7 homo sapien
1324	55	12.2	235	2	Q67AJ4_HUMAN	Q67AJ4 homo sapien
1325	55	12.2	235	2	Q67AJ3_HUMAN	Q67AJ3 homo sapien
1326	55	12.2	249	2	Q5FF04_EHRRG	Q5FF04 ehrlichia r
1327	55	12.2	249	2	Q5HCP5_EHRRW	Q5HCP5 ehrlichia r
1328	55	12.2	250	2	Q19711_HUMAN	Q19711 homo sapien
1329	55	12.2	250	2	Q19714_HUMAN	Q19714 homo sapien
1330	55	12.2	250	2	Q4Z2L8_PLABE	Q4Z2L8 plasmodium
1331	55	12.2	256	2	Q5SR06_HUMAN	Q5SR06 homo sapien
1332	55	12.2	258	2	Q6RKH9_GIBZE	Q6RKH9 gibberella
1333	55	12.2	260	2	P79551_HUMAN	P79551 homo sapien
1334	55	12.2	261	1	HB21_HUMAN	P01918 homo sapien
1335	55	12.2	261	1	HB23_HUMAN	P05537 homo sapien
1336	55	12.2	261	1	HB24_HUMAN	P01920 homo sapien
1337	55	12.2	261	2	Q30096_HUMAN	Q30096 homo sapien
1338	55	12.2	261	2	Q30091_HUMAN	Q30091 homo sapien
1339	55	12.2	261	2	Q95IH2_HUMAN	Q95IH2 homo sapien
1340	55	12.2	261	2	Q5Y7F6_HUMAN	Q5Y7F6 homo sapien
1341	55	12.2	261	2	Q30061_HUMAN	Q30061 homo sapien
1342	55	12.2	261	2	Q5ISH3_HUMAN	Q5ISH3 homo sapien
1343	55	12.2	261	2	Q5ISH1_HUMAN	Q5ISH1 homo sapien
1344	55	12.2	261	2	Q5Y7G8_HUMAN	Q5Y7G8 homo sapien
1345	55	12.2	261	2	Q31633_HUMAN	Q31633 homo sapien

1346	55	12.2	261	2	Q5Y7D3_HUMAN	Q5Y7D3 homo sapien
1347	55	12.2	264	2	Q29826_HUMAN	Q29826 homo sapien
1348	55	12.2	264	2	Q5SR05_HUMAN	Q5SR05 homo sapien
1349	55	12.2	267	2	Q54XR8_DICDI	Q54XR8 dictyosteli
1350	55	12.2	267	2	Q561R6_RAT	Q561R6 rattus norv
1351	55	12.2	268	1	HB2X_HUMAN	P05538 homo sapien
1352	55	12.2	274	2	Q9WEU7_9HIV1	Q9WEU7 human immun
1353	55	12.2	276	2	Q6BCY4_HUMAN	Q6BCY4 homo sapien
1354	55	12.2	283	2	Q8WLR4_HUMAN	Q8WLR4 homo sapien
1355	55	12.2	284	2	Q54GQ2_DICDI	Q54GQ2 dictyosteli
1356	55	12.2	287	2	Q9XX63_CABEL	Q9XX63 caenorhabdi
1357	55	12.2	297	2	Q4N7Q3_THEPA	Q4N7Q3 theileria p
1358	55	12.2	319	2	Q8ESD0_OCEIH	Q8ESD0 oceanobacil
1359	55	12.2	320	2	Q5ZMK0_CHICK	Q5ZMK0 gallus gall
1360	55	12.2	326	2	Q9NK73_DROME	Q9NK73 drosophila
1361	55	12.2	327	2	Q8MS18_DROME	Q8MS18 drosophila
1362	55	12.2	327	2	Q9VJM9_DROME	Q9VJM9 drosophila
1363	55	12.2	327	2	Q8LT49_9CAUD	Q8LT49 vibrionphage
1364	55	12.2	328	2	Q5AVC6_EMBENI	Q5AVC6 aspergillus
1365	55	12.2	328	2	Q4UI64_THEAN	Q4UI64 theileria a
1366	55	12.2	329	2	Q81NC7_BACAN	Q81NC7 bacillus an
1367	55	12.2	332	1	AXHA_ASPNG	P79019 aspergillus
1368	55	12.2	332	2	Q68170_9LACT	Q68170 lactococcus
1369	55	12.2	334	2	Q6FRW2_CANGA	Q6FRW2 candida gla
1370	55	12.2	348	2	Q4S271_TETNG	Q4S271 tetraodon n
1371	55	12.2	349	2	Q9FTT4_ORYSA	Q9FTT4 oryza sativ
1372	55	12.2	358	2	Q8PFW7_METMA	Q8PFW7 methanosarc
1373	55	12.2	359	2	Q9CHR9_LACLA	Q9CHR9 lactococcus
1374	55	12.2	363	1	VXS1_MOUSE	Q91VL0 mus musculu
1375	55	12.2	369	2	Q8SVZ6_ENCCU	Q8SVZ6 encephalito
1376	55	12.2	377	2	Q6Q906_9GAMM	Q6Q906 uncultured
1377	55	12.2	378	2	Q7MXM1_PORGI	Q7MXM1 porphyromon
1378	55	12.2	379	2	Q4KCG5_PSEFP5	Q4KCG5 pseudomonas
1379	55	12.2	399	2	Q5JE21_PYRKO	Q5JE21 pyrococcus
1380	55	12.2	401	2	Q60VB9_CAEBR	Q60VB9 caenorhabdi
1381	55	12.2	406	1	YNQ5_YEAST	P53891 saccharomyc
1382	55	12.2	410	1	CDA_CRYNV	P82476 cryptococcu
1383	55	12.2	410	2	Q4SXT0_TETNG	Q4SXT0 tetraodon n
1384	55	12.2	410	2	Q4TB78_TETNG	Q4TB78 tetraodon n
1385	55	12.2	412	1	AATC_BOVIN	P33097 bos taurus
1386	55	12.2	413	2	Q5E9R4_BOVIN	Q5E9R4 bos taurus
1387	55	12.2	416	2	Q9VY24_DROME	Q9VY24 drosophila
1388	55	12.2	421	2	Q4V4S5_DROME	Q4V4S5 drosophila
1389	55	12.2	421	2	Q4V6I6_DROME	Q4V6I6 drosophila
1390	55	12.2	429	2	Q7PZ84_ANOGA	Q7PZ84 anopheles g
1391	55	12.2	443	2	Q9A6Z5_CAUCR	Q9A6Z5 caulobacter
1392	55	12.2	454	2	Q96UM2_BOTCI	Q96UM2 botrytis ci
1393	55	12.2	458	1	YM51_YEAST	P42933 saccharomyc
1394	55	12.2	470	2	Q8IHU1_PLAF7	Q8IHU1 plasmodium
1395	55	12.2	485	2	Q86HV0_DICDI	Q86HV0 dictyosteli
1396	55	12.2	486	1	LAC1_BOTCI	Q12570 botrytis ci
1397	55	12.2	493	1	AERA_AERHY	P09167 aeromonas h
1398	55	12.2	499	2	Q54IM9_DICDI	Q54IM9 dictyosteli
1399	55	12.2	500	1	AMPA_RHOPA	Q6N5B9 rhodopsendo
1400	55	12.2	501	2	Q529G8_MAGGR	Q529G8 magnaporth
1401	55	12.2	510	2	Q8BG78_MOUSE	Q8BG78 m mus muscu
1402	55	12.2	519	2	Q8RCZ8_THETN	Q8RCZ8 thermoanaer
1403	55	12.2	534	2	Q54H08_DICDI	Q54H08 dictyosteli
1404	55	12.2	536	2	Q9ZNP4_COMTE	Q9ZNP4 comamonas t
1405	55	12.2	538	2	Q8QMF7_9CORO	Q8QMF7 avian infec
1406	55	12.2	542	2	Q726G4_DESVH	Q726G4 desulfovibr
1407	55	12.2	555	2	Q551H1_DICDI	Q551H1 dictyosteli
1408	55	12.2	559	2	Q7RWQ5_NEUCR	Q7RWQ5 neurospora
1409	55	12.2	561	2	Q96WN0_BOTCI	Q96WN0 botrytis ci
1410	55	12.2	565	2	Q4US47_XANCP	Q4US47 xanthomonas
1411	55	12.2	565	2	Q8PBF9_XANCP	Q8PBF9 xanthomonas
1412	55	12.2	565	2	Q8PN12_XANAC	Q8PN12 xanthomonas
1413	55	12.2	571	1	HEMA_PI2H	P25465 human parai
1414	55	12.2	571	1	HEMA_PI2HT	P25466 human parai
1415	55	12.2	571	2	Q4R4G4_PI2H	Q4R4G4 human parai
1416	55	12.2	582	1	YANB_SCHPO	Q10076 schizosacch
1417	55	12.2	586	2	Q6CAY8_YARLI	Q6CAY8 yarrowia li
1418	55	12.2	586	2	Q9NDR4_SARPE	Q9NDR4 sarcophaga

Q5Y7d3	homo sapien
Q29826	homo sapien
Q5ar05	homo sapien
Q54xr8	dictyosteli
Q561r6	rattus norv
P05538	homo sapien
Q9weu7	human immun
Q6bcy4	homo sapien
Q8wlr4	homo sapien
Q54gq2	dictyosteli
Q9xx63	caenorhabdi
Q4n7q3	theileria p
Q8ead0	oceanobacil
Q5zmk0	gallus gall
Q9nk73	drosophila
Q8ms18	drosophila
Q9vjm9	drosophila
Q8lt49	vibriophage
Q5avc6	aspergillus
Q4ui64	theileria a
Q81nc7	bacillus an
P79019	aspergillus
O68170	lactococcus
Q6frw2	candida gla
Q4s271	tetraodon n
Q9ftt4	oryza sativ
Q8pww7	methanosarc
Q9chr9	lactococcus
Q91vl0	mus musculu
Q8svz6	encephalito
Q6q906	uncultured
Q7mxm1	porphyromon
Q4kcg5	pseudomonas
Q5je21	pyrococcus
Q60vb9	caenorhabdi
P53891	saccharomyc
P82476	cryptococcu
Q4sxt0	tetraodon n
Q4tb78	tetraodon n
P33097	bos taurus
Q5e9r4	bos taurus
Q9vy24	drosophila
Q4v4s5	drosophila
Q4v6i6	drosophila
Q7pz84	anopheles g
Q9a6z5	caulobacter
Q96um2	botrytis ci
P42933	saccharomyc
Q8ihu1	plasmodium
Q86hv0	dictyosteli
Q12570	botrytis ci
P09167	aeromonas h
Q54im9	dictyosteli
Q6n5b9	rhodopsendo
Q529g8	magnaporth
Q8bg78	m mus muscu
Q8rcz8	thermoanaer
Q54h08	dictyosteli
Q9znp4	comamonas t
Q8qmf7	avian infec
Q726g4	desulfovibr
Q551h1	dictyosteli
Q7rwq5	neurospora
Q96wn0	botrytis ci
Q4us47	xanthomonas
Q8pbf9	xanthomonas
Q8pn12	xanthomonas
P25465	human parai
P25466	human parai
Q4r4g4	human parai
Q10076	schizosacch
Q6cay8	yarrowia li
Q9ndr4	sarcophaga

RT "The sequence of Homo sapiens BAC clone RP11-563C6.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25075 MW; 1718E0594997A1A1 CRC64;

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.6e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGW 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 RASSFHFDSEENKRLIHFS 80
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 RASSFHFDSEENKRLIHFS 190

RESULT 3
Q6UWS1 HUMAN
ID Q6UWS1_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q6UWS1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE TCCE518.
GN ORFNames=UNQ518;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358671; AAQ89034.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 229 AA; 25109 MW; 1718ED342C58C903 CRC64;

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.6e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGW 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGW 170
Qy 61 RASSFHFDSEENKRLIHFS 80
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 RASSFHFDSEENKRLIHFS 190

RESULT 4
Q5U609 HUMAN
ID Q5U609_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q5U609;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Transmembrane 4 L six family member 20.
GN Name=TM4SF20;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035754; AAH35754.1; -; mRNA.
DR Ensembl; ENSG00000168955; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
KW Transmembrane.
SQ SEQUENCE 229 AA; 25137 MW; B750504AFD7C247D CRC64;

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.6e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGW 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLOWFFNDSCAPPTGFNKPTSNDTMASGW 170
Qy 61 RASSFHFDSEENKRLIHFS 80
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 RASSFHFDSEENKRLIHFS 190

RESULT 5
Q9CQY8_MOUSE

ID Q9CQY8_MOUSE PRELIMINARY; PRT; 226 AA.

AC Q9CQY8;

DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)

DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,

DE RIKEN full-length enriched library, clone:5033426G15 product:similar

DE to cDNA: FLJ22800 FIS, CLONE KAI2630 (Mus musculus 10 day old male

DE pancreas cDNA, RIKEN full-length enriched library, clone:1810018L02

DE product:similar to cDNA: FLJ22800 FIS, CLONE KAI2630).

GN Name=Tm4sf20;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK017195; BAB30629.1; -; mRNA.

DR EMBL; AK007532; BAB25093.1; -; mRNA.

DR Ensembl; ENSMUSG00000026149; Mus musculus.

DR MGI; MGI:1913511; Tm4sf20.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR008661; L6 membrane.

DR Pfam; PF05805; L6 membrane; 1.

SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;

Query Match 52.9%; Score 237.5; DB 2; Length 226;

Best Local Similarity 53.8%; Pred. No. 3.3e-18;

Matches 43; Conservative 13; Mismatches 21; Indels 3; Gaps 2;

Qy 1 KGPLMCNPSNSNANCFSLKNISDIHPESFNLQWPFNDSCAPPTGTFNKPTSNDTMASGW 60

Db 111 EGPLICNTQANSTVTCFSLKNLSKFPDPSFNLLWFNGTCVSPTDFKNPTINN-MVSNW 169

Qy 61 RASSFHFDSSEENKRLIHFS 80

Db 170 KIP--NSNSEEDRRHIFHFS 187

RESULT 6

Q9D3R0_MOUSE

ID Q9D3R0_MOUSE PRELIMINARY; PRT; 226 AA.

AC Q9D3R0;

DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033405M13 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI2630.
GN Name=Tm4sf20; Synonyms=1810018L02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
The FANTOM Consortium,
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK017154; BAB30618.1; -, mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; 1810018L02Rik.
DR MGI; MGI:1913511; Tm4sf20.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008661; L6 membrane.
DR Pfam; PF05805; L6 membrane; 1.
SQ SEQUENCE 226 AA; 24714 MW; 8BE6BE5C2D1EDDC0 CRC64;

Query Match 52.9%; Score 237.5; DB 2; Length 226;
Best Local Similarity 53.8%; Pred. No. 3.3e-18;
Matches 43; Conservative 13; Mismatches 21; Indels 3; Gaps 2;

Qy 1 KGPLMCNPSNSNANCFSLKNISDIHPESFNLQWFNDSCAPPTGFNKPTSNDTMASGW 60
Db 111 EGPLICNTQANSTVTCTFSLKNLSKFDPEFNFLLWFPNGTCVPTDFKNPTINN-MVSNW 169
Qy 61 RASSFHEDSEENKRLIHFS 80
Db 170 KIP--NSNSEEDRRHIFHFS 187

RESULT 7
Q9D3Q0 MOUSE PRELIMINARY; PRT; 226 AA.
AC Q9D3Q0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033430P14 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI2630.
GN Name=Tm4sf20; Synonyms=1810018L02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,

RESULT 12
O65095 PICMA
ID O65095 PICMA PRELIMINARY; PRT; 148 AA.
AC O65095;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATAF1-like protein (Fragment).
GN Name=Sb29;
OS Picea mariana (black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98278823; PubMed=9611216;
RA Perry D.J., Bousquet J.;
RT "Sequence-tagged-site (STS) markers of arbitrary genes: development,
RT characterization and analysis of linkage in black spruce.";
RL Genetics 149:1089-1098(1998).
DR EMBL; AF051748; AAC32165.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 148 AA; 16658 MW; 78091616816D081A CRC64;

Query Match 18.3%; Score 82; DB 2; Length 148;
Best Local Similarity 29.7%; Pred. No. 0.43;
Matches 30; Conservative 14; Mismatches 27; Indels 30; Gaps 7;

QY 5 MCNSPNSNANCEFSLKNISD-----IHP--ESFNLQW-----PFND- 39
Db 20 LCVSPMNSNI-CLQNLDFPDSSTLKAPVQNTAFNPIYSSINHQTNCNSTDLMSGLEHDS 78

QY 40 SCAPPTGFNKPTS-NDTWASGWRASSFHFDSEENKRLIHF 79
Db 79 SCSKPSSEPISEKEFVQSSFRLENF---SQEQQSLPWF 116

RESULT 13
Q9PRJ8 XENLA
ID Q9PRJ8 XENLA PRELIMINARY; PRT; 352 AA.
AC Q9PRJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE XFD-12 protein (Fox protein) (Winged helix protein).
GN Name=xfd-12; Synonyms=FoxD5a, foxD5a;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20025545; PubMed=10559492; DOI=10.1016/S0925-4773(99)00195-1;
RA Soelter M., Koester M., Hollemann T., Brey A., Pieler T., Knoechel W.;
RT "Characterization of a subfamily of related winged helix genes, XFD-
RT 12/12/12" (XFLIP), during Xenopus embryogenesis.";
RL Mech. Dev. 89:161-165(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Schon C., Koster M., Knoechel W.;
RT "A downstream enhancer is essential for Xenopus FoxD5 transcription.";
RL Biochem. Biophys. Res. Commun. 325:1360-1366(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21294976; PubMed=11401404; DOI=10.1006/dbio.2001.0191;
RA Sullivan S.A., Akers L., Moody S.A.;
RT "foxD5a, a Xenopus winged helix gene, maintains an immature neural
RT ectoderm via transcriptional repression that is dependent on the C-
RT terminal domain.";
RL Dev. Biol. 232:439-457(2001).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AJ242676; CAB44728.1; -; mRNA.

DR EMBL; AJ850135; CAH64537.1; -; Genomic_DNA.
DR EMBL; AF162782; AAD47811.1; -; mRNA.
DR HSSP; Q63245; 2HDC.
DR SMR; Q9PRJ8; 96-192.
DR TRANSFAC; T04172; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 352 AA; 39719 MW; 24F3DA0EA2A6891C CRC64;

Query Match 17.8%; Score 80; DB 2; Length 352;
Best Local Similarity 33.3%; Pred. No. 2;
Matches 19; Conservative 8; Mismatches 18; Indels 12; Gaps 2;

QY 7 NSPSNSNANCEFSLKNI-----SDIHPEFNLQWFN-----DSCAPPTGFNKPT 51
Db 274 NHPNNSQSKCSFSIENIMRKPEPNIQSFNSHWYHVQRPSSCLLPVNLST 330

RESULT 14
Q70W02 CIOIN
ID Q70W02 CIOIN PRELIMINARY; PRT; 808 AA.
AC Q70W02;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SoxE protein (Fragment).
GN Name=soxE;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Leveugle M., Prat K., Popovici C., Birnbaum D., Coulrier F.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ534323; CAD58841.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS50118; HMG_BOX_2; 1.
FT NON TER 1
SQ SEQUENCE 808 AA; 89827 MW; 41DE23173A877B5E CRC64;

Query Match 17.6%; Score 79; DB 2; Length 808;
Best Local Similarity 32.2%; Pred. No. 7;
Matches 29; Conservative 13; Mismatches 26; Indels 22; Gaps 6;

QY 5 MCNSPNSNANCEFSLKNISDI-HPESFNLQWFNDS-----CAPPTGFN-----KPTS 52
Db 351 VCHSPSNQSPPHQGSITNIYEVHRE----QRGYHDSPDATVPCSPPTAINMDESKPHS 406

QY 53 -----NDTMAS-GWRASSFHFDSEENKRL 76
Db 407 TLHSRNSSFSGSKQQRGSSIDLTLTSECSHSM 436

RESULT 15
Q695B5 PICGL

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ID Q695B5_PICGL PRELIMINARY; PRT; 149 AA.
AC Q695B5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE NAM protein (Fragment).
GN Name=8b29;
OS Picea glauca (White spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3330;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bouille M., Bousquet J.;
RT "Trans-species shared polymorphisms at orthologous nuclear gene loci
RT among distant species in the conifer Picea (Pinaceae): implications
RT for the long-term maintenance of genetic diversity in trees.";
RL Am. J. Bot. 91:63-73 (2005).
DR EMBL; AY611045; AAT88043.1; -; Genomic DNA.
FT NON TER 1
SQ SEQUENCE 149 AA; 16691 MW; 1EA438165F833F93 CRC64;

Query Match 17.5%; Score 78.5; DB 2; Length 149;
Best Local Similarity 29.0%; Pred. No. 1.1;
Matches 31; Conservative 14; Mismatches 27; Indels 35; Gaps 8;

Qy 5 MCNSPNSN---ANCEF---SLKNISD-----IHP--ESFNLOW----- 35
   :|||  |||  :|  |||  |||  :|  |||  :|  |||  :|  |||
Db 14 LCVSPMNSNICVQNLPFQNSTTPFSDSTLKAPVQNTAFNPISSSINHMTNCNSTDLMS 73
   :|||  |||  :|  |||  |||  :|  |||  :|  |||  :|  |||

Qy 36 -FFND-SCAPPTGFNKPTS-NDTMASGWRASSFHFDSSENGKRLIHF 79
   |||  |||  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
Db 74 GLHNDSSCKPSSFSFSEPISEKEVQSSFLDNF---SQEQQSLFNF 117
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Search completed: December 22, 2005, 03:01:08
Job time : 292 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 03:01:15 ; Search time 96.3265 Seconds
(without alignments)
347.011 Million cell updates/sec

Perfect score: 449
Sequence: 1 KGPLMCNPSNSNANCEFSL.....RASSFHFDSEENKRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	100.0	227	4	US-10-331-053-36
28	449	100.0	229	3	US-09-997-428-258
75	449	100.0	229	4	US-10-087-192-66
564	449	100.0	229	4	US-10-174-587-198
628	449	100.0	229	4	US-10-763-742-48
743	449	100.0	229	4	US-10-055-889-508
744	449	100.0	229	5	US-10-972-317-48
746	449	100.0	229	5	US-10-950-374-258
749	237.5	52.9	228	4	US-10-331-053-33
750	237.5	52.9	230	4	US-10-087-192-63
751	70	15.6	1011	3	US-09-825-751A-65
752	70	15.6	1011	5	US-10-851-438-65
753	70	15.6	1079	6	US-11-097-143-40803
754	68	15.1	2108	4	US-10-236-392-184
755	68	15.1	2167	3	US-09-778-927A-61
756	68	15.1	2199	4	US-10-236-392-182
757	68	15.1	2200	3	US-09-796-575-2
758	68	15.1	2200	4	US-10-652-814-2
759	68	15.1	2201	4	US-10-465-572-12
760	68	15.1	2201	4	US-10-373-801-34
761	68	15.1	2201	5	US-10-723-860-2575
762	68	15.1	2201	5	US-10-719-993-775
763	68	15.1	2201	5	US-10-719-993-777
764	68	15.1	2201	5	US-10-719-993-777
765	68	15.1	2201	5	US-10-852-335A-132
766	68	15.1	2201	5	US-10-756-149-5410
767	67	14.9	500	5	US-10-450-763-40894
768	67	14.9	631	3	US-09-832-312-12
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					Sequence 66, Appl
					Sequence 198, Appl
					Sequence 48, Appl
					Sequence 508, Appl
					Sequence 48, Appl
					Sequence 258, Appl
					Sequence 33, Appl
					Sequence 63, Appl
					Sequence 65, Appl
					Sequence 40803, A
					Sequence 184, Appl
					Sequence 61, Appl
					Sequence 182, Appl
					Sequence 2, Appli
					Sequence 12, Appl
					Sequence 34, Appl
					Sequence 2575, Ap
					Sequence 775, App
					Sequence 777, App
					Sequence 132, App
					Sequence 5410, Ap
					Sequence 40894, A
					Sequence 12, Appl

769	67	14.9	631	3	US-09-829-495-12	Sequence 12, Appl
770	67	14.9	631	5	US-10-850-034-12	Sequence 12, Appl
771	67	14.9	632	4	US-10-114-153-92	Sequence 92, Appl
772	66.5	14.8	161	5	US-10-450-763-32096	Sequence 32096, A
773	66.5	14.8	677	4	US-10-476-924-9	Sequence 9, Appli
774	66	14.7	293	4	US-10-424-599-222366	Sequence 222366,
775	66	14.7	1217	5	US-10-509-307-3	Sequence 3, Appli
776	66	14.7	1219	5	US-10-450-763-43017	Sequence 43017, A
777	65.5	14.6	204	4	US-10-437-963-113089	Sequence 113089,
778	65.5	14.6	650	4	US-10-067-632-60	Sequence 60, Appl
779	65.5	14.6	771	6	US-11-097-143-19785	Sequence 19785, A
780	65.5	14.6	905	6	US-11-097-143-31641	Sequence 31641, A
781	64.5	14.4	79	3	US-09-864-761-40270	Sequence 40270, A
782	64.5	14.4	382	4	US-10-437-963-129067	Sequence 129067,
783	64.5	14.4	431	4	US-10-425-115-248601	Sequence 248601,
784	64.5	14.4	461	4	US-10-369-493-5084	Sequence 5084, Ap
785	64.5	14.4	1185	4	US-10-259-194A-246	Sequence 246, App
786	64.5	14.4	2070	4	US-10-437-963-154111	Sequence 154111,
787	64	14.3	61	4	US-10-425-115-232390	Sequence 232390,
788	64	14.3	228	4	US-10-363-493-6694	Sequence 6694, Ap
789	64	14.3	228	5	US-10-732-923-14744	Sequence 14744, A
790	64	14.3	594	4	US-10-437-963-110864	Sequence 110864,
791	63	14.0	68	4	US-10-425-115-198835	Sequence 198835,
792	63	14.0	87	4	US-10-425-115-365472	Sequence 365472,
793	63	14.0	130	4	US-10-425-115-346439	Sequence 346439,
794	63	14.0	181	4	US-10-425-115-365474	Sequence 365474,
795	63	14.0	213	4	US-10-818-765-3	Sequence 3, Appli
796	63	14.0	213	5	US-10-861-049-15	Sequence 15, Appl
797	63	14.0	213	5	US-10-861-049-18	Sequence 18, Appl
798	63	14.0	213	5	US-10-861-049-19	Sequence 19, Appl
799	63	14.0	213	5	US-10-861-049-21	Sequence 21, Appl
800	63	14.0	213	6	US-11-021-874-15	Sequence 15, Appl
801	63	14.0	213	6	US-11-021-874-18	Sequence 18, Appl
802	63	14.0	213	6	US-11-021-874-19	Sequence 19, Appl
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805	63	14.0	213	6	US-11-006-136-3	Sequence 3, Appli
806	63	14.0	232	5	US-10-877-363-3	Sequence 3, Appli
807	63	14.0	232	5	US-10-922-651-3	Sequence 3, Appli
808	63	14.0	232	5	US-10-861-049-3	Sequence 3, Appli
809	63	14.0	232	6	US-11-021-874-3	Sequence 3, Appli
810	63	14.0	418	4	US-10-225-066A-288	Sequence 288, App
811	63	14.0	418	4	US-10-374-780A-2592	Sequence 2592, Ap
812	63	14.0	418	5	US-10-225-066A-288	Sequence 288, App
813	63	14.0	452	4	US-10-424-599-277835	Sequence 277835,
814	63	14.0	548	4	US-10-424-599-153769	Sequence 153769,
815	63	14.0	684	4	US-10-687-732-23	Sequence 23, Appl
816	63	14.0	816	6	US-11-097-143-25482	Sequence 25482, A
817	63	14.0	925	4	US-10-369-493-21137	Sequence 21137, A
818	63	14.0	1165	3	US-09-801-368-76	Sequence 76, Appl
819	63	14.0	1165	4	US-10-369-493-1432	Sequence 1432, Ap
820	62.5	13.9	368	4	US-10-424-599-245634	Sequence 245634,
821	62.5	13.9	413	4	US-10-408-765A-429	Sequence 429, App
822	62.5	13.9	413	4	US-10-722-357-2	Sequence 2, Appli
823	62.5	13.9	437	4	US-10-425-115-248603	Sequence 248603,
824	62.5	13.9	443	4	US-10-425-114-70967	Sequence 70967, A
825	62.5	13.9	513	4	US-10-437-963-195563	Sequence 195563,
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and is derived by analysis of the total score distribution.

SUMMARIES

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86	50.5	11.2	243	7	US-11-046-456-10	Sequence 10, Appl
87	50.5	11.2	243	7	US-11-046-456-180	Sequence 180, App
88	50.5	11.2	243	7	US-11-046-644-10	Sequence 10, Appl
89	50.5	11.2	252	7	US-11-046-456-16	Sequence 16, Appl
90	50.5	11.2	252	7	US-11-046-644-16	Sequence 16, Appl
91	50.5	11.2	263	7	US-11-046-456-4	Sequence 4, Appli
92	50.5	11.2	263	7	US-11-046-456-18	Sequence 18, Appl
93	50.5	11.2	263	7	US-11-046-456-179	Sequence 179, App
94	50.5	11.2	263	7	US-11-046-644-4	Sequence 4, Appli
95	50.5	11.2	263	7	US-11-046-644-18	Sequence 18, Appl
96	50.5	11.2	290	6	US-10-467-657-1882	Sequence 1882, Ap
97	50.5	11.2	308	7	US-11-046-456-6	Sequence 6, Appli
98	50.5	11.2	308	7	US-11-046-644-6	Sequence 6, Appli
99	50.5	11.2	529	7	US-11-174-150-46	Sequence 46, Appl
100	50.5	11.2	629	6	US-10-467-657-250	Sequence 250, App
101	50.5	11.2	629	6	US-10-467-657-3084	Sequence 3084, Ap

102	50.5	11.2	666	7	US-11-096-046-27	Sequence 27, Appl	177	48	10.7	384	7	US-11-000-463-804	Sequence 804, App
103	50.5	11.2	667	7	US-11-096-046-25	Sequence 25, Appl	178	48	10.7	384	7	US-11-000-463-805	Sequence 805, App
104	50.5	11.2	667	7	US-11-096-046-28	Sequence 28, Appl	179	48	10.7	384	7	US-11-000-463-806	Sequence 806, App
105	50.5	11.2	667	7	US-11-096-046-30	Sequence 30, Appl	180	48	10.7	384	7	US-11-000-463-807	Sequence 807, App
106	50.5	11.2	695	7	US-11-096-046-26	Sequence 26, Appl	181	48	10.7	423	6	US-10-467-962B-85	Sequence 85, Appl
107	50	11.1	175	6	US-10-821-234-1543	Sequence 1543, Ap	182	48	10.7	497	6	US-10-999-866-34	Sequence 34, Appl
108	50	11.1	230	6	US-10-884-730-370	Sequence 370, App	183	48	10.7	497	7	US-11-061-821-34	Sequence 34, Appl
109	50	11.1	230	6	US-10-884-730-371	Sequence 371, App	184	48	10.7	552	7	US-11-074-176-204	Sequence 204, App
110	50	11.1	230	6	US-10-884-730-373	Sequence 373, App	185	48	10.7	661	6	US-10-467-657-1266	Sequence 1266, Ap
111	50	11.1	230	6	US-10-884-730-374	Sequence 374, App	186	48	10.7	758	7	US-11-089-551A-31	Sequence 31, Appl
112	50	11.1	230	6	US-10-884-730-375	Sequence 375, App	187	48	10.7	760	6	US-10-821-234-1141	Sequence 1141, Ap
113	50	11.1	230	6	US-10-884-730-376	Sequence 376, App	188	48	10.7	2828	7	US-11-080-991-54	Sequence 54, Appl
114	50	11.1	230	6	US-10-884-730-377	Sequence 377, App	189	48	10.7	2828	7	US-11-080-991-54	Sequence 49, Appl
115	50	11.1	289	6	US-10-884-730-377	Sequence 377, App	190	47.5	10.6	58	6	US-11-186-284-49	Sequence 325, App
116	50	11.1	367	7	US-11-093-626-3312	Sequence 3312, Ap	191	47.5	10.6	108	7	US-11-093-274-22	Sequence 22, Appl
117	50	11.1	459	6	US-11-000-463-899	Sequence 899, App	192	47.5	10.6	113	6	US-10-932-334-67	Sequence 67, Appl
118	50	11.1	1005	7	US-10-641-678-72	Sequence 72, Appl	193	47.5	10.6	129	7	US-11-116-144-102	Sequence 102, App
119	49.5	11.0	160	6	US-11-080-991-90	Sequence 90, Appl	194	47.5	10.6	173	6	US-10-746-959C-9	Sequence 9, Appl
120	49.5	11.0	235	7	US-10-793-626-1044	Sequence 1044, Ap	196	47.5	10.6	282	7	US-11-080-991-34	Sequence 34, Appl
121	49.5	11.0	235	7	US-11-046-456-178	Sequence 178, App	197	47.5	10.6	417	7	US-11-080-528-66	Sequence 66, Appl
122	49.5	11.0	250	7	US-11-046-644-178	Sequence 178, App	198	47.5	10.6	500	7	US-11-087-100-8	Sequence 8, Appl
123	49.5	11.0	254	6	US-11-054-515-1174	Sequence 1174, Ap	199	47.5	10.6	500	7	US-11-087-100-8	Sequence 8, Appl
124	49.5	11.0	257	6	US-10-467-657-1534	Sequence 1534, Ap	200	47.5	10.6	500	7	US-11-087-084-8	Sequence 8, Appl
125	49.5	11.0	258	6	US-10-821-234-1484	Sequence 1484, Ap	201	47.5	10.6	526	6	US-11-087-085-2	Sequence 2, Appl
126	49.5	11.0	295	6	US-10-995-561-583	Sequence 583, App	202	47.5	10.6	530	6	US-10-606-302-7	Sequence 7, Appl
127	49.5	11.0	305	6	US-10-995-561-581	Sequence 581, App	203	47.5	10.6	530	6	US-10-858-730-232	Sequence 232, App
128	49.5	11.0	317	7	US-10-995-561-582	Sequence 582, App	204	47.5	10.6	676	6	US-10-510-947-1	Sequence 1, Appl
129	49.5	11.0	451	6	US-10-129-143-114	Sequence 114, App	206	47.5	10.6	2910	7	US-11-02-240-34	Sequence 34, Appl
131	49	10.9	136	7	US-10-821-234-1491	Sequence 1491, Ap	207	47.5	10.6	2910	7	US-11-087-100-2	Sequence 2, Appl
132	49	10.9	146	6	US-11-144-248-2	Sequence 2, Appli	208	47.5	10.6	2910	7	US-11-087-084-2	Sequence 2, Appli
133	49	10.9	213	7	US-10-485-517-193	Sequence 193, App	209	47	10.5	114	6	US-11-087-085-2	Sequence 2, Appli
134	49	10.9	236	7	US-11-102-621-118	Sequence 118, App	210	47	10.5	139	6	US-10-821-234-938	Sequence 938, App
136	49	10.9	524	6	US-11-144-248-51	Sequence 51, Appl	211	47	10.5	214	7	US-10-510-386-142	Sequence 142, App
137	49	10.9	554	7	US-10-467-657-8258	Sequence 8258, Ap	212	47	10.5	307	7	US-11-035-712-11	Sequence 11, Appl
138	49	10.9	845	7	US-11-055-822-998	Sequence 998, App	213	47	10.5	312	6	US-11-000-463-332	Sequence 332, App
139	49	10.9	926	6	US-11-147-047-46	Sequence 46, Appl	214	47	10.5	312	6	US-10-723-207-2	Sequence 2, Appli
140	49	10.9	1637	6	US-10-841-129-2	Sequence 2, Appli	215	47	10.5	334	7	US-11-000-463-334	Sequence 334, App
141	48.5	10.8	58	6	US-10-821-234-1204	Sequence 1204, Ap	216	47	10.5	531	6	US-11-035-822-980	Sequence 980, App
142	48.5	10.8	96	7	US-10-925-366A-328	Sequence 328, App	217	47	10.5	606	6	US-10-878-556A-90	Sequence 90, Appl
143	48.5	10.8	97	7	US-11-144-248-40	Sequence 40, Appl	218	46.5	10.4	71	6	US-10-624-932-18	Sequence 18, Appl
144	48.5	10.8	107	7	US-11-084-554-122	Sequence 122, Appl	219	46.5	10.4	72	6	US-10-467-657-750	Sequence 750, App
145	48.5	10.8	112	7	US-11-093-274-24	Sequence 24, Appl	220	46.5	10.4	73	6	US-10-467-657-1502	Sequence 1502, Ap
146	48.5	10.8	241	7	US-11-125-837-25	Sequence 25, Appl	221	46.5	10.4	107	7	US-10-467-657-5022	Sequence 5022, Ap
147	48.5	10.8	242	7	US-11-054-515-1577	Sequence 1577, Ap	222	46.5	10.4	108	7	US-11-077-978-6	Sequence 6, Appli
148	48.5	10.8	247	7	US-11-054-515-1915	Sequence 1915, Ap	223	46.5	10.4	175	6	US-11-093-274-23	Sequence 23, Appl
149	48.5	10.8	248	7	US-11-054-515-3240	Sequence 3240, Ap	224	46.5	10.4	185	7	US-10-667-295-48	Sequence 48, Appl
150	48.5	10.8	251	7	US-11-054-515-1446	Sequence 1446, Ap	225	46.5	10.4	248	7	US-11-098-662-136	Sequence 136, App
151	48.5	10.8	251	7	US-11-054-515-88	Sequence 88, Appl	226	46.5	10.4	422	7	US-11-054-515-1104	Sequence 1104, Ap
152	48.5	10.8	251	7	US-11-054-515-240	Sequence 240, App	228	46.5	10.4	493	7	US-11-120-543-20	Sequence 20, Appl
153	48.5	10.8	380	7	US-11-054-515-1921	Sequence 1921, Ap	229	46.5	10.4	526	6	US-11-067-121-20	Sequence 20, Appl
154	48.5	10.8	668	6	US-11-089-551A-25	Sequence 25, Appl	230	46.5	10.4	568	6	US-10-606-302-5	Sequence 5, Appli
155	48.5	10.8	742	6	US-10-995-561-619	Sequence 619, App	231	46.5	10.4	568	6	US-10-997-247-4	Sequence 4, Appli
156	48.5	10.8	742	6	US-10-995-561-615	Sequence 615, App	232	46.5	10.4	1211	7	US-10-793-626-1066	Sequence 1066, Ap
157	48.5	10.8	768	6	US-10-995-561-618	Sequence 618, App	233	46.5	10.4	1211	7	US-11-186-284-4	Sequence 4, Appli
158	48.5	10.8	790	6	US-10-995-561-956	Sequence 956, App	234	46	10.2	107	7	US-11-105-268-22	Sequence 22, Appl
159	48.5	10.8	830	6	US-10-995-561-955	Sequence 955, App	235	46	10.2	108	6	US-10-925-366A-3	Sequence 3, Appli
160	48.5	10.8	830	6	US-10-995-561-957	Sequence 957, App	236	46	10.2	108	6	US-10-925-366A-6	Sequence 6, Appli
161	48.5	10.8	847	6	US-10-995-561-958	Sequence 958, App	237	46	10.2	139	6	US-11-127-677-36	Sequence 36, Appl
162	48.5	10.8	1259	6	US-10-995-561-634	Sequence 634, App	238	46	10.2	232	6	US-10-995-561-667	Sequence 667, App
163	48.5	10.8	1286	6	US-10-995-561-625	Sequence 625, App	239	46	10.2	232	6	US-10-884-730-363	Sequence 363, App
164	48.5	10.8	1315	6	US-10-995-561-628	Sequence 628, App	240	46	10.2	232	6	US-10-884-730-364	Sequence 364, App
165	48.5	10.8	1341	6	US-10-995-561-630	Sequence 630, App	241	46	10.2	232	6	US-10-884-730-365	Sequence 365, App
166	48.5	10.8	1348	6	US-10-995-561-621	Sequence 621, App	242	46	10.2	232	6	US-10-884-730-366	Sequence 366, App
167	48.5	10.8	2296	6	US-10-995-561-624	Sequence 624, App	243	46	10.2	240	6	US-10-884-730-366	Sequence 366, App
168	48.5	10.8	2355	6	US-10-995-561-623	Sequence 623, App	244	46	10.2	248	7	US-10-925-366A-219	Sequence 219, App
169	48.5	10.8	2355	6	US-10-995-561-633	Sequence 633, App	245	46	10.2	248	7	US-11-054-515-1360	Sequence 1360, Ap
170	48.5	10.8	2384	6	US-10-995-561-627	Sequence 627, App	246	46	10.2	317	6	US-10-689-742-166	Sequence 166, App
171	48.5	10.8	2386	6	US-10-995-561-627	Sequence 627, App	247	46	10.2	367	7	US-11-109-157A-4	Sequence 4, Appli
172	48	10.7	185	6	US-10-995-561-627	Sequence 1545, Ap	248	46	10.2	375	7	US-11-109-157A-40	Sequence 40, Appl
173	48	10.7	214	7	US-10-821-234-1130	Sequence 626, App	249	46	10.2	461	7	US-11-132-285-6	Sequence 6, Appli
174	48	10.7	214	7	US-11-094-625-9	Sequence 1130, Ap	250	46	10.2	461	7	US-11-182-946-4	Sequence 4, Appli
175	48	10.7	292	6	US-10-995-561-627	Sequence 9, Appli	251	46	10.2	463	6	US-10-641-678-71	Sequence 71, Appl
176	48	10.7	325	6	US-11-102-621-129	Sequence 129, App	252	46	10.2	599	7	US-11-109-157A-3	Sequence 3, Appli
					Sequence 18, Appl	Sequence 18, Appl				606	6	US-10-624-932-16	Sequence 16, Appl
					Sequence 1, Appli	Sequence 1, Appli				618	6	US-10-512-184-48	Sequence 48, Appl

254	46	10.2	735	7	US-11-184-380-24	Sequence 24, Appl	328	45	10.0	859	7	US-11-000-463-423	Sequence 423, App
255	46	10.2	741	7	US-11-191-374-18	Sequence 18, Appl	329	45	10.0	859	7	US-11-000-463-895	Sequence 895, App
256	46	10.2	741	7	US-11-191-375-18	Sequence 18, Appl	330	45	10.0	3623	6	US-10-995-561-593	Sequence 593, App
257	46	10.2	742	7	US-11-191-374-46	Sequence 46, Appl	331	44.5	9.9	78	6	US-10-467-657-4846	Sequence 4846, Ap
258	46	10.2	742	7	US-11-191-375-46	Sequence 46, Appl	332	44.5	9.9	104	7	US-11-075-351-54	Sequence 54, Appl
259	46	10.2	756	6	US-10-467-657-8694	Sequence 8694, Ap	333	44.5	9.9	106	7	US-11-155-775-8	Sequence 8, Appl
260	46	10.2	791	6	US-10-821-234-962	Sequence 962, App	334	44.5	9.9	107	7	US-11-107-028-40	Sequence 40, Appl
261	46	10.2	970	6	US-10-770-726-86	Sequence 86, Appl	335	44.5	9.9	107	7	US-11-107-028-42	Sequence 42, Appl
262	46	10.2	1042	7	US-11-067-811-1	Sequence 1, Appli	336	44.5	9.9	108	6	US-10-925-366A-193	Sequence 193, App
263	46	10.2	1454	7	US-11-109-157A-2	Sequence 2, Appli	337	44.5	9.9	112	7	US-11-012-353-54	Sequence 54, Appl
264	46	10.2	1649	6	US-10-995-561-974	Sequence 974, App	338	44.5	9.9	112	7	US-11-125-837-34	Sequence 34, Appl
265	46	10.2	1686	7	US-11-109-157A-1	Sequence 1, Appli	339	44.5	9.9	113	6	US-10-932-334-60	Sequence 60, Appl
266	46	10.2	1694	7	US-11-135-855-36	Sequence 36, Appl	340	44.5	9.9	113	6	US-10-932-334-62	Sequence 62, Appl
267	46	10.2	1709	7	US-10-995-561-973	Sequence 973, App	341	44.5	9.9	113	6	US-10-932-334-69	Sequence 69, Appl
268	46	10.2	1709	7	US-11-135-855-35	Sequence 35, Appl	342	44.5	9.9	122	7	US-11-012-353-49	Sequence 49, Appl
269	46	10.2	3588	6	US-10-995-561-672	Sequence 672, App	343	44.5	9.9	127	7	US-11-193-512-92	Sequence 92, Appl
270	46	10.2	4346	6	US-10-995-561-671	Sequence 671, App	344	44.5	9.9	127	7	US-11-193-512-98	Sequence 98, Appl
271	46	10.2	4347	6	US-10-995-561-670	Sequence 670, App	345	44.5	9.9	129	7	US-11-116-144-93	Sequence 93, Appl
272	46	10.2	4419	6	US-10-821-234-1155	Sequence 1155, Ap	346	44.5	9.9	129	7	US-11-116-144-94	Sequence 94, Appl
273	45.5	10.1	105	7	US-11-155-775-56	Sequence 56, Appl	347	44.5	9.9	129	7	US-11-116-144-95	Sequence 95, Appl
274	45.5	10.1	108	6	US-10-925-366A-233	Sequence 233, App	348	44.5	9.9	131	7	US-11-125-837-19	Sequence 19, Appl
275	45.5	10.1	122	7	US-11-046-456-103	Sequence 103, App	349	44.5	9.9	188	6	US-10-980-388-101	Sequence 101, App
276	45.5	10.1	122	7	US-11-046-644-103	Sequence 103, App	350	44.5	9.9	279	6	US-10-467-657-3032	Sequence 3032, Ap
277	45.5	10.1	181	7	US-11-098-662-32	Sequence 32, Appl	351	44.5	9.9	305	7	US-11-000-463-391	Sequence 391, App
278	45.5	10.1	181	7	US-11-098-662-50	Sequence 50, Appl	352	44.5	9.9	305	7	US-11-000-463-863	Sequence 863, App
279	45.5	10.1	181	7	US-11-098-662-70	Sequence 70, Appl	353	44.5	9.9	372	7	US-11-143-986-5	Sequence 5, Appli
280	45.5	10.1	181	7	US-11-098-662-78	Sequence 78, Appl	354	44.5	9.9	372	7	US-11-143-986-6	Sequence 6, Appli
281	45.5	10.1	181	7	US-11-098-662-110	Sequence 110, App	355	44.5	9.9	384	6	US-10-999-866-33	Sequence 33, Appl
282	45.5	10.1	182	7	US-11-098-662-34	Sequence 34, Appl	356	44.5	9.9	384	7	US-11-061-821-33	Sequence 33, Appl
283	45.5	10.1	182	7	US-11-098-662-38	Sequence 38, Appl	357	44.5	9.9	391	6	US-10-821-234-1487	Sequence 1487, Ap
284	45.5	10.1	182	7	US-11-098-662-52	Sequence 52, Appl	358	44.5	9.9	397	7	US-11-032-562-223	Sequence 223, App
285	45.5	10.1	182	7	US-11-098-662-72	Sequence 72, Appl	359	44.5	9.9	494	6	US-10-971-560-7	Sequence 7, Appli
286	45.5	10.1	182	7	US-11-098-662-80	Sequence 80, Appl	360	44.5	9.9	691	6	US-10-995-561-617	Sequence 617, App
287	45.5	10.1	182	7	US-11-098-662-112	Sequence 112, App	362	44.5	9.9	1308	7	US-11-113-202-16	Sequence 16, Appl
288	45.5	10.1	183	7	US-11-098-662-126	Sequence 126, App	363	44	9.8	108	7	US-11-127-677-40	Sequence 40, Appl
289	45.5	10.1	183	7	US-11-098-662-130	Sequence 130, App	364	44	9.8	108	7	US-11-127-677-67	Sequence 67, Appl
290	45.5	10.1	200	7	US-11-098-662-4	Sequence 4, Appli	365	44	9.8	112	7	US-11-012-353-55	Sequence 55, Appl
291	45.5	10.1	200	7	US-11-098-662-20	Sequence 20, Appl	366	44	9.8	135	6	US-10-793-626-536	Sequence 536, App
292	45.5	10.1	206	6	US-10-793-626-832	Sequence 832, App	367	44	9.8	237	7	US-11-054-515-1906	Sequence 1906, Ap
293	45.5	10.1	207	6	US-10-467-657-4678	Sequence 4678, Ap	368	44	9.8	237	7	US-11-054-515-2003	Sequence 2003, Ap
294	45.5	10.1	277	6	US-10-467-657-1170	Sequence 1170, Ap	369	44	9.8	237	7	US-11-054-515-2005	Sequence 2005, Ap
295	45.5	10.1	302	6	US-10-793-626-1144	Sequence 1144, Ap	370	44	9.8	237	7	US-11-054-515-2017	Sequence 2017, Ap
296	45.5	10.1	461	7	US-11-067-425A-81	Sequence 81, Appl	371	44	9.8	237	7	US-11-054-515-2019	Sequence 2019, Ap
298	45.5	10.1	637	7	US-11-154-324-4	Sequence 4, Appli	372	44	9.8	237	7	US-11-054-515-2020	Sequence 2020, Ap
299	45.5	10.1	693	6	US-10-995-561-632	Sequence 632, App	373	44	9.8	237	7	US-11-054-515-2027	Sequence 2027, Ap
300	45.5	10.1	769	6	US-10-467-657-3280	Sequence 3280, Ap	374	44	9.8	237	7	US-11-054-515-2028	Sequence 2028, Ap
301	45.5	10.1	828	6	US-10-467-962B-99	Sequence 99, Appl	375	44	9.8	237	7	US-11-054-515-2040	Sequence 2040, Ap
302	45.5	10.1	879	7	US-11-022-562-340	Sequence 340, App	376	44	9.8	237	7	US-11-054-515-2043	Sequence 2043, Ap
303	45.5	10.1	919	7	US-11-102-240-70	Sequence 70, Appl	377	44	9.8	237	7	US-11-054-515-2104	Sequence 2104, Ap
304	45	10.0	126	6	US-10-467-657-888	Sequence 888, App	378	44	9.8	237	7	US-11-054-515-2111	Sequence 2111, Ap
305	45	10.0	129	7	US-11-116-144-104	Sequence 104, App	379	44	9.8	237	7	US-11-054-515-2114	Sequence 2114, Ap
306	45	10.0	174	7	US-11-113-424-185	Sequence 185, App	380	44	9.8	237	7	US-11-054-515-2115	Sequence 2115, Ap
307	45	10.0	205	6	US-10-485-517-318	Sequence 318, App	381	44	9.8	237	7	US-11-054-515-2118	Sequence 2118, Ap
308	45	10.0	218	6	US-10-923-327-6	Sequence 6, Appli	382	44	9.8	238	7	US-11-054-515-2053	Sequence 2053, Ap
309	45	10.0	218	6	US-10-923-327-8	Sequence 8, Appli	383	44	9.8	242	7	US-11-054-515-1580	Sequence 1580, Ap
310	45	10.0	218	6	US-10-923-327-10	Sequence 10, Appl	384	44	9.8	245	7	US-11-054-515-1291	Sequence 1291, Ap
311	45	10.0	218	6	US-10-923-327-12	Sequence 12, Appl	385	44	9.8	248	7	US-11-054-515-1004	Sequence 1004, Ap
312	45	10.0	218	6	US-10-923-327-17	Sequence 17, Appl	386	44	9.8	248	7	US-11-054-515-1385	Sequence 1385, Ap
313	45	10.0	218	7	US-11-084-554-11	Sequence 11, Appl	387	44	9.8	248	7	US-11-054-515-1717	Sequence 1717, Ap
314	45	10.0	223	6	US-10-793-626-2824	Sequence 2824, Ap	388	44	9.8	248	7	US-11-054-515-1719	Sequence 1719, Ap
315	45	10.0	237	7	US-11-054-669-109	Sequence 109, App	389	44	9.8	248	7	US-11-054-515-1733	Sequence 1733, Ap
316	45	10.0	239	7	US-11-139-499-6	Sequence 6, Appli	390	44	9.8	248	7	US-11-054-515-1737	Sequence 1737, Ap
317	45	10.0	265	7	US-11-170-653-62	Sequence 62, Appl	391	44	9.8	248	7	US-11-054-515-1876	Sequence 1876, Ap
318	45	10.0	318	6	US-10-873-528-192	Sequence 192, App	392	44	9.8	248	7	US-11-054-515-1879	Sequence 1879, Ap
319	45	10.0	477	7	US-11-089-551A-34	Sequence 34, Appl	393	44	9.8	249	7	US-11-054-515-1321	Sequence 1321, Ap
320	45	10.0	498	6	US-10-510-947-9	Sequence 9, Appli	394	44	9.8	250	7	US-11-054-515-1410	Sequence 1410, Ap
321	45	10.0	619	6	US-10-485-517-374	Sequence 374, App	395	44	9.8	270	6	US-10-495-597-12	Sequence 12, Appl
322	45	10.0	633	6	US-10-821-234-1146	Sequence 1146, Ap	396	44	9.8	317	6	US-10-674-767-2	Sequence 2, Appli
323	45	10.0	664	6	US-10-821-234-1670	Sequence 1670, Ap	397	44	9.8	337	6	US-10-821-234-1004	Sequence 1004, Ap
324	45	10.0	664	6	US-10-995-561-964	Sequence 964, App	398	44	9.8	406	7	US-11-107-028-7	Sequence 7, Appli
325	45	10.0	664	6	US-10-995-561-965	Sequence 965, App	399	44	9.8	432	7	US-11-055-822-224	Sequence 224, App
326	45	10.0	744	6	US-10-873-528-184	Sequence 184, App	400	44	9.8	448	6	US-10-967-527A-16	Sequence 16, Appl
327	45	10.0	809	6	US-10-467-657-1106	Sequence 1106, Ap	401	44	9.8	471	6	US-10-336-263A-6	Sequence 6, Appli

402	44	9.8	478	7	US-11-055-822-220	Sequence 220, App	476	43	9.6	313	6	US-10-723-207-3	Sequence 3, Appli
403	44	9.8	558	6	US-10-467-657-4258	Sequence 4258, Ap	477	43	9.6	336	6	US-10-793-626-1858	Sequence 1858, Ap
404	44	9.8	567	6	US-10-485-517-216	Sequence 216, App	478	43	9.6	394	6	US-10-467-657-8414	Sequence 8414, Ap
405	44	9.8	585	7	US-11-108-172-1067	Sequence 1067, Ap	479	43	9.6	397	6	US-10-485-517-172	Sequence 172, App
406	44	9.8	717	6	US-10-793-626-3022	Sequence 3022, Ap	480	43	9.6	459	6	US-10-793-626-2666	Sequence 2666, Ap
407	44	9.8	743	6	US-10-485-517-351	Sequence 351, App	481	43	9.6	504	6	US-10-999-782-2	Sequence 2, Appli
408	44	9.8	792	7	US-11-088-686-29	Sequence 29, Appl	482	43	9.6	588	6	US-10-550-326B-7	Sequence 7, Appli
409	44	9.8	877	6	US-10-485-517-200	Sequence 200, App	483	43	9.6	638	6	US-10-995-561-1025	Sequence 1025, Ap
410	44	9.8	1001	7	US-11-132-285-40	Sequence 40, Appl	484	43	9.6	651	6	US-10-821-234-1666	Sequence 1666, Ap
412	44	9.8	1613	7	US-11-108-528-84	Sequence 84, Appl	485	43	9.6	934	7	US-11-077-386-17	Sequence 17, Appl
413	43.5	9.7	77	6	US-10-925-366A-305	Sequence 305, App	486	43	9.6	979	6	US-10-636-320-6	Sequence 6, Appli
414	43.5	9.7	108	7	US-11-127-677-32	Sequence 32, Appl	487	43	9.6	1018	7	US-11-067-121-17	Sequence 17, Appl
415	43.5	9.7	112	6	US-10-502-145-23	Sequence 23, Appl	488	43	9.6	1028	7	US-11-067-121-7	Sequence 7, Appli
416	43.5	9.7	113	6	US-10-932-334-59	Sequence 59, Appl	490	43	9.6	1160	6	US-10-995-561-1019	Sequence 1019, Ap
417	43.5	9.7	113	6	US-10-932-334-61	Sequence 61, Appl	491	43	9.6	1302	6	US-10-995-561-1024	Sequence 1024, Ap
418	43.5	9.7	129	7	US-11-116-144-92	Sequence 92, Appl	492	43	9.6	1304	6	US-10-821-234-1648	Sequence 1648, Ap
419	43.5	9.7	129	7	US-11-116-144-96	Sequence 96, Appl	493	43	9.6	1306	6	US-10-995-561-1027	Sequence 1027, Ap
420	43.5	9.7	140	6	US-10-467-657-852	Sequence 852, App	494	43	9.6	1458	7	US-11-096-274-2	Sequence 2, Appli
421	43.5	9.7	147	7	US-11-144-296	Sequence 296, App	495	43	9.6	1613	7	US-11-108-528-86	Sequence 86, Appl
422	43.5	9.7	160	6	US-10-793-626-2372	Sequence 2372, Ap	496	43	9.6	2897	6	US-10-499-715-2	Sequence 2, Appli
423	43.5	9.7	181	6	US-10-873-528-189	Sequence 189, App	497	43	9.6	4655	6	US-10-995-561-556	Sequence 556, App
424	43.5	9.7	181	7	US-11-098-662-54	Sequence 54, Appl	498	43	9.6	4868	7	US-11-044-111-24	Sequence 24, Appl
425	43.5	9.7	181	7	US-11-098-662-62	Sequence 62, Appl	499	42.5	9.5	91	7	US-11-102-476-12	Sequence 12, Appl
426	43.5	9.7	182	7	US-11-098-662-56	Sequence 56, Appl	500	42.5	9.5	96	7	US-11-144-248-42	Sequence 42, Appl
427	43.5	9.7	182	7	US-11-098-662-64	Sequence 64, Appl	501	42.5	9.5	100	7	US-11-144-248-10	Sequence 10, Appl
428	43.5	9.7	245	7	US-11-046-456-69	Sequence 69, Appl	502	42.5	9.5	106	7	US-11-155-775-20	Sequence 20, Appl
429	43.5	9.7	245	7	US-11-046-644-69	Sequence 69, Appl	503	42.5	9.5	106	7	US-11-155-775-32	Sequence 32, Appl
430	43.5	9.7	251	6	US-10-512-184-30	Sequence 30, Appl	504	42.5	9.5	108	7	US-11-127-677-76	Sequence 76, Appl
431	43.5	9.7	259	7	US-11-054-515-1485	Sequence 1485, Ap	505	42.5	9.5	112	6	US-10-502-145-15	Sequence 15, Appl
432	43.5	9.7	261	7	US-11-056-825-2	Sequence 2, Appli	506	42.5	9.5	112	7	US-11-012-353-56	Sequence 56, Appl
433	43.5	9.7	302	7	US-11-182-592-6	Sequence 6, Appli	507	42.5	9.5	113	6	US-10-932-334-66	Sequence 66, Appl
434	43.5	9.7	320	6	US-10-512-184-67	Sequence 47, Appl	508	42.5	9.5	113	6	US-10-932-334-68	Sequence 68, Appl
435	43.5	9.7	353	7	US-11-182-592-4	Sequence 67, Appl	509	42.5	9.5	116	7	US-11-065-943-49	Sequence 49, Appl
436	43.5	9.7	404	6	US-10-793-626-398	Sequence 398, App	510	42.5	9.5	131	7	US-11-125-837-23	Sequence 23, Appl
437	43.5	9.7	417	7	US-11-108-528-64	Sequence 64, Appl	511	42.5	9.5	153	6	US-10-821-234-1355	Sequence 1355, Ap
438	43.5	9.7	431	6	US-10-995-561-807	Sequence 807, App	512	42.5	9.5	189	6	US-10-821-234-1432	Sequence 1432, Ap
439	43.5	9.7	431	6	US-10-995-561-808	Sequence 808, App	513	42.5	9.5	189	6	US-10-878-556A-193	Sequence 193, App
440	43.5	9.7	431	7	US-11-186-284-161	Sequence 161, App	514	42.5	9.5	230	6	US-10-467-657-7800	Sequence 7800, Ap
441	43.5	9.7	569	6	US-10-512-184-66	Sequence 66, Appl	515	42.5	9.5	232	7	US-10-467-657-7800	Sequence 1534, Ap
442	43.5	9.7	652	6	US-10-821-234-1016	Sequence 1016, Ap	516	42.5	9.5	255	7	US-11-054-515-1137	Sequence 1137, Ap
443	43.5	9.7	730	7	US-11-113-424-50	Sequence 50, Appl	517	42.5	9.5	259	7	US-11-056-825-7	Sequence 7, Appli
444	43.5	9.7	734	6	US-10-995-561-770	Sequence 770, App	518	42.5	9.5	301	6	US-10-512-184-37	Sequence 37, Appl
445	43.5	9.7	944	7	US-11-057-058-68	Sequence 68, Appl	519	42.5	9.5	382	7	US-11-000-463-447	Sequence 447, App
446	43.5	9.7	964	7	US-11-089-551A-30	Sequence 30, Appl	520	42.5	9.5	384	6	US-10-995-561-518	Sequence 518, App
447	43.5	9.7	1155	6	US-10-793-626-1780	Sequence 1780, Ap	521	42.5	9.5	391	6	US-10-996-628-2	Sequence 2, Appli
448	43.5	9.7	1207	6	US-10-821-234-1109	Sequence 1109, Ap	522	42.5	9.5	397	7	US-11-060-008-8	Sequence 8, Appli
449	43.5	9.7	1388	6	US-10-821-234-1143	Sequence 1143, Ap	524	42.5	9.5	437	6	US-10-521-596-2	Sequence 2, Appli
450	43.5	9.7	2769	7	US-11-113-424-14	Sequence 14, Appl	525	42.5	9.5	530	6	US-10-878-556A-71	Sequence 71, Appl
451	43.5	9.7	3690	6	US-10-995-561-1016	Sequence 1016, Ap	526	42.5	9.5	530	6	US-10-878-556A-148	Sequence 148, App
452	43.5	9.7	3714	6	US-10-995-561-1015	Sequence 1015, Ap	527	42.5	9.5	541	6	US-10-995-561-519	Sequence 519, App
453	43.5	9.7	3717	6	US-10-821-234-1076	Sequence 1076, Ap	528	42.5	9.5	541	6	US-10-995-561-521	Sequence 521, App
454	43	9.6	17	7	US-10-110-748A-293	Sequence 293, App	529	42.5	9.5	576	6	US-10-512-184-65	Sequence 65, Appl
455	43	9.6	102	6	US-10-793-626-122	Sequence 122, App	530	42.5	9.5	595	7	US-11-102-476-33	Sequence 33, Appl
456	43	9.6	105	7	US-11-155-775-48	Sequence 48, Appl	531	42.5	9.5	615	6	US-10-512-184-50	Sequence 50, Appl
457	43	9.6	108	6	US-10-665-658-3	Sequence 3, Appli	532	42.5	9.5	625	6	US-10-512-184-47	Sequence 47, Appl
458	43	9.6	108	7	US-11-120-338-3	Sequence 3, Appli	533	42.5	9.5	626	6	US-10-512-184-49	Sequence 49, Appl
459	43	9.6	108	7	US-11-127-677-39	Sequence 39, Appl	535	42.5	9.5	815	7	US-11-073-112-3	Sequence 3, Appli
460	43	9.6	109	7	US-11-096-046-5	Sequence 5, Appli	536	42.5	9.5	902	7	US-11-057-058-64	Sequence 64, Appl
461	43	9.6	198	6	US-10-467-657-98	Sequence 98, Appl	537	42.5	9.5	987	6	US-10-949-720-395	Sequence 395, App
462	43	9.6	198	6	US-10-467-657-5714	Sequence 5714, Ap	538	42.5	9.5	990	6	US-10-821-234-1201	Sequence 1201, Ap
463	43	9.6	215	6	US-10-793-626-828	Sequence 828, App	539	42.5	9.5	1133	6	US-10-821-234-1219	Sequence 1219, Ap
464	43	9.6	227	6	US-10-510-386-60	Sequence 60, Appl	540	42.5	9.5	1225	7	US-11-102-476-2	Sequence 2, Appli
465	43	9.6	237	6	US-10-884-730-273	Sequence 273, App	541	42.5	9.5	2314	7	US-11-097-728-2	Sequence 2, Appli
466	43	9.6	259	7	US-11-054-515-1552	Sequence 1552, Ap	542	42.5	9.5	2353	7	US-11-097-728-6	Sequence 6, Appli
467	43	9.6	261	7	US-11-055-822-430	Sequence 430, App	543	42.5	9.5	2725	7	US-11-113-424-52	Sequence 52, Appl
468	43	9.6	262	6	US-10-884-730-289	Sequence 289, App	544	42	9.4	99	7	US-11-090-439-56	Sequence 56, Appl
469	43	9.6	262	6	US-10-884-730-270	Sequence 289, App	545	42	9.4	107	6	US-10-925-366A-99	Sequence 99, Appl
470	43	9.6	266	6	US-10-884-730-285	Sequence 285, App	546	42	9.4	130	7	US-11-116-144-143	Sequence 143, App
471	43	9.6	266	6	US-10-884-730-287	Sequence 285, App	547	42	9.4	231	6	US-10-527-771-10	Sequence 10, Appl
472	43	9.6	266	6	US-10-884-730-287	Sequence 287, App	548	42	9.4	266	7	US-11-082-389-340	Sequence 340, App
473	43	9.6	280	7	US-11-080-991-44	Sequence 44, Appl	549	42	9.4	269	6	US-10-495-597-14	Sequence 14, Appl
474	43	9.6	282	7	US-11-102-240-60	Sequence 60, Appl	550	42	9.4	270	6	US-10-495-597-11	Sequence 11, Appl
475	43	9.6	297	6	US-10-967-527A-17	Sequence 17, Appl	551	42	9.4	310	7	US-11-000-463-357	Sequence 357, App

552	42	9.4	311	7	US-11-000-463-345	Sequence 345, App	627	41.5	9.2	375	6	US-10-667-295-119	Sequence 119, App
553	42	9.4	311	7	US-11-000-463-817	Sequence 817, App	628	41.5	9.2	383	6	US-10-793-626-1564	Sequence 1564, Ap
554	42	9.4	311	7	US-11-000-463-829	Sequence 829, App	629	41.5	9.2	485	6	US-10-630-203-2	Sequence 2, Appli
555	42	9.4	354	6	US-10-821-234-1605	Sequence 1605, Ap	630	41.5	9.2	485	7	US-11-103-037-1	Sequence 1, Appli
556	42	9.4	354	7	US-11-089-551A-4	Sequence 4, Appli	631	41.5	9.2	493	7	US-11-067-121-10	Sequence 10, Appl
557	42	9.4	356	7	US-11-012-762-46	Sequence 46, Appl	632	41.5	9.2	504	7	US-11-055-822-136	Sequence 136, App
558	42	9.4	363	7	US-11-000-463-335	Sequence 335, App	633	41.5	9.2	569	6	US-10-632-150-2	Sequence 2, Appli
559	42	9.4	366	6	US-10-661-426-7	Sequence 4, Appli	634	41.5	9.2	569	7	US-11-073-457-2	Sequence 2, Appli
560	42	9.4	366	6	US-10-661-426-13	Sequence 7, Appli	635	41.5	9.2	569	7	US-11-099-691-12	Sequence 12, Appl
561	42	9.4	366	6	US-10-661-426-13	Sequence 13, Appl	636	41.5	9.2	569	7	US-11-073-460-2	Sequence 2, Appli
562	42	9.4	374	7	US-11-097-728-4	Sequence 4, Appli	637	41.5	9.2	576	6	US-10-508-442-2	Sequence 2, Appli
563	42	9.4	392	6	US-10-793-626-2494	Sequence 2494, Ap	638	41.5	9.2	672	7	US-11-004-057-2	Sequence 2, Appli
564	42	9.4	473	6	US-10-509-464-5	Sequence 5, Appli	639	41.5	9.2	703	6	US-10-467-657-7158	Sequence 7158, Ap
565	42	9.4	491	6	US-10-793-626-1798	Sequence 1798, Ap	641	41.5	9.2	852	6	US-10-645-441-15	Sequence 15, Appl
566	42	9.4	496	7	US-11-186-284-103	Sequence 103, App	642	41.5	9.2	859	7	US-11-053-100-52	Sequence 52, Appl
567	42	9.4	505	6	US-10-519-447-4	Sequence 4, Appli	643	41.5	9.2	862	7	US-11-128-420-11	Sequence 11, Appl
568	42	9.4	514	6	US-10-641-678-54	Sequence 54, Appl	644	41.5	9.2	1213	7	US-11-074-176-256	Sequence 256, App
569	42	9.4	532	6	US-10-467-657-820	Sequence 820, App	645	41.5	9.2	1302	7	US-11-004-057-6	Sequence 6, Appli
570	42	9.4	572	6	US-10-878-556A-47	Sequence 47, Appl	646	41.5	9.2	1309	7	US-11-053-100-53	Sequence 53, Appl
571	42	9.4	598	7	US-11-074-176-258	Sequence 258, App	647	41.5	9.2	1311	6	US-10-509-422-5	Sequence 5, Appli
573	42	9.4	651	6	US-10-821-234-1480	Sequence 1480, Ap	648	41.5	9.2	1476	6	US-10-647-956A-4	Sequence 4, Appli
574	42	9.4	651	6	US-10-770-726-67	Sequence 67, Appl	649	41.5	9.2	1493	7	US-11-004-057-4	Sequence 4, Appli
576	42	9.4	685	7	US-11-078-735-19	Sequence 19, Appl	650	41.5	9.2	2107	6	US-10-995-561-827	Sequence 827, App
577	42	9.4	693	6	US-10-873-528-185	Sequence 185, App	651	41.5	9.2	2480	6	US-10-995-561-825	Sequence 825, App
578	42	9.4	761	6	US-10-485-517-252	Sequence 252, App	652	41.5	9.2	3011	6	US-10-985-205-3	Sequence 3, Appli
579	42	9.4	783	7	US-11-186-284-59	Sequence 59, Appl	653	41.5	9.2	3116	6	US-10-995-561-826	Sequence 826, App
580	42	9.4	998	6	US-10-510-524-1	Sequence 1, Appli	654	41.5	9.2	5935	6	US-10-995-561-776	Sequence 776, App
581	42	9.4	1199	6	US-10-821-234-1126	Sequence 1126, Ap	655	41	9.1	54	6	US-10-914-165-19	Sequence 19, Appl
582	42	9.4	1263	7	US-11-076-163-3	Sequence 3, Appli	656	41	9.1	57	6	US-10-821-234-1698	Sequence 1698, Ap
583	42	9.4	2214	7	US-11-080-991-94	Sequence 94, Appl	657	41	9.1	73	6	US-10-986-501-123	Sequence 123, App
584	42	9.4	2491	6	US-10-995-561-769	Sequence 769, App	658	41	9.1	76	6	US-10-925-366A-319	Sequence 319, App
585	41.5	9.2	58	6	US-10-925-366A-308	Sequence 308, App	659	41	9.1	77	7	US-11-123-896-308	Sequence 308, App
586	41.5	9.2	71	6	US-10-467-657-358	Sequence 358, App	660	41	9.1	84	7	US-11-123-896-386	Sequence 386, App
587	41.5	9.2	76	6	US-10-925-366A-322	Sequence 322, App	661	41	9.1	91	6	US-10-467-657-5566	Sequence 5566, Ap
588	41.5	9.2	95	7	US-11-054-669-59	Sequence 59, Appl	662	41	9.1	91	7	US-11-054-669-71	Sequence 71, Appl
589	41.5	9.2	95	7	US-11-054-669-60	Sequence 60, Appl	663	41	9.1	95	7	US-11-084-554-123	Sequence 123, App
590	41.5	9.2	95	7	US-11-054-669-67	Sequence 67, Appl	664	41	9.1	106	6	US-10-793-626-794	Sequence 794, App
591	41.5	9.2	95	7	US-11-084-554-116	Sequence 116, App	665	41	9.1	106	6	US-10-793-626-2140	Sequence 2140, Ap
592	41.5	9.2	95	7	US-11-084-554-125	Sequence 125, App	666	41	9.1	108	7	US-11-127-677-28	Sequence 28, Appl
593	41.5	9.2	95	7	US-11-084-554-139	Sequence 139, App	667	41	9.1	109	7	US-11-127-677-69	Sequence 69, Appl
594	41.5	9.2	100	6	US-10-932-334-56	Sequence 56, Appl	668	41	9.1	111	7	US-11-125-837-37	Sequence 37, Appl
595	41.5	9.2	107	7	US-11-144-248-6	Sequence 6, Appli	669	41	9.1	112	6	US-10-502-145-19	Sequence 19, Appl
596	41.5	9.2	107	7	US-11-144-248-14	Sequence 14, Appl	670	41	9.1	114	6	US-10-923-327-1	Sequence 1, Appli
597	41.5	9.2	107	7	US-11-105-268-24	Sequence 24, Appl	671	41	9.1	114	6	US-10-923-327-2	Sequence 2, Appli
598	41.5	9.2	108	7	US-11-127-677-25	Sequence 25, Appl	672	41	9.1	114	6	US-10-923-327-3	Sequence 3, Appli
599	41.5	9.2	108	7	US-11-127-677-38	Sequence 38, Appl	673	41	9.1	129	6	US-10-467-657-910	Sequence 910, App
600	41.5	9.2	112	7	US-11-012-353-61	Sequence 61, Appl	674	41	9.1	140	6	US-10-467-657-1278	Sequence 1278, Ap
601	41.5	9.2	112	7	US-11-012-353-65	Sequence 65, Appl	675	41	9.1	230	6	US-10-884-730-372	Sequence 372, App
602	41.5	9.2	113	6	US-10-932-334-65	Sequence 65, Appl	676	41	9.1	231	6	US-10-454-437-414	Sequence 414, App
603	41.5	9.2	113	7	US-11-009-939-17	Sequence 17, Appl	677	41	9.1	238	6	US-10-927-641-68	Sequence 68, Appl
604	41.5	9.2	120	6	US-10-932-334-74	Sequence 74, Appl	678	41	9.1	247	7	US-11-056-825-8	Sequence 8, Appli
605	41.5	9.2	127	7	US-11-193-512-103	Sequence 103, App	679	41	9.1	248	6	US-10-923-327-15	Sequence 15, Appl
606	41.5	9.2	129	7	US-11-116-144-97	Sequence 97, Appl	680	41	9.1	248	6	US-10-923-327-16	Sequence 16, Appl
607	41.5	9.2	129	7	US-11-116-144-98	Sequence 98, Appl	681	41	9.1	249	7	US-11-056-825-4	Sequence 4, Appli
608	41.5	9.2	129	7	US-11-116-144-99	Sequence 99, Appl	682	41	9.1	254	7	US-11-054-515-905	Sequence 905, App
609	41.5	9.2	129	7	US-11-116-144-100	Sequence 100, App	683	41	9.1	256	6	US-10-467-657-7902	Sequence 7902, Ap
610	41.5	9.2	131	6	US-10-789-273-14	Sequence 14, Appl	684	41	9.1	259	6	US-10-467-657-5466	Sequence 5466, Ap
611	41.5	9.2	131	7	US-11-012-353-63	Sequence 63, Appl	685	41	9.1	292	6	US-10-858-730-127	Sequence 127, App
612	41.5	9.2	131	7	US-11-012-353-67	Sequence 67, Appl	686	41	9.1	299	7	US-11-074-176-198	Sequence 198, App
613	41.5	9.2	236	6	US-10-927-641-72	Sequence 72, Appl	687	41	9.1	310	7	US-11-025-834A-13	Sequence 13, Appl
614	41.5	9.2	251	7	US-11-054-515-1238	Sequence 1238, Ap	688	41	9.1	410	6	US-10-467-657-3024	Sequence 3024, Ap
615	41.5	9.2	251	7	US-11-054-515-1310	Sequence 1310, Ap	689	41	9.1	414	7	US-11-089-551A-28	Sequence 28, Appl
616	41.5	9.2	253	7	US-11-054-515-936	Sequence 936, App	690	41	9.1	429	6	US-10-878-556A-17	Sequence 17, Appl
617	41.5	9.2	264	6	US-11-054-515-936	Sequence 78, Appl	691	41	9.1	430	6	US-10-793-626-130	Sequence 130, App
618	41.5	9.2	303	7	US-11-186-284-193	Sequence 193, App	692	41	9.1	442	6	US-10-467-657-1614	Sequence 1614, Ap
619	41.5	9.2	305	6	US-10-502-972-2	Sequence 2, Appli	693	41	9.1	473	6	US-10-509-464-6	Sequence 6, Appli
620	41.5	9.2	341	6	US-10-515-481-3	Sequence 3, Appli	694	41	9.1	473	6	US-10-467-657-1874	Sequence 1874, Ap
621	41.5	9.2	341	6	US-10-515-481-6	Sequence 6, Appli	695	41	9.1	497	7	US-11-021-441-22	Sequence 22, Appl
622	41.5	9.2	341	6	US-10-515-481-9	Sequence 9, Appli	696	41	9.1	497	7	US-11-021-441-24	Sequence 24, Appl
623	41.5	9.2	341	6	US-10-515-481-12	Sequence 12, Appl	697	41	9.1	514	6	US-10-878-556A-32	Sequence 32, Appl
624	41.5	9.2	348	6	US-10-667-295-121	Sequence 121, App	698	41	9.1	528	7	US-11-118-809-2	Sequence 2, Appli
625	41.5	9.2	350	6	US-10-667-295-120	Sequence 120, App	699	41	9.1	587	6	US-10-925-970-6	Sequence 6, Appli
626	41.5	9.2	358	7	US-11-129-143-111	Sequence 111, App	700	41	9.1	591	6	US-10-510-386-22	Sequence 22, Appl

701	41	9.1	609	7	US-11-062-225-3	Sequence 3, Appli	774	40.5	9.0	344	6	US-10-967-527A-24	Sequence 24, Appl
702	41	9.1	609	7	US-11-062-225-4	Sequence 4, Appli	775	40.5	9.0	396	7	US-11-120-543-10	Sequence 10, Appl
703	41	9.1	609	7	US-11-062-225-5	Sequence 5, Appli	776	40.5	9.0	398	6	US-10-996-628-4	Sequence 4, Appli
704	41	9.1	609	7	US-11-062-225-6	Sequence 6, Appli	777	40.5	9.0	415	6	US-10-821-234-936	Sequence 936, App
705	41	9.1	609	7	US-11-062-225-8	Sequence 8, Appli	778	40.5	9.0	441	6	US-10-454-437-56	Sequence 56, Appl
706	41	9.1	686	6	US-10-821-234-1027	Sequence 1027, Ap	779	40.5	9.0	446	6	US-10-467-657-6244	Sequence 6244, Ap
707	41	9.1	693	7	US-11-189-301-20	Sequence 20, Appl	780	40.5	9.0	456	7	US-11-059-867-4	Sequence 4, Appli
708	41	9.1	701	7	US-11-189-301-19	Sequence 19, Appl	781	40.5	9.0	462	7	US-11-132-142-10	Sequence 10, Appl
709	41	9.1	766	7	US-11-189-301-21	Sequence 21, Appl	782	40.5	9.0	489	6	US-10-835-475-11	Sequence 11, Appl
710	41	9.1	783	7	US-11-082-389-354	Sequence 354, App	783	40.5	9.0	514	6	US-10-835-475-2	Sequence 2, Appli
711	41	9.1	792	6	US-10-793-626-1492	Sequence 1492, Ap	784	40.5	9.0	521	6	US-10-821-234-1546	Sequence 1546, Ap
712	41	9.1	805	6	US-10-485-517-297	Sequence 297, App	785	40.5	9.0	523	6	US-10-641-678-45	Sequence 45, Appl
713	41	9.1	880	6	US-10-513-786-5	Sequence 5, Appli	786	40.5	9.0	527	7	US-11-120-543-18	Sequence 18, Appl
714	41	9.1	897	7	US-11-137-465-35	Sequence 35, Appl	787	40.5	9.0	627	6	US-10-467-657-5432	Sequence 5432, Ap
715	41	9.1	927	7	US-11-189-301-10	Sequence 10, Appl	788	40.5	9.0	703	6	US-10-821-234-1412	Sequence 1412, Ap
716	41	9.1	984	7	US-11-113-424-60	Sequence 60, Appl	789	40.5	9.0	767	6	US-10-467-962B-91	Sequence 91, Appl
717	41	9.1	993	7	US-11-137-465-36	Sequence 36, Appl	790	40.5	9.0	770	6	US-10-821-234-1269	Sequence 1269, Ap
718	41	9.1	997	7	US-11-113-424-37	Sequence 37, Appl	791	40.5	9.0	794	6	US-10-485-517-355	Sequence 355, App
719	41	9.1	1005	7	US-11-113-424-63	Sequence 63, Appl	792	40.5	9.0	798	6	US-10-770-726-64	Sequence 64, Appl
720	41	9.1	1059	7	US/11/062	Sequence 5, Appli	793	40.5	9.0	825	7	US-11-074-176-20	Sequence 20, Appl
721	41	9.1	1061	7	US-11-059-814-18	Sequence 18, Appl	794	40.5	9.0	830	6	US-10-995-561-899	Sequence 899, App
722	41	9.1	1076	6	US-10-467-657-7916	Sequence 7916, Ap	795	40.5	9.0	871	7	US-11-097-864-765	Sequence 765, App
723	41	9.1	1084	7	US/11/062	Sequence 8, Appli	796	40.5	9.0	871	7	US-11-097-912-765	Sequence 765, App
724	41	9.1	1238	7	US-11-078-735-21	Sequence 21, Appl	797	40.5	9.0	875	7	US-11-097-864-743	Sequence 743, App
725	41	9.1	1316	7	US-11-091-643-4	Sequence 4, Appli	798	40.5	9.0	875	7	US-11-097-864-745	Sequence 745, App
726	41	9.1	1627	6	US-10-821-234-1283	Sequence 1283, Ap	799	40.5	9.0	875	7	US-11-097-864-747	Sequence 747, App
727	41	9.1	1734	7	US-11-192-967-6	Sequence 6, Appli	800	40.5	9.0	875	7	US-11-097-864-748	Sequence 748, App
728	41	9.1	1734	7	US-11-193-715-6	Sequence 6, Appli	801	40.5	9.0	875	7	US-11-097-864-751	Sequence 751, App
729	41	9.1	1900	6	US-10-513-786-3	Sequence 3, Appli	802	40.5	9.0	875	7	US-11-097-912-743	Sequence 743, App
730	41	9.1	3507	7	US-11-075-185-7	Sequence 7, Appli	803	40.5	9.0	875	7	US-11-097-912-745	Sequence 745, App
731	41	9.1	3704	6	US-10-513-786-1	Sequence 1, Appli	804	40.5	9.0	875	7	US-11-097-912-747	Sequence 747, App
732	40.5	9.0	49	6	US-10-467-657-2178	Sequence 2178, Ap	805	40.5	9.0	875	7	US-11-097-912-748	Sequence 748, App
733	40.5	9.0	78	6	US-10-925-366A-314	Sequence 314, App	806	40.5	9.0	875	7	US-11-097-912-751	Sequence 751, App
734	40.5	9.0	96	7	US-11-054-669-88	Sequence 88, Appl	807	40.5	9.0	1032	6	US-10-835-475-1	Sequence 1, Appli
735	40.5	9.0	96	7	US-11-084-554-135	Sequence 135, App	808	40.5	9.0	1032	7	US-11-014-367-1	Sequence 3, Appli
736	40.5	9.0	106	7	US-11-107-028-28	Sequence 28, Appl	809	40.5	9.0	1032	7	US-11-014-367-3	Sequence 4, Appli
737	40.5	9.0	107	7	US-11-120-338-1	Sequence 1, Appli	810	40.5	9.0	1138	6	US-10-509-422-4	Sequence 2494, Ap
738	40.5	9.0	108	7	US-11-054-669-94	Sequence 94, Appl	812	40	8.9	47	6	US-10-467-657-2494	Sequence 798, App
739	40.5	9.0	112	7	US-11-012-353-57	Sequence 57, Appl	813	40	8.9	58	6	US-10-467-657-798	Sequence 110, App
740	40.5	9.0	112	7	US-11-127-932-15	Sequence 15, Appl	814	40	8.9	103	6	US-10-467-657-110	Sequence 6246, Ap
741	40.5	9.0	121	7	US-11-107-028-16	Sequence 16, Appl	815	40	8.9	103	6	US-10-467-657-6246	Sequence 60, Appl
742	40.5	9.0	121	7	US-11-107-028-18	Sequence 18, Appl	816	40	8.9	105	7	US-11-155-775-60	Sequence 64, Appl
743	40.5	9.0	124	6	US-10-467-657-2914	Sequence 2914, Ap	817	40	8.9	105	7	US-11-155-775-64	Sequence 316, App
744	40.5	9.0	124	7	US-11-096-074-14	Sequence 14, Appl	818	40	8.9	108	6	US-10-925-366A-316	Sequence 330, App
745	40.5	9.0	128	7	US-11-116-144-147	Sequence 147, App	819	40	8.9	108	6	US-10-925-366A-330	Sequence 19, Appl
746	40.5	9.0	129	7	US-11-194-246-423	Sequence 423, App	820	40	8.9	108	7	US-11-127-932-19	Sequence 30, Appl
747	40.5	9.0	143	7	US-11-096-074-10	Sequence 10, Appl	821	40	8.9	109	7	US/11/020	Sequence 62, Appl
748	40.5	9.0	143	7	US-11-096-074-12	Sequence 12, Appl	822	40	8.9	109	7	US-11-127-677-62	Sequence 14, Appl
749	40.5	9.0	177	6	US-10-467-657-1658	Sequence 1658, Ap	823	40	8.9	109	7	US-11-127-932-14	Sequence 18, Appl
750	40.5	9.0	178	6	US-10-363-924-4	Sequence 4, Appli	824	40	8.9	109	7	US-11-127-932-18	Sequence 3, Appli
751	40.5	9.0	181	6	US-10-467-657-300	Sequence 300, App	825	40	8.9	116	7	US-11-096-046-3	Sequence 32, Appl
752	40.5	9.0	224	6	US-10-467-657-6360	Sequence 6360, Ap	826	40	8.9	121	7	US-11-009-939-32	Sequence 11, App
753	40.5	9.0	281	6	US-10-467-657-3144	Sequence 3144, Ap	827	40	8.9	129	7	US-11-116-144-115	Sequence 115, App
754	40.5	9.0	246	7	US-11-054-515-2075	Sequence 2075, Ap	828	40	8.9	130	6	US-10-793-626-2902	Sequence 2902, Ap
755	40.5	9.0	250	7	US-11-054-515-49	Sequence 49, Appl	829	40	8.9	135	6	US-10-467-657-2858	Sequence 2858, Ap
756	40.5	9.0	251	7	US-11-054-515-126	Sequence 126, App	830	40	8.9	145	7	US-11-084-858-11	Sequence 11, Appl
757	40.5	9.0	251	7	US-11-054-515-142	Sequence 142, App	831	40	8.9	153	6	US-10-467-657-914	Sequence 914, App
758	40.5	9.0	251	7	US-11-054-515-145	Sequence 145, App	832	40	8.9	174	6	US-10-884-730-173	Sequence 173, App
759	40.5	9.0	251	7	US-11-054-515-148	Sequence 148, App	833	40	8.9	179	6	US-10-884-730-84	Sequence 84, Appl
760	40.5	9.0	251	7	US-11-054-515-154	Sequence 154, App	834	40	8.9	183	6	US-10-884-730-86	Sequence 86, Appl
761	40.5	9.0	251	7	US-11-054-515-156	Sequence 156, App	835	40	8.9	188	6	US-10-884-730-88	Sequence 88, Appl
762	40.5	9.0	251	7	US-11-054-515-157	Sequence 157, App	836	40	8.9	188	6	US-10-884-730-294	Sequence 294, App
763	40.5	9.0	251	7	US-11-054-515-162	Sequence 162, App	837	40	8.9	188	6	US-10-884-730-322	Sequence 322, App
764	40.5	9.0	251	7	US-11-054-515-176	Sequence 176, App	838	40	8.9	209	6	US-10-884-730-172	Sequence 172, App
765	40.5	9.0	251	7	US-11-054-515-285	Sequence 285, App	839	40	8.9	210	7	US-11-022-562-221	Sequence 221, App
766	40.5	9.0	251	7	US-11-054-515-286	Sequence 286, App	840	40	8.9	225	6	US-10-884-730-5	Sequence 5, Appli
767	40.5	9.0	251	7	US-11-054-515-303	Sequence 303, App	841	40	8.9	237	6	US-10-884-730-2	Sequence 2, Appli
768	40.5	9.0	251	7	US-11-054-515-314	Sequence 314, App	842	40	8.9	237	6	US-10-884-730-10	Sequence 10, Appl
769	40.5	9.0	259	7	US-11-054-515-1270	Sequence 1270, Ap	843	40	8.9	237	6	US-10-884-730-12	Sequence 12, Appl
770	40.5	9.0	266	6	US-10-884-730-295	Sequence 295, App	844	40	8.9	237	6	US-10-884-730-22	Sequence 22, Appl
771	40.5	9.0	266	6	US-10-884-730-296	Sequence 296, App	845	40	8.9	237	6	US-10-884-730-113	Sequence 113, App
772	40.5	9.0	266	7	US-11-000-463-464	Sequence 464, App	846	40	8.9	237	6	US-10-884-730-120	Sequence 120, App
773	40.5	9.0	336	6	US-10-499-715-8	Sequence 8, Appli	847	40	8.9	237	6	US-10-884-730-175	Sequence 175, App

848	40	8.9	237	6	US-10-884-730-177	Sequence 177, App	922	39.5	8.8	105	7	US-11-025-712-6	Sequence 6, Appli
849	40	8.9	237	6	US-10-884-730-307	Sequence 307, App	923	39.5	8.8	105	7	US-11-075-351-62	Sequence 62, Appli
850	40	8.9	237	6	US-10-884-730-317	Sequence 317, App	924	39.5	8.8	105	7	US-11-102-621-5	Sequence 5, Appli
851	40	8.9	237	6	US-10-884-730-318	Sequence 318, App	925	39.5	8.8	107	6	US-10-999-866-41	Sequence 41, Appli
852	40	8.9	256	7	US-11-054-515-1027	Sequence 1027, Ap	926	39.5	8.8	107	7	US-11-061-821-41	Sequence 41, Appli
853	40	8.9	266	6	US-10-884-730-1	Sequence 1, Appli	927	39.5	8.8	107	7	US-11-107-028-51	Sequence 51, Appli
854	40	8.9	266	6	US-10-884-730-4	Sequence 4, Appli	928	39.5	8.8	108	6	US-10-925-366A-173	Sequence 173, App
855	40	8.9	266	6	US-10-884-730-79	Sequence 79, Appl	929	39.5	8.8	108	6	US-10-665-658-1	Sequence 1, Appli
856	40	8.9	266	6	US-10-884-730-85	Sequence 85, Appl	930	39.5	8.8	108	7	US-11-127-677-35	Sequence 35, Appli
857	40	8.9	266	6	US-10-884-730-116	Sequence 116, App	931	39.5	8.8	108	7	US-11-127-932-12	Sequence 12, Appl
858	40	8.9	266	6	US-10-884-730-121	Sequence 121, App	932	39.5	8.8	108	7	US-11-127-932-13	Sequence 13, Appl
859	40	8.9	266	6	US-10-884-730-165	Sequence 165, App	933	39.5	8.8	110	6	US-10-648-816-1	Sequence 1, Appli
860	40	8.9	266	6	US-10-884-730-166	Sequence 166, App	934	39.5	8.8	110	6	US-10-648-816-2	Sequence 2, Appli
861	40	8.9	266	6	US-10-884-730-306	Sequence 306, App	935	39.5	8.8	110	6	US-10-648-816-3	Sequence 3, Appli
862	40	8.9	266	7	US-11-000-463-381	Sequence 381, App	936	39.5	8.8	110	6	US-10-648-816-4	Sequence 4, Appli
863	40	8.9	266	7	US-11-000-463-853	Sequence 853, App	937	39.5	8.8	110	6	US-10-648-816-5	Sequence 5, Appli
864	40	8.9	313	7	US-11-000-463-427	Sequence 427, App	938	39.5	8.8	110	6	US-10-648-816-6	Sequence 6, Appli
865	40	8.9	318	6	US-10-821-234-1590	Sequence 1590, Ap	939	39.5	8.8	110	6	US-10-648-816-7	Sequence 7, Appli
866	40	8.9	318	7	US-11-186-284-69	Sequence 69, Appl	940	39.5	8.8	110	6	US-10-648-816-8	Sequence 8, Appli
867	40	8.9	340	6	US-10-873-528-188	Sequence 188, App	941	39.5	8.8	113	7	US-11-096-074-53	Sequence 53, Appl
868	40	8.9	354	6	US-10-821-234-1618	Sequence 1618, Ap	942	39.5	8.8	121	7	US-11-107-028-20	Sequence 20, Appl
869	40	8.9	358	7	US-11-095-624-6	Sequence 6, Appli	943	39.5	8.8	129	7	US-11-116-144-101	Sequence 101, App
870	40	8.9	368	7	US-11-000-463-916	Sequence 916, App	944	39.5	8.8	129	7	US-11-116-144-103	Sequence 103, App
871	40	8.9	386	7	US-11-143-986-2	Sequence 2, Appli	945	39.5	8.8	132	7	US-11-108-172-200	Sequence 200, App
872	40	8.9	386	7	US-11-143-986-3	Sequence 3, Appli	946	39.5	8.8	143	7	US-11-096-074-18	Sequence 18, Appl
873	40	8.9	388	7	US-11-000-463-444	Sequence 444, App	947	39.5	8.8	172	6	US-10-746-959C-8	Sequence 8, Appli
874	40	8.9	398	6	US-10-873-528-61	Sequence 61, Appl	948	39.5	8.8	180	6	US-10-689-742-84	Sequence 84, Appl
875	40	8.9	433	6	US-10-821-234-1353	Sequence 1353, Ap	949	39.5	8.8	180	7	US-11-098-662-114	Sequence 114, App
876	40	8.9	440	7	US-11-102-240-52	Sequence 52, Appl	950	39.5	8.8	182	7	US-11-098-662-128	Sequence 128, App
877	40	8.9	472	6	US-10-508-263-62	Sequence 62, Appl	951	39.5	8.8	182	7	US-11-098-662-132	Sequence 132, App
878	40	8.9	472	6	US-10-508-263-64	Sequence 64, Appl	952	39.5	8.8	208	6	US-10-821-234-1118	Sequence 1118, Ap
879	40	8.9	472	7	US-11-008-331-3	Sequence 3, Appli	953	39.5	8.8	225	6	US-10-118-590-30	Sequence 30, Appl
880	40	8.9	473	7	US-11-069-642-5	Sequence 5, Appli	954	39.5	8.8	231	7	US-11-000-463-283	Sequence 283, App
881	40	8.9	488	6	US-10-508-263-12	Sequence 12, Appl	955	39.5	8.8	232	7	US-11-000-463-755	Sequence 755, App
882	40	8.9	490	6	US-10-508-263-10	Sequence 10, Appl	956	39.5	8.8	233	6	US-10-467-657-5890	Sequence 5890, Ap
883	40	8.9	501	6	US-10-630-203-25	Sequence 25, Appl	957	39.5	8.8	234	7	US-11-139-499-2	Sequence 2, Appli
884	40	8.9	506	6	US-10-641-678-69	Sequence 69, Appl	958	39.5	8.8	236	7	US-11-139-499-10	Sequence 10, Appl
885	40	8.9	508	7	US-11-093-274-41	Sequence 41, Appl	959	39.5	8.8	240	7	US-11-000-463-248	Sequence 248, App
887	40	8.9	513	7	US-11-102-240-124	Sequence 124, App	960	39.5	8.8	248	7	US-11-054-515-111	Sequence 111, App
888	40	8.9	532	7	US-11-152-747-2	Sequence 2, Appli	961	39.5	8.8	250	7	US-11-054-515-48	Sequence 48, Appl
889	40	8.9	563	6	US-10-873-528-27	Sequence 27, Appl	962	39.5	8.8	250	7	US-11-054-515-50	Sequence 50, Appl
890	40	8.9	563	6	US-10-873-528-28	Sequence 28, Appl	963	39.5	8.8	250	7	US-11-054-515-51	Sequence 51, Appl
891	40	8.9	609	7	US-11-062-225-7	Sequence 7, Appli	964	39.5	8.8	250	7	US-11-054-515-52	Sequence 52, Appl
892	40	8.9	615	7	US-11-172-145-6	Sequence 6, Appli	965	39.5	8.8	250	7	US-11-054-515-53	Sequence 53, Appl
893	40	8.9	617	7	US-11-172-145-8	Sequence 8, Appli	966	39.5	8.8	250	7	US-11-054-515-54	Sequence 54, Appl
894	40	8.9	621	6	US-10-632-150-56	Sequence 56, Appl	967	39.5	8.8	250	7	US-11-054-515-56	Sequence 56, Appl
895	40	8.9	621	7	US-11-073-457-56	Sequence 56, Appl	968	39.5	8.8	250	7	US-11-054-515-57	Sequence 57, Appl
896	40	8.9	621	7	US-11-073-460-56	Sequence 56, Appl	969	39.5	8.8	250	7	US-11-054-515-58	Sequence 58, Appl
897	40	8.9	658	6	US-10-467-657-4782	Sequence 4782, Ap	970	39.5	8.8	250	7	US-11-054-515-59	Sequence 59, Appl
898	40	8.9	697	7	US-11-074-176-62	Sequence 62, Appl	971	39.5	8.8	250	7	US-11-054-515-62	Sequence 62, Appl
899	40	8.9	710	7	US-11-089-551A-33	Sequence 33, Appl	972	39.5	8.8	250	7	US-11-054-515-63	Sequence 63, Appl
900	40	8.9	756	7	US-11-113-837-20	Sequence 20, Appl	973	39.5	8.8	250	7	US-11-054-515-66	Sequence 66, Appl
901	40	8.9	883	6	US-10-858-730-207	Sequence 207, App	974	39.5	8.8	250	7	US-11-054-515-69	Sequence 69, Appl
902	40	8.9	987	6	US-10-770-726-61	Sequence 61, Appl	975	39.5	8.8	250	7	US-11-054-515-73	Sequence 73, Appl
903	40	8.9	995	7	US-11-113-424-62	Sequence 62, Appl	976	39.5	8.8	250	7	US-11-054-515-74	Sequence 74, Appl
904	40	8.9	1011	7	US-11-069-642-111	Sequence 111, App	977	39.5	8.8	250	7	US-11-054-515-75	Sequence 75, Appl
905	40	8.9	1141	6	US-10-601-368-6	Sequence 6, Appli	978	39.5	8.8	250	7	US-11-054-515-76	Sequence 76, Appl
906	40	8.9	1166	6	US-10-601-368-4	Sequence 4, Appli	979	39.5	8.8	250	7	US-11-054-515-77	Sequence 77, Appl
907	40	8.9	1188	6	US-10-601-368-3	Sequence 3, Appli	980	39.5	8.8	250	7	US-11-054-515-78	Sequence 78, Appl
908	40	8.9	1188	7	US-11-000-463-338	Sequence 338, App	981	39.5	8.8	250	7	US-11-054-515-80	Sequence 80, Appl
909	40	8.9	1188	7	US-11-000-463-810	Sequence 810, App	982	39.5	8.8	250	7	US-11-054-515-81	Sequence 81, Appl
910	40	8.9	1189	6	US-10-821-234-1209	Sequence 1209, Ap	983	39.5	8.8	250	7	US-11-054-515-100	Sequence 100, App
911	40	8.9	1263	6	US-10-485-517-127	Sequence 127, App	984	39.5	8.8	250	7	US-11-054-515-107	Sequence 107, App
912	40	8.9	1452	6	US-10-821-234-1102	Sequence 1102, Ap	985	39.5	8.8	250	7	US-11-054-515-140	Sequence 140, App
913	40	8.9	1463	6	US-10-971-982-3	Sequence 3, Appli	986	39.5	8.8	251	7	US-11-054-515-9	Sequence 9, Appli
914	40	8.9	1857	7	US-11-057-058-60	Sequence 60, Appl	987	39.5	8.8	251	7	US-11-054-515-10	Sequence 10, Appl
915	40	8.9	1857	7	US-11-057-058-61	Sequence 61, Appl	988	39.5	8.8	251	7	US-11-054-515-11	Sequence 11, Appl
916	40	8.9	2333	7	US-11-096-281-13	Sequence 13, Appl	989	39.5	8.8	251	7	US-11-054-515-12	Sequence 12, Appl
917	40	8.9	3063	7	US-11-186-284-26	Sequence 26, Appl	990	39.5	8.8	251	7	US-11-054-515-13	Sequence 13, Appl
918	40	8.9	4128	6	US-10-770-726-77	Sequence 77, Appl	991	39.5	8.8	251	7	US-11-054-515-14	Sequence 14, Appl
919	39.5	8.8	20	7	US-11-022-562-146	Sequence 146, App	992	39.5	8.8	251	7	US-11-054-515-15	Sequence 15, Appl
920	39.5	8.8	92	7	US-11-144-248-18	Sequence 18, Appl	993	39.5	8.8	251	7	US-11-054-515-16	Sequence 16, Appl
921	39.5	8.8	102	6	US-10-793-626-2616	Sequence 2616, Ap	994	39.5	8.8	251	7	US-11-054-515-17	Sequence 17, Appl

1141	39.5	8.8	251	7	US-11-054-515-223	Sequence 223, App	1214	39.5	8.8	251	7	US-11-054-515-308	Sequence 308, App
1142	39.5	8.8	251	7	US-11-054-515-224	Sequence 224, App	1215	39.5	8.8	251	7	US-11-054-515-309	Sequence 309, App
1143	39.5	8.8	251	7	US-11-054-515-225	Sequence 225, App	1216	39.5	8.8	251	7	US-11-054-515-310	Sequence 310, App
1144	39.5	8.8	251	7	US-11-054-515-226	Sequence 226, App	1217	39.5	8.8	251	7	US-11-054-515-312	Sequence 312, App
1145	39.5	8.8	251	7	US-11-054-515-227	Sequence 227, App	1218	39.5	8.8	251	7	US-11-054-515-313	Sequence 313, App
1146	39.5	8.8	251	7	US-11-054-515-228	Sequence 228, App	1219	39.5	8.8	251	7	US-11-054-515-315	Sequence 315, App
1147	39.5	8.8	251	7	US-11-054-515-229	Sequence 229, App	1220	39.5	8.8	251	7	US-11-054-515-318	Sequence 318, App
1148	39.5	8.8	251	7	US-11-054-515-230	Sequence 230, App	1221	39.5	8.8	251	7	US-11-054-515-319	Sequence 319, App
1149	39.5	8.8	251	7	US-11-054-515-231	Sequence 231, App	1222	39.5	8.8	276	6	US-10-467-657-4172	Sequence 4172, Ap
1150	39.5	8.8	251	7	US-11-054-515-232	Sequence 232, App	1223	39.5	8.8	276	6	US-10-467-657-7078	Sequence 7078, Ap
1151	39.5	8.8	251	7	US-11-054-515-233	Sequence 233, App	1224	39.5	8.8	349	7	US-11-055-822-186	Sequence 186, App
1152	39.5	8.8	251	7	US-11-054-515-234	Sequence 234, App	1225	39.5	8.8	376	6	US-10-454-437-412	Sequence 412, App
1153	39.5	8.8	251	7	US-11-054-515-235	Sequence 235, App	1226	39.5	8.8	376	7	US-11-182-752-2	Sequence 2, Appli
1154	39.5	8.8	251	7	US-11-054-515-236	Sequence 236, App	1227	39.5	8.8	409	7	US-11-113-424-73	Sequence 73, Appli
1155	39.5	8.8	251	7	US-11-054-515-237	Sequence 237, App	1228	39.5	8.8	417	7	US-11-182-752-4	Sequence 4, Appli
1156	39.5	8.8	251	7	US-11-054-515-238	Sequence 238, App	1229	39.5	8.8	426	7	US-11-087-100-10	Sequence 10, Appl
1157	39.5	8.8	251	7	US-11-054-515-239	Sequence 239, App	1230	39.5	8.8	426	7	US-11-087-084-10	Sequence 10, Appl
1158	39.5	8.8	251	7	US-11-054-515-241	Sequence 241, App	1231	39.5	8.8	426	7	US-11-087-085-10	Sequence 10, Appl
1159	39.5	8.8	251	7	US-11-054-515-242	Sequence 242, App	1232	39.5	8.8	429	7	US-11-093-274-37	Sequence 37, Appl
1160	39.5	8.8	251	7	US-11-054-515-243	Sequence 243, App	1233	39.5	8.8	449	7	US-11-055-822-142	Sequence 142, App
1161	39.5	8.8	251	7	US-11-054-515-244	Sequence 244, App	1234	39.5	8.8	450	7	US-11-186-284-14	Sequence 14, Appl
1162	39.5	8.8	251	7	US-11-054-515-245	Sequence 245, App	1235	39.5	8.8	459	6	US-10-990-276-3	Sequence 3, Appli
1163	39.5	8.8	251	7	US-11-054-515-246	Sequence 246, App	1236	39.5	8.8	488	6	US-10-821-234-1000	Sequence 1000, Ap
1164	39.5	8.8	251	7	US-11-054-515-247	Sequence 247, App	1237	39.5	8.8	503	7	US-11-113-424-72	Sequence 72, Appl
1165	39.5	8.8	251	7	US-11-054-515-248	Sequence 248, App	1238	39.5	8.8	506	6	US-10-501-098-3	Sequence 3, Appli
1166	39.5	8.8	251	7	US-11-054-515-249	Sequence 249, App	1239	39.5	8.8	516	6	US-10-641-678-59	Sequence 59, Appl
1167	39.5	8.8	251	7	US-11-054-515-250	Sequence 250, App	1241	39.5	8.8	539	6	US-10-467-657-3870	Sequence 3870, Ap
1168	39.5	8.8	251	7	US-11-054-515-251	Sequence 251, App	1242	39.5	8.8	551	7	US-11-000-463-346	Sequence 346, App
1169	39.5	8.8	251	7	US-11-054-515-252	Sequence 252, App	1243	39.5	8.8	556	6	US-10-821-234-1509	Sequence 1509, Ap
1170	39.5	8.8	251	7	US-11-054-515-253	Sequence 253, App	1244	39.5	8.8	558	6	US-10-501-098-1	Sequence 1, Appli
1171	39.5	8.8	251	7	US-11-054-515-254	Sequence 254, App	1245	39.5	8.8	570	7	US-11-113-424-69	Sequence 69, Appl
1172	39.5	8.8	251	7	US-11-054-515-255	Sequence 255, App	1246	39.5	8.8	570	7	US-11-113-424-71	Sequence 71, Appl
1173	39.5	8.8	251	7	US-11-054-515-256	Sequence 256, App	1247	39.5	8.8	594	7	US-11-012-762-4	Sequence 4, Appli
1174	39.5	8.8	251	7	US-11-054-515-258	Sequence 258, App	1248	39.5	8.8	620	7	US-11-113-424-70	Sequence 70, Appl
1175	39.5	8.8	251	7	US-11-054-515-259	Sequence 259, App	1249	39.5	8.8	720	7	US-11-113-424-28	Sequence 28, Appl
1176	39.5	8.8	251	7	US-11-054-515-260	Sequence 260, App	1250	39.5	8.8	747	7	US-11-113-424-26	Sequence 26, Appl
1177	39.5	8.8	251	7	US-11-054-515-262	Sequence 262, App	1251	39.5	8.8	794	7	US-11-102-476-34	Sequence 34, Appl
1178	39.5	8.8	251	7	US-11-054-515-263	Sequence 263, App	1252	39.5	8.8	805	6	US-10-927-641-77	Sequence 77, Appl
1179	39.5	8.8	251	7	US-11-054-515-264	Sequence 264, App	1253	39.5	8.8	835	6	US-10-501-039-4	Sequence 4, Appli
1180	39.5	8.8	251	7	US-11-054-515-265	Sequence 265, App	1254	39.5	8.8	836	6	US-10-821-234-1559	Sequence 1559, Ap
1181	39.5	8.8	251	7	US-11-054-515-267	Sequence 267, App	1255	39.5	8.8	883	6	US-10-793-626-754	Sequence 754, App
1182	39.5	8.8	251	7	US-11-054-515-268	Sequence 268, App	1256	39.5	8.8	900	7	US-11-144-987-4	Sequence 4, Appli
1183	39.5	8.8	251	7	US-11-054-515-269	Sequence 269, App	1257	39.5	8.8	900	7	US-11-144-987-10	Sequence 10, Appl
1184	39.5	8.8	251	7	US-11-054-515-270	Sequence 270, App	1258	39.5	8.8	902	7	US-11-144-987-6	Sequence 6, Appli
1185	39.5	8.8	251	7	US-11-054-515-271	Sequence 271, App	1259	39.5	8.8	902	7	US-11-144-987-8	Sequence 8, Appli
1186	39.5	8.8	251	7	US-11-054-515-272	Sequence 272, App	1260	39.5	8.8	902	7	US-11-144-987-12	Sequence 12, Appl
1187	39.5	8.8	251	7	US-11-054-515-273	Sequence 273, App	1261	39.5	8.8	902	7	US-11-144-987-14	Sequence 14, Appl
1188	39.5	8.8	251	7	US-11-054-515-274	Sequence 274, App	1262	39.5	8.8	910	7	US-11-144-987-2	Sequence 2, Appli
1189	39.5	8.8	251	7	US-11-054-515-275	Sequence 275, App	1263	39.5	8.8	915	7	US-11-144-987-16	Sequence 16, Appl
1190	39.5	8.8	251	7	US-11-054-515-276	Sequence 276, App	1264	39.5	8.8	915	7	US-11-144-987-22	Sequence 22, Appl
1191	39.5	8.8	251	7	US-11-054-515-277	Sequence 277, App	1265	39.5	8.8	917	7	US-11-144-987-18	Sequence 18, Appl
1192	39.5	8.8	251	7	US-11-054-515-278	Sequence 278, App	1266	39.5	8.8	917	7	US-11-144-987-20	Sequence 20, Appl
1193	39.5	8.8	251	7	US-11-054-515-282	Sequence 282, App	1267	39.5	8.8	917	7	US-11-144-987-24	Sequence 24, Appl
1194	39.5	8.8	251	7	US-11-054-515-283	Sequence 283, App	1268	39.5	8.8	917	7	US-11-144-987-26	Sequence 26, Appl
1195	39.5	8.8	251	7	US-11-054-515-287	Sequence 287, App	1269	39.5	8.8	943	6	US-10-475-204-34	Sequence 34, Appl
1196	39.5	8.8	251	7	US-11-054-515-288	Sequence 288, App	1270	39.5	8.8	965	7	US-11-172-145-4	Sequence 4, Appli
1197	39.5	8.8	251	7	US-11-054-515-289	Sequence 289, App	1271	39.5	8.8	972	7	US-11-124-215-1	Sequence 1, Appli
1198	39.5	8.8	251	7	US-11-054-515-290	Sequence 290, App	1272	39.5	8.8	972	7	US-11-124-215-3	Sequence 3, Appli
1199	39.5	8.8	251	7	US-11-054-515-291	Sequence 291, App	1273	39.5	8.8	972	7	US-11-124-215-7	Sequence 7, Appli
1200	39.5	8.8	251	7	US-11-054-515-292	Sequence 292, App	1274	39.5	8.8	972	7	US-11-172-145-2	Sequence 2, Appli
1201	39.5	8.8	251	7	US-11-054-515-293	Sequence 293, App	1275	39.5	8.8	1050	6	US-10-523-477-12	Sequence 12, Appl
1202	39.5	8.8	251	7	US-11-054-515-294	Sequence 294, App	1276	39.5	8.8	1050	6	US-10-770-726-47	Sequence 47, Appl
1203	39.5	8.8	251	7	US-11-054-515-295	Sequence 295, App	1277	39.5	8.8	1126	6	US-10-485-517-248	Sequence 248, App
1204	39.5	8.8	251	7	US-11-054-515-296	Sequence 296, App	1278	39.5	8.8	1219	7	US-11-032-236-4	Sequence 4, Appli
1205	39.5	8.8	251	7	US-11-054-515-297	Sequence 297, App	1279	39.5	8.8	1424	7	US-11-102-476-4	Sequence 4, Appli
1206	39.5	8.8	251	7	US-11-054-515-298	Sequence 298, App	1280	39.5	8.8	4384	6	US-10-821-234-1120	Sequence 1120, Ap
1207	39.5	8.8	251	7	US-11-054-515-299	Sequence 299, App	1281	39	8.7	78	6	US-10-925-366A-311	Sequence 311, App
1208	39.5	8.8	251	7	US-11-054-515-300	Sequence 300, App	1282	39	8.7	85	6	US-10-467-657-9150	Sequence 9150, Ap
1209	39.5	8.8	251	7	US-11-054-515-301	Sequence 301, App	1283	39	8.7	87	7	US-11-053-076-1	Sequence 1, Appli
1210	39.5	8.8	251	7	US-11-054-515-302	Sequence 302, App	1284	39	8.7	105	7	US-11-053-076-5	Sequence 5, Appli
1211	39.5	8.8	251	7	US-11-054-515-304	Sequence 304, App	1285	39	8.7	105	7	US-11-075-351-56	Sequence 56, Appl
1212	39.5	8.8	251	7	US-11-054-515-305	Sequence 305, App	1286	39	8.7	107	6	US-10-925-366A-153	Sequence 153, App
1213	39.5	8.8	251	7	US-11-054-515-306	Sequence 306, App	1287	39	8.7	108	6	US-10-925-366A-142	Sequence 142, App

1288	39	8.7	108	6	US-10-925-366A-143	Sequence 143, App	1361	39	8.7	394	7	US-11-055-822-1094	Sequence 1094, Ap
1289	39	8.7	108	6	US-10-925-366A-144	Sequence 144, App	1362	39	8.7	400	7	US-11-077-386-26	Sequence 26, Appl
1290	39	8.7	108	6	US-10-925-366A-145	Sequence 145, App	1363	39	8.7	407	6	US-10-793-626-886	Sequence 886, App
1291	39	8.7	108	6	US-10-925-366A-146	Sequence 146, App	1364	39	8.7	415	6	US-10-467-657-10	Sequence 10, Appl
1292	39	8.7	108	6	US-10-925-366A-149	Sequence 149, App	1365	39	8.7	415	6	US-10-467-657-5468	Sequence 5468, Ap
1293	39	8.7	108	6	US-10-925-366A-151	Sequence 151, App	1366	39	8.7	432	6	US-10-793-626-2942	Sequence 2942, App
1294	39	8.7	108	6	US-10-925-366A-152	Sequence 152, App	1367	39	8.7	441	7	US-11-196-475-120	Sequence 120, App
1295	39	8.7	108	6	US-10-925-366A-154	Sequence 154, App	1369	39	8.7	445	7	US-11-115-564-1	Sequence 1, Appli
1296	39	8.7	108	6	US-10-925-366A-155	Sequence 155, App	1370	39	8.7	445	7	US-11-115-564-2	Sequence 2, Appli
1297	39	8.7	108	6	US-10-925-366A-156	Sequence 156, App	1371	39	8.7	476	6	US-10-999-866-39	Sequence 39, Appl
1298	39	8.7	108	6	US-10-925-366A-157	Sequence 157, App	1372	39	8.7	476	7	US-11-061-821-39	Sequence 39, Appl
1299	39	8.7	108	6	US-10-925-366A-158	Sequence 158, App	1373	39	8.7	479	7	US-11-024-251-33	Sequence 33, Appl
1300	39	8.7	108	6	US-10-925-366A-159	Sequence 159, App	1374	39	8.7	519	6	US-10-485-517-220	Sequence 220, App
1301	39	8.7	108	6	US-10-925-366A-160	Sequence 160, App	1376	39	8.7	534	7	US-11-077-386-25	Sequence 25, Appl
1302	39	8.7	108	6	US-10-925-366A-161	Sequence 161, App	1377	39	8.7	544	6	US-10-432-483-20	Sequence 20, Appl
1303	39	8.7	108	6	US-10-925-366A-162	Sequence 162, App	1378	39	8.7	556	6	US-10-995-561-766	Sequence 766, App
1304	39	8.7	108	6	US-10-925-366A-163	Sequence 163, App	1379	39	8.7	556	6	US-10-995-561-767	Sequence 767, App
1305	39	8.7	108	6	US-10-925-366A-164	Sequence 164, App	1380	39	8.7	581	7	US-11-067-231-153	Sequence 153, App
1306	39	8.7	108	6	US-10-925-366A-165	Sequence 165, App	1381	39	8.7	594	6	US-10-997-247-2	Sequence 2, Appli
1307	39	8.7	108	6	US-10-925-366A-166	Sequence 166, App	1382	39	8.7	609	7	US-11-110-082-40	Sequence 40, Appl
1308	39	8.7	108	6	US-10-925-366A-167	Sequence 167, App	1383	39	8.7	660	6	US-10-878-556A-102	Sequence 102, App
1309	39	8.7	108	6	US-10-925-366A-168	Sequence 168, App	1384	39	8.7	694	6	US-10-467-657-4602	Sequence 4602, Ap
1310	39	8.7	108	6	US-10-925-366A-169	Sequence 169, App	1385	39	8.7	703	6	US-10-821-234-1317	Sequence 1317, Ap
1311	39	8.7	108	6	US-10-925-366A-170	Sequence 170, App	1386	39	8.7	712	6	US-10-770-726-66	Sequence 66, Appl
1312	39	8.7	108	6	US-10-925-366A-171	Sequence 171, App	1387	39	8.7	721	7	US-11-060-920-5	Sequence 5, Appli
1313	39	8.7	108	6	US-10-925-366A-176	Sequence 176, App	1388	39	8.7	750	7	US-11-070-627-6	Sequence 6, Appli
1314	39	8.7	108	6	US-10-925-366A-178	Sequence 178, App	1389	39	8.7	768	7	US-11-147-109-10	Sequence 10, Appl
1315	39	8.7	108	6	US-10-925-366A-179	Sequence 179, App	1390	39	8.7	795	6	US-10-821-234-1002	Sequence 1002, Ap
1316	39	8.7	108	6	US-10-925-366A-180	Sequence 180, App	1391	39	8.7	858	6	US-10-878-556A-113	Sequence 113, App
1317	39	8.7	108	6	US-10-925-366A-182	Sequence 182, App	1392	39	8.7	944	6	US-10-793-626-3324	Sequence 3324, Ap
1318	39	8.7	108	6	US-10-925-366A-183	Sequence 183, App	1393	39	8.7	1073	6	US-10-467-657-5230	Sequence 5230, Ap
1319	39	8.7	108	6	US-10-925-366A-186	Sequence 186, App	1394	39	8.7	1206	7	US-11-058-727-2	Sequence 2, Appli
1320	39	8.7	108	6	US-10-925-366A-187	Sequence 187, App	1395	39	8.7	1206	7	US-11-108-389-2	Sequence 2, Appli
1321	39	8.7	108	6	US-10-925-366A-188	Sequence 188, App	1396	39	8.7	1210	7	US-11-058-727-4	Sequence 4, Appli
1322	39	8.7	108	6	US-10-925-366A-189	Sequence 189, App	1398	39	8.7	1210	7	US-11-108-172-692	Sequence 692, App
1323	39	8.7	108	6	US-10-925-366A-203	Sequence 203, App	1399	39	8.7	1342	6	US-10-770-726-63	Sequence 63, Appl
1325	39	8.7	108	6	US-10-925-366A-332	Sequence 332, App	1400	39	8.7	1342	7	US-11-113-202-12	Sequence 12, Appl
1326	39	8.7	108	7	US-11-075-351-63	Sequence 63, Appli	1401	39	8.7	1342	7	US-11-113-202-14	Sequence 14, Appl
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1328	39	8.7	108	7	US-11-127-932-11	Sequence 11, Appl	1403	39	8.7	1548	7	US-11-108-172-1095	Sequence 1095, Ap
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1330	39	8.7	129	6	US-10-721-763-23	Sequence 23, Appl	1405	39	8.7	2339	7	US-11-096-281-11	Sequence 11, Appl
1331	39	8.7	134	6	US-10-793-626-2374	Sequence 2374, Ap	1406	39	8.7	3002	6	US-10-821-234-916	Sequence 916, App
1332	39	8.7	158	6	US-10-995-561-1031	Sequence 1031, Ap	1407	39	8.7	7968	7	US-11-143-980-49	Sequence 49, Appl
1333	39	8.7	158	6	US-10-995-561-1032	Sequence 1032, Ap	1408	38.5	8.6	32	7	US-11-105-268-41	Sequence 41, Appl
1334	39	8.7	160	6	US-10-793-626-2940	Sequence 8, Appli	1409	38.5	8.6	74	6	US-10-925-366A-295	Sequence 295, App
1335	39	8.7	177	7	US-11-068-717-8	Sequence 1645, Ap	1410	38.5	8.6	78	6	US-10-925-366A-302	Sequence 302, App
1336	39	8.7	201	6	US-10-821-234-1645	Sequence 610, App	1411	38.5	8.6	93	6	US-10-999-866-10	Sequence 10, Appl
1337	39	8.7	208	6	US-10-793-626-610	Sequence 32, Appl	1412	38.5	8.6	93	7	US-11-061-821-10	Sequence 10, Appl
1338	39	8.7	222	7	US-11-170-653-32	Sequence 86, Appl	1413	38.5	8.6	93	7	US-11-186-284-179	Sequence 179, App
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1340	39	8.7	229	7	US-11-063-343-34	Sequence 84, Appl	1415	38.5	8.6	95	7	US-11-054-669-54	Sequence 54, Appl
1341	39	8.7	248	7	US-11-054-515-2086	Sequence 2086, Ap	1416	38.5	8.6	95	7	US-11-054-669-55	Sequence 55, Appl
1342	39	8.7	249	7	US-11-054-515-1160	Sequence 1160, Ap	1417	38.5	8.6	95	7	US-11-054-669-61	Sequence 61, Appl
1343	39	8.7	251	7	US-11-054-515-201	Sequence 201, App	1418	38.5	8.6	95	7	US-11-054-669-62	Sequence 62, Appl
1344	39	8.7	287	7	US-11-080-991-66	Sequence 66, Appl	1419	38.5	8.6	95	7	US-11-054-669-63	Sequence 63, Appl
1345	39	8.7	295	7	US-11-192-374-4	Sequence 4, Appli	1420	38.5	8.6	95	7	US-11-054-669-64	Sequence 64, Appl
1346	39	8.7	295	7	US-11-192-374-24	Sequence 24, Appl	1421	38.5	8.6	95	7	US-11-054-669-65	Sequence 65, Appl
1347	39	8.7	297	6	US-10-510-386-16	Sequence 16, Appl	1422	38.5	8.6	95	7	US-11-054-669-66	Sequence 66, Appl
1348	39	8.7	298	7	US-11-110-082-28	Sequence 28, Appl	1423	38.5	8.6	95	7	US-11-054-669-72	Sequence 72, Appl
1349	39	8.7	309	6	US-10-510-386-84	Sequence 84, Appl	1424	38.5	8.6	95	7	US-11-054-669-86	Sequence 86, Appl
1350	39	8.7	324	6	US-10-995-561-765	Sequence 765, App	1425	38.5	8.6	95	7	US-11-084-554-121	Sequence 121, App
1351	39	8.7	327	6	US-10-667-295-59	Sequence 59, Appl	1426	38.5	8.6	95	7	US-11-084-554-124	Sequence 124, App
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1354	39	8.7	346	7	US-11-077-386-24	Sequence 24, Appl	1429	38.5	8.6	95	7	US-11-084-554-129	Sequence 129, App
1355	39	8.7	348	6	US-10-878-556A-111	Sequence 111, App	1430	38.5	8.6	95	7	US-11-084-554-136	Sequence 136, App
1356	39	8.7	371	7	US-11-137-671-16	Sequence 16, Appl	1431	38.5	8.6	95	7	US-11-084-554-137	Sequence 137, App
1357	39	8.7	373	6	US-10-793-626-890	Sequence 890, App	1432	38.5	8.6	95	7	US-11-084-554-138	Sequence 138, App
1358	39	8.7	374	6	US-10-467-657-3088	Sequence 3088, Ap	1433	38.5	8.6	95	7	US-11-084-554-143	Sequence 143, App
1359	39	8.7	380	7	US-11-196-475-118	Sequence 118, App	1434	38.5	8.6	95	7	US-11-084-554-146	Sequence 146, App
1360	39	8.7	386	6	US-10-858-730-236	Sequence 236, App	1435	38.5	8.6	100	6	US-10-925-366A-172	Sequence 172, App

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1456	38.5	8.6	108	6	US-10-925-366A-194	Sequence 194, App
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1458	38.5	8.6	108	6	US-10-925-366A-196	Sequence 196, App
1459	38.5	8.6	108	6	US-10-925-366A-197	Sequence 197, App
1460	38.5	8.6	108	6	US-10-925-366A-198	Sequence 198, App
1461	38.5	8.6	108	6	US-10-925-366A-200	Sequence 200, App
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1463	38.5	8.6	108	6	US-10-925-366A-202	Sequence 202, App
1464	38.5	8.6	108	6	US-10-925-366A-205	Sequence 205, App
1465	38.5	8.6	108	6	US-10-925-366A-206	Sequence 206, App
1466	38.5	8.6	108	6	US-10-925-366A-207	Sequence 207, App
1467	38.5	8.6	108	6	US-10-925-366A-232	Sequence 232, App
1468	38.5	8.6	108	6	US-10-925-366A-237	Sequence 237, App
1469	38.5	8.6	108	6	US-10-925-366A-239	Sequence 239, App
1470	38.5	8.6	108	6	US-10-925-366A-284	Sequence 284, App
1471	38.5	8.6	108	6	US-10-925-366A-288	Sequence 288, App
1472	38.5	8.6	108	6	US-10-925-366A-290	Sequence 290, App
1473	38.5	8.6	108	6	US-10-925-366A-292	Sequence 292, App
1474	38.5	8.6	108	6	US-10-925-366A-297	Sequence 297, App
1475	38.5	8.6	108	6	US-10-665-658-2	Sequence 2, Appli
1476	38.5	8.6	108	7	US-11-173-071-16	Sequence 16, Appl
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1479	38.5	8.6	109	7	US-11-127-677-29	Sequence 29, Appl
1480	38.5	8.6	109	7	US-11-127-932-16	Sequence 16, Appl
1481	38.5	8.6	109	7	US-11-127-932-17	Sequence 17, Appl
1482	38.5	8.6	109	7	US-11-127-932-20	Sequence 20, Appl
1483	38.5	8.6	111	7	US-11-077-978-1	Sequence 1, Appli
1484	38.5	8.6	114	6	US-10-925-366A-12	Sequence 12, Appl
1485	38.5	8.6	127	7	US-11-193-512-71	Sequence 71, Appl
1486	38.5	8.6	127	7	US-11-193-512-88	Sequence 88, Appl
1487	38.5	8.6	128	6	US-10-721-763-31	Sequence 31, Appl
1488	38.5	8.6	131	6	US-10-721-763-27	Sequence 27, Appl
1489	38.5	8.6	140	6	US-10-967-093-4	Sequence 4, Appli
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1491	38.5	8.6	153	6	US-10-977-334-4	Sequence 4, Appli
1492	38.5	8.6	182	6	US-10-510-386-70	Sequence 70, Appl
1493	38.5	8.6	182	6	US-10-510-386-182	Sequence 182, App
1494	38.5	8.6	204	6	US-10-980-388-102	Sequence 102, App
1495	38.5	8.6	211	7	US-11-170-653-18	Sequence 18, Appl
1496	38.5	8.6	219	7	US-11-134-795-14	Sequence 14, Appl
1497	38.5	8.6	231	6	US-10-884-730-367	Sequence 367, App
1498	38.5	8.6	231	6	US-10-884-730-368	Sequence 368, App
1499	38.5	8.6	231	6	US-10-884-730-369	Sequence 369, App
1500	38.5	8.6	237	6	US-10-884-730-336	Sequence 336, App

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OM protein - protein search, using sw model
Run on: December 22, 2005, 02:28:47 ; Search time 228.571 Seconds
(without alignments)
153.783 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KGPLMCNSPSNSNANCEPSL.....RASSFHFDSEENKRLIHFS 80
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66703	standard; protein; 229 AA.				
DE	Membrane-bound protein PRO994.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 449;	DB 3;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.8e-43;				
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ID	AAU29122	standard; protein; 229 AA.				
DE	Human PRO polypeptide sequence #99.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
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RESULT 3						
ID	AAB87549	standard; protein; 229 AA.				
DE	Human PRO994.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
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RESULT 4						
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PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
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RESULT 5						
ID	ABG95874	standard; protein; 229 AA.				
DE	Human secreted/transmembrane protein PRO994.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 449;	DB 5;	Length 229;		
Best Local Similarity	100.0%;	Pred. No. 2.8e-43;				
RESULT 6						
ID	ABU58498	standard; protein; 229 AA.				

DE Human PRO polypeptide #99.
PN US2003027272-A1.
PD 06-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABU8046 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 8
ID ABU84361 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032112-A1.
PD 13-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABR66235 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027278-A1.
PD 06-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABR65625 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036159-A1.
PD 20-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 11
ID ABU99565 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040070-A1.
PD 27-FEB-2003.
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RESULT 12
ID ABU58041 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027163-A1.
PD 06-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 13
ID ABU59119 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO994.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 14
ID ABU82631 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003032023-A1.
PD 13-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 15
ID ABU82804 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 16
ID ABU89925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036147-A1.

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PD 20-FEB-2003.
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RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
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RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
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ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 30
ID ABU9450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 36
ID ABO33958 standard; protein; 229 AA.
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DE Human secreted/transmembrane protein PRO994.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 46
ID ABO11532 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

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PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID 198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.
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PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 80
ID ABUS9266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 81
ID ABUS371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 82
ID ABUS9061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 83
ID ABUS3141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 84
ID ABUS4997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 85
ID ABUS0545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 86
ID ABUS4056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 87
ID ABUS3707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 94
ID ABUS7029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 95
ID ABUS5981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 96
ID ABUS2268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human secreted polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.
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PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 147
ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
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RESULT 157
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 161
ID ABR8518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 166
ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 180
ID ABM77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 181
ID ABM27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 182
ID ABM06155 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 183
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 184
ID ABM35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 185
ID ABM26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 190
ID ABM11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 191
ID ABM02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 192
ID ABM16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 194
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 194
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ID ABM29094 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 222
ID ABO4940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 223
ID ABM08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 232
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
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PD 27-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 258
ID ABR88823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 449; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 270
ID ABM02441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 298

ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 310
ID ABM77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 312
ID ABM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 326
ID ABO51791 standard; protein; 229 AA.


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DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 334
ID ABM12555 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
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PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 355
ID ABR73111 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 365
ID ABO30553 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 367
ID ABM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 368
ID ABM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 369
ID ABM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 371
ID ABM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 375
ID ABM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 383
ID ABM26959 standard; protein; 229 AA.

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DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 388
ID ABO5332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
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PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 403
ID ABM03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 404
ID ABM19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 405
ID ABM19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 414
ID ABM01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 415
ID ABM02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 417
ID ABM12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 418
ID ABM30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 419
ID ABM24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 421
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ID ABO31263 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 422
ID ABM14390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 423
ID ABM09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 425
ID ABM34705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 430
ID ABR7720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 433
ID ABR93788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 434
ID ABM01831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 435
ID ABM78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 438
ID ABM27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 439
ID ABM13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
  RESULT 440
ID ABO31873 standard; protein; 229 AA.
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DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 443
ID ABO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 465
ID ABO41075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 466
ID ABO36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 467
ID ABO37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 469
ID ABM32449 standard; protein; 229 AA.

Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 470
ID ABO46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 474
ID ABM31839 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 478
ID ABM32449 standard; protein; 229 AA.

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DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 481
ID ABM31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 482
ID ABM30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 498
ID ADC82448 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 499
ID ADD05671 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 500
ID ADD08628 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 501
ID ADD06877 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 502
ID ADC83124 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 503
ID ADD55231 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 504
ID ADD36052 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 505
ID ADD56189 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 506
ID ADD54627 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 507
ID ADE26781 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 508
ID ADE26248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 509
ID ADF67185 standard; protein; 229 AA.
DE Human PRO994 amino acid sequence SEQ ID NO:258.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 510
ID ADG01053 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 511
ID ADG08606 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 512
ID ADG02666 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 513
ID ADG01373 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 514
ID ADF95548 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 515
ID ADF95227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 516
ID ADG12363 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;


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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 535
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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ID ADH57383 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 544
ID ADI35439 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 7; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 554
ID ADH9080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 555
ID ADI05068 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 556
ID ADI03418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 557
ID ADI04813 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 558
ID ADH78267 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 559
ID ADI19611 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 560
ID ADH90359 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 561
ID ADI03078 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 562
ID ADH77927 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 563

ID ADH97910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 564

ID ADI01295 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190665-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 565

ID ADI01990 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 566

ID ADI03248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 567

ID ADI11435 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 568

ID ADI02337 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 569

ID ADI11775 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 570

ID ADI05412 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 571

ID ADH79484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 7; Length 229;
RESULT 572

ID ADH79484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

ID ABM85217 standard; protein; 229 AA.
DE Human protein sequence hCP1734062.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 591
ID ADC52186 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 592
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 593
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 594
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 595
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 596
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 597
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 598
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 599
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 600
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 601
ID ADG6869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 602
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 603
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 604
ID ADH33732 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 605
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 606
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 607
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 608
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 609
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.


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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 627
ID ADH02205 standard; protein; 229 AA.
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DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 636
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 644
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 449; DB 8; Length 229;
  Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 645
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
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PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 646
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 647
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 648
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 649
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 650
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 651
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 652
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 653
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 654
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 655
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 656
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 657
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 658
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 659
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 660
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 661
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 662
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 663
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 664
ID ADRI4507 standard; protein; 229 AA.
DE Human NF-kappaB pathway-associated protein SeqID508.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 665
ID ADY77743 standard; protein; 229 AA.
DE Neoplastic disease detection protein PRO994.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 449; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 666
ID AEA38511 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #141.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 667
ID ABM85216 standard; protein; 230 AA.
DE Mouse protein sequence MCP5099.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 52.9%; Score 237.5; DB 7; Length 230;
Best Local Similarity 53.8%; Pred. No. 7.3e-19;
RESULT 668
ID ADT66602 standard; protein; 413 AA.
DE Murine aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match 16.3%; Score 73; DB 8; Length 413;
Best Local Similarity 26.2%; Pred. No. 15;
RESULT 669
ID ADP90666 standard; protein; 527 AA.
DE Mouse extracellular matrix protein #6.
PN JP2004180541-A.
PD 02-JUL-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (DANA-) DANAFOMU KK.
Query Match 15.7%; Score 70.5; DB 8; Length 527;
Best Local Similarity 30.9%; Pred. No. 39;
RESULT 670
ID AAB61263 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor.
PN WO200100810-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.6%; Score 70; DB 4; Length 631;
Best Local Similarity 24.0%; Pred. No. 56;
RESULT 671
ID ABB71337 standard; protein; 1079 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40803.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 15.6%; Score 70; DB 4; Length 1079;
Best Local Similarity 28.3%; Pred. No. 1.1e+02;
RESULT 672
ID AAG84914 standard; protein; 610 AA.
DE Shrimp white spot Bacilliform virus (WSBV) protein 5.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match 15.5%; Score 69.5; DB 4; Length 610;
Best Local Similarity 30.8%; Pred. No. 62;
RESULT 673
ID ABB98338 standard; protein; 292 AA.
DE Human anti-tenascin C monoclonal antibody SEQ ID NO 2.
PN JP2002234900-A.
PD 23-AUG-2002.
PA (MIED-) MIE DAIGAKUCHO.
Query Match 15.1%; Score 68; DB 6; Length 292;
Best Local Similarity 66.7%; Pred. No. 36;
RESULT 674
ID ADP04284 standard; protein; 292 AA.
DE Human tenascin C fibronectin III-like domain BCD domain polypeptide.
PN JP2004138489-A.
PD 13-MAY-2004.
PA (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 15.1%; Score 68; DB 8; Length 292;
Best Local Similarity 66.7%; Pred. No. 36;
RESULT 675
ID ADW18489 standard; protein; 362 AA.
DE Pinus radiata transcription factor protein NAC family Seq 2279.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 15.1%; Score 68; DB 9; Length 362;
Best Local Similarity 26.7%; Pred. No. 48;
RESULT 676
ID ADN05803 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #1065.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 15.1%; Score 68; DB 8; Length 2000;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
RESULT 677
ID ABO01379 standard; protein; 2108 AA.
DE Human protein NOV35b.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 68; DB 6; Length 2108;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 678
ID ADN96130 standard; protein; 2108 AA.
DE Human NOVX polypeptide #92.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (TCHE/) TCHERNEV V T.

PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2108;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 679
ID AAO30847 standard; protein; 2110 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.1%; Score 68; DB 7; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 680
ID ADM80773 standard; protein; 2110 AA.
DE Human CADECM-2 protein SEQ ID NO:2.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 681
ID ABM83292 standard; protein; 2116 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3541.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2116;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 682
ID ABM83291 standard; protein; 2122 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3540.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2122;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 683
ID ABG70361 standard; protein; 2167 AA.
DE Novel human thrombopoietin variant protein, NV-20.
PN US2002068342-A1.
PD 06-JUN-2002.
PA (KHOS/) KHOSRAVI R.
PA (BERN/) BERNSTEIN J.
Query Match 15.1%; Score 68; DB 5; Length 2167;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
RESULT 684
ID AAR94562 standard; protein; 2199 AA.
DE Human cytotoxicin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI) SCRIPPS RES INST.
Query Match 15.1%; Score 68; DB 2; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 685
ID ABO01378 standard; protein; 2199 AA.
DE Human protein NOV35a.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 68; DB 6; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 686
ID ADN96128 standard; protein; 2199 AA.
DE Human NOVX polypeptide #91.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 687
ID AAB36935 standard; protein; 2201 AA.
DE Human tenascin-C.
PN WO2000066628-A1.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 15.1%; Score 68; DB 4; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 688
ID ABP97745 standard; protein; 2201 AA.
DE Amino acid sequence of human HXB polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 15.1%; Score 68; DB 6; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 689
ID ABM78955 standard; protein; 2201 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.


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PD 12-SEP-2003.
PA (GEOU ) UNIV GEORGETOWN.
  Query Match      15.1%; Score 68; DB 7; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 690
ID ADD69400 standard; protein; 2201 AA.
DE Human tenascin protein - SEQ ID 136.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
  Query Match      15.1%; Score 68; DB 7; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 691
ID ADD47935 standard; protein; 2201 AA.
DE Human Protein XP_005348, SEQ ID NO 13631.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      15.1%; Score 68; DB 7; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 692
ID ADE62224 standard; protein; 2201 AA.
DE Human Protein P24821, SEQ ID NO 8153.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      15.1%; Score 68; DB 7; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 693
ID ADO17766 standard; protein; 2201 AA.
DE Differentially expressed protein Lul, SEQ ID 1.
PN WO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
  Query Match      15.1%; Score 68; DB 8; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 694
ID ADQ19756 standard; protein; 2201 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match      15.1%; Score 68; DB 8; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 695
ID ADU06359 standard; protein; 2201 AA.
DE Novel bronchial cancer-associated human protein SeqID583.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
  Query Match      15.1%; Score 68; DB 8; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 696
ID ADV70208 standard; protein; 2201 AA.
DE Tumor-associated antigenic target polypeptide TAT450.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH ) GENENTECH INC.
  Query Match      15.1%; Score 68; DB 9; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 697
ID ADW88533 standard; peptide; 2201 AA.
DE Human tenascin-C.
PN WO2005009366-A2.
PD 03-FEB-2005.
PA (CORR ) CORNELL RES FOUND INC.
  Query Match      15.1%; Score 68; DB 9; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 698
PD 12-SEP-2003.
PA (GEOU ) UNIV GEORGETOWN.
  Query Match      15.1%; Score 68; DB 7; Length 2201;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 699
ID ABM83293 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3543.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
  Query Match      15.1%; Score 68; DB 8; Length 2207;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 700
ID ABM83295 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3544.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
  Query Match      15.1%; Score 68; DB 8; Length 2207;
  Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 701
ID ABB49395 standard; protein; 296 AA.
DE Listeria monocytogenes protein #2099.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP ) INST PASTEUR.
  Query Match      14.9%; Score 67; DB 5; Length 296;
  Best Local Similarity 28.4%; Pred. No. 48;
RESULT 702
ID ABR41213 standard; protein; 337 AA.
DE Human DITHP receptor.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match      14.9%; Score 67; DB 6; Length 337;
  Best Local Similarity 24.0%; Pred. No. 57;
RESULT 703
ID AAE10579 standard; protein; 500 AA.
DE Human macrophage-expressed protein #4.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
  Query Match      14.9%; Score 67; DB 4; Length 500;
  Best Local Similarity 24.0%; Pred. No. 93;
RESULT 704
ID ABG10535 standard; protein; 500 AA.
DE Novel human diagnostic protein #10526.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match      14.9%; Score 67; DB 4; Length 500;
  Best Local Similarity 24.0%; Pred. No. 93;
RESULT 705
ID ADE62222 standard; protein; 619 AA.
DE Rat Protein AAA50761, SEQ ID NO 8151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match      14.9%; Score 67; DB 7; Length 619;
  Best Local Similarity 40.0%; Pred. No. 1.2e+02;
RESULT 706
ID ABU11229 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor protein.
PN WO200280968-A1.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match      14.9%; Score 67; DB 6; Length 631;
  Best Local Similarity 24.0%; Pred. No. 1.2e+02;
RESULT 707
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ID ABU12086 standard; protein; 632 AA.
DE Human NOV27a CG93884-01 protein SEQ ID 92.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
  Query Match 14.9%; Score 67; DB 6; Length 632;
  Best Local Similarity 24.0%; Pred. No. 1.3e+02;
RESULT 708
ID ABG01737 standard; protein; 161 AA.
DE Novel human diagnostic protein #1728.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 14.8%; Score 66.5; DB 4; Length 161;
  Best Local Similarity 29.5%; Pred. No. 26;
RESULT 709
ID ABR82240 standard; protein; 677 AA.
DE Human nucleic acid-associated protein (NAAP)-Id 2848827CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 14.8%; Score 66.5; DB 6; Length 677;
  Best Local Similarity 31.6%; Pred. No. 1.6e+02;
RESULT 710
ID ADQ66763 standard; protein; 926 AA.
DE Novel human protein sequence #1736.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 14.8%; Score 66.5; DB 8; Length 926;
  Best Local Similarity 31.6%; Pred. No. 2.3e+02;
RESULT 711
ID ABM92081 standard; protein; 1627 AA.
DE M. xanthus protein sequence, seq id 11280.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS ) MONSANTO TECHNOLOGY LLC.
  Query Match 14.8%; Score 66.5; DB 9; Length 1627;
  Best Local Similarity 28.6%; Pred. No. 4.7e+02;
RESULT 712
ID ADU82617 standard; protein; 1725 AA.
DE Human MDDT polypeptide (ID 7526175CD1).
PN WO200409390-A2.
PD 18-NOV-2004.
PA (INCY-) INCYTE CORP.
  Query Match 14.8%; Score 66.5; DB 8; Length 1725;
  Best Local Similarity 31.6%; Pred. No. 5.1e+02;
RESULT 713
ID ADT77471 standard; protein; 2046 AA.
DE Human nucleic acid-associated protein 7526176CD1.
PN WO2004087875-A2.
PD 14-OCT-2004.
PA (INCY-) INCYTE CORP.
  Query Match 14.8%; Score 66.5; DB 8; Length 2046;
  Best Local Similarity 31.6%; Pred. No. 6.3e+02;
RESULT 714
ID ADD47933 standard; protein; 575 AA.
DE Rat Protein AAA56909, SEQ ID NO 13629.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match 14.7%; Score 66; DB 7; Length 575;
  Best Local Similarity 66.7%; Pred. No. 1.4e+02;
RESULT 715
ID ADP09773 standard; protein; 1217 AA.
DE JNK3 human KIAA0569 protein.
PN WO2003086462-A1.
PD 23-OCT-2003.
PA (CELE-) CELESTAR LEXICO SCI INC.
PA (DAUC ) DAIICHI PHARM CO LTD.
  Query Match 14.7%; Score 66; DB 7; Length 1217;
  Best Local Similarity 27.5%; Pred. No. 3.7e+02;
RESULT 716
ID ABG12658 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12649.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 14.7%; Score 66; DB 4; Length 1219;
  Best Local Similarity 27.5%; Pred. No. 3.7e+02;
RESULT 717
ID AAM78969 standard; protein; 1279 AA.
DE Human protein SEQ ID NO 1631.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 14.7%; Score 66; DB 4; Length 1279;
  Best Local Similarity 27.5%; Pred. No. 4e+02;
RESULT 718
ID AAM79953 standard; protein; 1301 AA.
DE Human protein SEQ ID NO 3599.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 14.7%; Score 66; DB 4; Length 1301;
  Best Local Similarity 27.5%; Pred. No. 4e+02;
RESULT 719
ID AAR71382 standard; protein; 650 AA.
DE Drosophila semaphorin I protein.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC ) UNIV CALIFORNIA.
  Query Match 14.6%; Score 65.5; DB 2; Length 650;
  Best Local Similarity 31.8%; Pred. No. 1.9e+02;
RESULT 720
ID ABB64331 standard; protein; 771 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19785.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match 14.6%; Score 65.5; DB 4; Length 771;
  Best Local Similarity 31.8%; Pred. No. 2.4e+02;
RESULT 721
ID ABB68283 standard; protein; 905 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31641.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match 14.6%; Score 65.5; DB 4; Length 905;
  Best Local Similarity 27.3%; Pred. No. 2.9e+02;
RESULT 722
ID ABM84660 standard; protein; 452 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4909.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
  Query Match 14.5%; Score 65; DB 8; Length 452;
  Best Local Similarity 24.0%; Pred. No. 1.4e+02;
RESULT 723
ID ABM84659 standard; protein; 481 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4908.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
  Query Match 14.5%; Score 65; DB 8; Length 481;
  Best Local Similarity 24.0%; Pred. No. 1.5e+02;
RESULT 724
ID ADN99607 standard; protein; 512 AA.
DE Novel human protein sequence #423.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match 14.5%; Score 65; DB 8; Length 512;
  Best Local Similarity 24.0%; Pred. No. 1.6e+02;
RESULT 725
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ID AAM20306 standard; protein; 79 AA.
DE Peptide #6740 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 726
ID ABB40757 standard; peptide; 79 AA.
DE Peptide #8263 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 727
ID AAM34523 standard; protein; 79 AA.
DE Peptide #8560 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 728
ID ABB24972 standard; protein; 79 AA.
DE Protein #6971 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 729
ID AAM74409 standard; protein; 79 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34715.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 730
ID AAM61617 standard; protein; 79 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33722.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 731
ID ABG56204 standard; peptide; 79 AA.
DE Human liver peptide, SEQ ID NO 34852.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 732
ID ABG44311 standard; peptide; 79 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33976.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 5; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 733
ID ADN22431 standard; protein; 461 AA.
DE Bacterial polypeptide #5084.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 14.4%; Score 64.5; DB 8; Length 461;
Best Local Similarity 26.5%; Pred. No. 1.6e+02;
RESULT 734
ID ADI45315 standard; protein; 1185 AA.
DE Rice isoprenoid biosynthesis-associated protein #123.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match 14.4%; Score 64.5; DB 8; Length 1185;
Best Local Similarity 27.8%; Pred. No. 5.4e+02;
RESULT 735
ID ADN24041 standard; protein; 228 AA.
DE Bacterial polypeptide #6694.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 64; DB 8; Length 228;
Best Local Similarity 31.9%; Pred. No. 77;
RESULT 736
ID ABM87753 standard; protein; 959 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5999.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 14.3%; Score 64; DB 7; Length 959;
Best Local Similarity 26.6%; Pred. No. 4.7e+02;
RESULT 737
ID ADR43499 standard; protein; 3056 AA.
DE CSA-binding malarial variant surface antigen.
PN WO2004067559-A1.
PD 12-AUG-2004.
PA (UYKO-) UNIV KOBENHAVNS.
Query Match 14.3%; Score 64; DB 8; Length 3056;
Best Local Similarity 29.7%; Pred. No. 2e+03;
RESULT 738
ID AAB11524 standard; protein; 166 AA.
DE SEN virus protein fragment SEQ ID NO: 70.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 14.1%; Score 63.5; DB 3; Length 166;
Best Local Similarity 24.2%; Pred. No. 59;
RESULT 739
ID AEB27727 standard; protein; 155 AA.
DE Humanized 2H7 antibody light chain sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 155;
Best Local Similarity 29.9%; Pred. No. 62;
RESULT 740
ID ADS33303 standard; protein; 213 AA.
DE Anti-CD20 humanised antibody hu2H7v16, light chain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;

RESULT 741
ID ADW03409 standard; protein; 213 AA.
DE Humanized anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 15.
PN WO200500351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;
RESULT 742
ID AEB17637 standard; peptide; 213 AA.
DE Light chain peptide sequence of intact humanized 2H7 antibody.
PN WO2005061542-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;
RESULT 743
ID ADP79583 standard; protein; 232 AA.
DE 2H7.v16 L chain amino acid sequence SEQ ID NO:21.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 92;
RESULT 744
ID ADW03398 standard; protein; 232 AA.
DE Human anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 3.
PN WO200500351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 745
ID ADW21318 standard; protein; 232 AA.
DE Mouse anti-CD20 antibody 2H7 humanized clone v16, light chain.
PN WO200505462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 746
ID ADX00804 standard; protein; 232 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 3.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 747
ID ADY62624 standard; protein; 232 AA.
DE Humanized 2H7 antibody light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 748
ID ADD30256 standard; protein; 418 AA.
DE Plant yield-related protein from clone G1360.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 14.0%; Score 63; DB 7; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.2e+02;
RESULT 749
ID ADI44129 standard; protein; 418 AA.
DE Plant transcription factor related polypeptide #1653.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.

PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 14.0%; Score 63; DB 8; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.2e+02;
RESULT 750
ID ABB66230 standard; protein; 816 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25482.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.0%; Score 63; DB 4; Length 816;
Best Local Similarity 28.2%; Pred. No. 5e+02;
RESULT 751
ID ADS42707 standard; protein; 925 AA.
DE Bacterial polypeptide #21137.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 925;
Best Local Similarity 29.8%; Pred. No. 5.9e+02;
RESULT 752
ID ADN18779 standard; protein; 1165 AA.
DE Bacterial polypeptide #1432.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 1165;
Best Local Similarity 28.1%; Pred. No. 7.8e+02;
RESULT 753
ID AAB11504 standard; protein; 379 AA.
DE SEN virus protein fragment SEQ ID NO: 21.
PN WO20028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 379;
Best Local Similarity 25.6%; Pred. No. 2.2e+02;
RESULT 754
ID ADW08812 standard; protein; 412 AA.
DE Human protein which is up-regulated in HCV-infected tissue - SEQ ID 149.
PN EP1493750-A2.
PD 05-JAN-2005.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 13.9%; Score 62.5; DB 9; Length 412;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 755
ID ADJ68623 standard; protein; 413 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID429.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.9%; Score 62.5; DB 7; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 756
ID ADO55165 standard; protein; 413 AA.
DE Protein #67 with increased gene expression in renal cell carcinoma.

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PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 757
ID ADO19653 standard; protein; 413 AA.
DE Human PRO polypeptide #291.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 758
ID ABM81188 standard; protein; 413 AA.
DE Tumor-associated antigenic target (TAT) polypeptide PRO61502, SEQ:3067.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 759
ID ADP54767 standard; protein; 413 AA.
DE Human PRO protein sequence SEQ ID NO:743.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 760
ID ADP24138 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO:1316.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 761
ID ADT66598 standard; protein; 413 AA.
DE Human aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF ) GRUENENTHAL GMBH.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 762
ID ADY16030 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO 1836.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH ) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 9; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 763
ID ADY23183 standard; protein; 443 AA.
DE Plant full length insert polypeptide seqid 70967.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.9%; Score 62.5; DB 8; Length 443;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 764
ID AAB11509 standard; protein; 679 AA.
DE SEN virus protein fragment SEQ ID NO: 36.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 679;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 765
ID ADH87440 standard; protein; 711 AA.
DE Enterococcus faecalis polypeptide #1920.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 13.9%; Score 62.5; DB 7; Length 711;
Best Local Similarity 31.2%; Pred. No. 4.8e+02;
RESULT 766
ID AAE14710 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP ) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 734;
Best Local Similarity 30.3%; Pred. No. 5e+02;
RESULT 767
ID ADJ32529 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 734;
Best Local Similarity 30.3%; Pred. No. 5e+02;
RESULT 768
ID ABB64648 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20736.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 13.9%; Score 62.5; DB 4; Length 826;
Best Local Similarity 28.1%; Pred. No. 5.8e+02;
RESULT 769
ID AAE14709 standard; protein; 1466 AA.
DE Mouse beta4 integrin.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP ) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 770
ID ADJ32527 standard; protein; 1466 AA.
DE Mouse integrin beta4 subunit protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 771
ID ABO69591 standard; protein; 290 AA.
DE Pseudomonas aeruginosa polypeptide #1766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 290;
Best Local Similarity 24.6%; Pred. No. 1.8e+02;
RESULT 772
ID ABO77973 standard; protein; 372 AA.
DE Pseudomonas aeruginosa polypeptide #10148.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 372;
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
RESULT 773
ID AAG70883 standard; protein; 592 AA.
DE C albicans apoptosis associated protein #63.
PN WO200102550-A2.
PD 11-JAN-2001.
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PA (JANC) JANSSEN PHARM NV.
Query Match 13.8%; Score 62; DB 4; Length 592;
Best Local Similarity 27.3%; Pred. No. 4.4e+02;
RESULT 774
ID ADX95117 standard; protein; 823 AA.
DE Plant full length insert polypeptide seqid 57781.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.8%; Score 62; DB 8; Length 823;
Best Local Similarity 28.6%; Pred. No. 6.6e+02;
RESULT 775
ID ADN18993 standard; protein; 891 AA.
DE Bacterial polypeptide #1646.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.8%; Score 62; DB 8; Length 891;
Best Local Similarity 27.1%; Pred. No. 7.3e+02;
RESULT 776
ID ABR53813 standard; protein; 971 AA.
DE Protein sequence #SEQ ID 2491.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 6; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.1e+02;
RESULT 777
ID ADK65020 standard; protein; 971 AA.
DE Disease treating protein complex-derived protein #1506.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 7; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.1e+02;
RESULT 778
ID AAB84882 standard; protein; 1530 AA.
DE Human protein, SEQ ID 6.
PN WO200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 1530;
Best Local Similarity 28.2%; Pred. No. 1.4e+03;
RESULT 779
ID AEB41562 standard; protein; 1921 AA.
DE L. pneumophila protein SEQ ID NO 5894.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1921;
Best Local Similarity 25.6%; Pred. No. 1.9e+03;
RESULT 780
ID AEB38280 standard; protein; 1956 AA.
DE L. pneumophila protein SEQ ID NO 2612.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1956;

Best Local Similarity 25.6%; Pred. No. 2e+03;
RESULT 781
ID AAB84885 standard; protein; 2266 AA.
DE Human protein, SEQ ID 14.
PN WO200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.4e+03;
RESULT 782
ID ADX06502 standard; protein; 2266 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1067.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.8%; Score 62; DB 9; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.4e+03;
RESULT 783
ID ABG22400 standard; protein; 102 AA.
DE Novel human diagnostic protein #22391.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 61.5; DB 4; Length 102;
Best Local Similarity 27.3%; Pred. No. 54;
RESULT 784
ID ADM05710 standard; protein; 122 AA.
DE Human protein of the invention SEQ ID NO:4395.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.7%; Score 61.5; DB 7; Length 122;
Best Local Similarity 25.6%; Pred. No. 68;
RESULT 785
ID ADO05882 standard; peptide; 130 AA.
DE C. jacchus M3-24 MOG-specific Ig kappa light chain Fab fragment.
PN WO2004034031-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 13.7%; Score 61.5; DB 8; Length 130;
Best Local Similarity 30.3%; Pred. No. 74;
RESULT 786
ID ADC85015 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 787
ID ADC85018 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 788
ID ADC85012 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 789
ID ADY24666 standard; protein; 616 AA.
DE Plant full length insert polypeptide seqid 72450.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.

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PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match      13.7%; Score 61.5; DB 8; Length 616;
  Best Local Similarity 25.0%; Pred. No. 5.2e+02;
RESULT 790
ID ADW18493 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 2283.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
  Query Match      13.7%; Score 61.5; DB 9; Length 1024;
  Best Local Similarity 27.1%; Pred. No. 9.9e+02;
RESULT 791
ID ADW17829 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 1606.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
  Query Match      13.7%; Score 61.5; DB 9; Length 1024;
  Best Local Similarity 27.1%; Pred. No. 9.9e+02;
RESULT 792
ID AD943681 standard; protein; 1034 AA.
DE Bacterial polypeptide #22111.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
  Query Match      13.7%; Score 61.5; DB 8; Length 1034;
  Best Local Similarity 28.8%; Pred. No. 1e+03;
RESULT 793
ID ADS05365 standard; protein; 45 AA.
DE Staphylococcus epidermis polypeptide seqid 4660.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
  Query Match      13.6%; Score 61; DB 8; Length 45;
  Best Local Similarity 42.9%; Pred. No. 22;
RESULT 794
ID AAB56760 standard; protein; 187 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1338.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
  Query Match      13.6%; Score 61; DB 3; Length 187;
  Best Local Similarity 26.2%; Pred. No. 1.3e+02;
RESULT 795
ID ADZ59470 standard; protein; 283 AA.
DE L19 antibody protein with N-terminal linker & C-terminal tagged peptide.
PN WO2005037312-A2.
PD 28-APR-2005.
PA (SCHD ) SCHERING AG.
  Query Match      13.6%; Score 61; DB 9; Length 283;
  Best Local Similarity 27.5%; Pred. No. 2.2e+02;
RESULT 796
ID AAR20807 standard; protein; 311 AA.
DE Human CDw32 antigen.
PN WO201049-A.
PD 23-JAN-1992.
PA (GEOH ) GEN HOSPITAL CORP.
  Query Match      13.6%; Score 61; DB 2; Length 311;
  Best Local Similarity 40.6%; Pred. No. 2.5e+02;
RESULT 797
ID AAM48902 standard; protein; 365 AA.
DE Aminotransferase related human protein.
PN WO200192490-A2.
PD 06-DEC-2001.
PA (APPL-) APPLERA CORP.

  Query Match      13.6%; Score 61; DB 5; Length 365;
  Best Local Similarity 25.0%; Pred. No. 3.1e+02;
RESULT 798
ID ADB85178 standard; protein; 413 AA.
DE Rat aspartate aminotransferase SEQ ID NO:59.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN ) WARNER LAMBERT CO.
  Query Match      13.6%; Score 61; DB 7; Length 413;
  Best Local Similarity 25.0%; Pred. No. 3.6e+02;
RESULT 799
ID ADT66600 standard; protein; 413 AA.
DE Rat aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF ) GRUENENTHAL GMBH.
  Query Match      13.6%; Score 61; DB 8; Length 413;
  Best Local Similarity 25.0%; Pred. No. 3.6e+02;
RESULT 800
ID AAU15075 standard; protein; 715 AA.
DE Protein encoded by C. albicans essential gene CayJL090C (DPB11).
PN WO200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
  Query Match      13.6%; Score 61; DB 4; Length 715;
  Best Local Similarity 35.9%; Pred. No. 7.2e+02;
RESULT 801
ID ABP73165 standard; protein; 715 AA.
DE Candida albicans essential protein SEQ ID NO 7002.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match      13.6%; Score 61; DB 5; Length 715;
  Best Local Similarity 35.9%; Pred. No. 7.2e+02;
RESULT 802
ID ABB62311 standard; protein; 788 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match      13.6%; Score 61; DB 4; Length 788;
  Best Local Similarity 26.6%; Pred. No. 8.1e+02;
RESULT 803
ID AAR94563 standard; protein; 1810 AA.
DE Chicken cytotoxin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI ) SCRIPPS RES INST.
  Query Match      13.6%; Score 61; DB 2; Length 1810;
  Best Local Similarity 46.2%; Pred. No. 2.3e+03;
RESULT 804
ID ADS85087 standard; protein; 2019 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID89.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
  Query Match      13.6%; Score 61; DB 8; Length 2019;
  Best Local Similarity 55.6%; Pred. No. 2.7e+03;
RESULT 805
ID ADY24980 standard; protein; 436 AA.
DE Plant full length insert polypeptide seqid 72764.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match      13.5%; Score 60.5; DB 8; Length 436;
  Best Local Similarity 26.0%; Pred. No. 4.4e+02;
RESULT 806
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ID ABU24178 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #9705.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match      13.5%; Score 60.5; DB 6; Length 444;
  Best Local Similarity 29.3%; Pred. No. 4.5e+02;
RESULT 807
ID ABG92810 standard; protein; 588 AA.
DE Protein encoded by fungal peptide synthetase gene cluster ORF16.
PN WO200242444-A2.
PD 30-MAY-2002.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA (CORR ) CORNELL RES FOUND INC.
PA (YODE/) YODER O.
PA (TURG/) TURGEON B G.
PA (LUSS/) LU S.
  Query Match      13.5%; Score 60.5; DB 5; Length 588;
  Best Local Similarity 25.0%; Pred. No. 6.4e+02;
RESULT 808
ID AAU96804 standard; protein; 890 AA.
DE Human immunodeficiency virus type 2 derived polypeptide #4.
PN US2002051967-A1.
PD 02-MAY-2002.
PA (INSP ) INST PASTEUR.
  Query Match      13.5%; Score 60.5; DB 5; Length 890;
  Best Local Similarity 22.9%; Pred. No. 1.1e+03;
RESULT 809
ID ADO00996 standard; protein; 937 AA.
DE Mouse homologue of Fruit fly AD-related protein CG10198.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
  Query Match      13.5%; Score 60.5; DB 8; Length 937;
  Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 810
ID ADO07917 standard; protein; 937 AA.
DE Rat polypeptide.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
  Query Match      13.5%; Score 60.5; DB 8; Length 937;
  Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 811
ID ABR53184 standard; protein; 992 AA.
DE Protein sequence #SEQ ID 1233.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
  Query Match      13.5%; Score 60.5; DB 6; Length 992;
  Best Local Similarity 19.8%; Pred. No. 1.2e+03;
RESULT 812
ID ADK63220 standard; protein; 992 AA.
DE Disease treating protein complex-derived protein #736.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
  Query Match      13.5%; Score 60.5; DB 7; Length 992;
  Best Local Similarity 19.8%; Pred. No. 1.2e+03;
RESULT 813
ID ADI27180 standard; protein; 1611 AA.
DE Human LRP binding family protein #11.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
  Query Match      13.5%; Score 60.5; DB 8; Length 1611;
  Best Local Similarity 28.1%; Pred. No. 2.3e+03;
RESULT 814
ID ABP31105 standard; protein; 116 AA.
DE Human ORF78 protein, SEQ ID NO:156.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.

  Query Match      13.4%; Score 60; DB 5; Length 116;
  Best Local Similarity 26.5%; Pred. No. 95;
RESULT 815
ID AAO03609 standard; protein; 141 AA.
DE Human polypeptide SEQ ID NO 17501.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
  Query Match      13.4%; Score 60; DB 4; Length 141;
  Best Local Similarity 24.2%; Pred. No. 1.2e+02;
RESULT 816
ID AAE35326 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.
PN EP1258255-A1.
PD 20-NOV-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
  Query Match      13.4%; Score 60; DB 6; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 817
ID AAE34878 standard; protein; 213 AA.
DE BIWA4/8 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
  Query Match      13.4%; Score 60; DB 6; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 818
ID AAE34877 standard; protein; 213 AA.
DE BIWA4 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
  Query Match      13.4%; Score 60; DB 6; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 819
ID ADL15441 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.
PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
  Query Match      13.4%; Score 60; DB 8; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 820
ID ADL15445 standard; protein; 213 AA.
DE Humanised murine antibody BIWA8 light chain protein.
PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
  Query Match      13.4%; Score 60; DB 8; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 821
ID ADO00849 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 4 light chain protein SEQ ID NO:4.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
  Query Match      13.4%; Score 60; DB 8; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 822
ID ADO00853 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
  Query Match      13.4%; Score 60; DB 8; Length 213;
  Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 823
ID AEB29787 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain A.
PN WO2005065717-A2.
PD 21-JUL-2005.
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PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 824
ID AEB29791 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain B.
PN WO2005065717-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 825
ID AEB29782 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain B.
PN WO2005065709-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 826
ID AEB29778 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain A.
PN WO2005065709-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 827
ID ADY70960 standard; protein; 214 AA.
DE Human monoclonal antibody CRJA light chain.
PN WO2005023849-A2.
PD 17-MAR-2005.
PA (CRUC-) CRUCELL HOLLAND BV.
Query Match 13.4%; Score 60; DB 9; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.1e+02;
RESULT 828
ID ABR01492 standard; protein; 215 AA.
DE Human anti-TIMP-1 antibody light chain #33.
PN WO200286085-A2.
PD 31-OCT-2002.
PA (FARB) BAYER CORP.
PA (MORP-) MORPHOSYS AG.
Query Match 13.4%; Score 60; DB 6; Length 215;
Best Local Similarity 29.9%; Pred. No. 2.1e+02;
RESULT 829
ID AAO14066 standard; protein; 234 AA.
DE Light chain protein of the monoclonal antibody from clone JA.
PN WO200188132-A2.
PD 22-NOV-2001.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 5; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.3e+02;
RESULT 830
ID ABU08018 standard; protein; 234 AA.
DE Human monoclonal rabies virus antibody light chain, clone JH, protein.
PN WO2003016501-A2.
PD 27-FEB-2003.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 6; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.3e+02;
RESULT 831
ID ADF65776 standard; protein; 234 AA.
DE Human monoclonal rabies virus antibody light chain.
PN US2003157112-A1.
PD 21-AUG-2003.
PA (HOOP/) HOOPER D C.
PA (DIET/) DIETZSCHOLD B.
Query Match 13.4%; Score 60; DB 7; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.3e+02;

RESULT 832
ID ADJ92516 standard; protein; 234 AA.
DE Human SOJA monoclonal antibody light chain protein.
PN US2004013672-A1.
PD 22-JAN-2004.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.3e+02;
RESULT 833
ID AAB82912 standard; protein; 241 AA.
DE Human immune response protein HIRP1.
PN WO200168696-A1.
PD 20-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.4%; Score 60; DB 4; Length 241;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 834
ID ADV86419 standard; protein; 482 AA.
DE Novel Clq domain-containing protein #40.
PN US2004248156-A1.
PD 09-DEC-2004.
PA (HUTT/) HU T.
PA (TANG/) TANG Y T.
PA (GHOS/) GHOSH M J.
PA (WANG/) WANG J.
PA (WANG/) WANG Z.
PA (ZHAO/) ZHAO Q.
PA (XUCC/) XU C.
PA (MULE/) MULERO J.
Query Match 13.4%; Score 60; DB 9; Length 482;
Best Local Similarity 29.3%; Pred. No. 5.7e+02;
RESULT 835
ID ABM68541 standard; protein; 920 AA.
DE Photorhabdus luminescens protein sequence #1638.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.4%; Score 60; DB 6; Length 920;
Best Local Similarity 29.8%; Pred. No. 1.3e+03;
RESULT 836
ID AAU30825 standard; protein; 962 AA.
DE Novel human secreted protein #1316.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 60; DB 4; Length 962;
Best Local Similarity 24.6%; Pred. No. 1.4e+03;
RESULT 837
ID AAU48592 standard; protein; 1341 AA.
DE Propionibacterium acnes immunogenic protein #9488.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 60; DB 4; Length 1341;
Best Local Similarity 26.5%; Pred. No. 2.1e+03;
RESULT 838
ID ABM45111 standard; protein; 1341 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9787.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 60; DB 6; Length 1341;
Best Local Similarity 26.5%; Pred. No. 2.1e+03;
RESULT 839
ID ADL70800 standard; protein; 213 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 73.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 13.3%; Score 59.5; DB 8; Length 213;
Best Local Similarity 28.8%; Pred. No. 2.3e+02;
RESULT 840

ID ABM84937 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5186.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.3%; Score 59.5; DB 8; Length 225;
Best Local Similarity 32.1%; Pred. No. 2.5e+02;
RESULT 841
ID ABP63108 standard; protein; 384 AA.
DE FLO11 gene expression regulator At27.
PN WO200257456-A2.
PD 25-JUL-2002.
PA (MICR-) MICROBIA.
Query Match 13.3%; Score 59.5; DB 5; Length 384;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
RESULT 842
ID ABM85836 standard; protein; 393 AA.
DE Mouse protein sequence mCPI3663.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.3%; Score 59.5; DB 7; Length 393;
Best Local Similarity 27.7%; Pred. No. 5.1e+02;
RESULT 843
ID AAB42218 standard; protein; 436 AA.
DE Human ORFX ORF1982 polypeptide sequence SEQ ID NO:3964.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 3; Length 436;
Best Local Similarity 28.4%; Pred. No. 5.8e+02;
RESULT 844
ID AEA20121 standard; protein; 650 AA.
DE Novel human polypeptide SEQ ID NO 815.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 650;
Best Local Similarity 28.4%; Pred. No. 9.5e+02;
RESULT 845
ID ADZ84991 standard; protein; 668 AA.
DE Partial FHOS interacting protein, mAK044679(668).
PN US2005100966-A1.
PD 12-MAY-2005.
PA (SAKA/) SAKAMOTO T.
PA (TAKE/) TAKEDA S.
Query Match 13.3%; Score 59.5; DB 9; Length 668;
Best Local Similarity 28.4%; Pred. No. 9.9e+02;
RESULT 846
ID AEA20120 standard; protein; 725 AA.
DE Novel human polypeptide SEQ ID NO 814.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 725;
Best Local Similarity 28.4%; Pred. No. 1.1e+03;
RESULT 847
ID ADS44222 standard; protein; 821 AA.
DE Bacterial polypeptide #22652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 59.5; DB 8; Length 821;
Best Local Similarity 28.9%; Pred. No. 1.3e+03;
RESULT 848
ID ABG79353 standard; protein; 884 AA.
DE Human GPCR15 protein.
PN WO200264793-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 5; Length 884;
Best Local Similarity 30.0%; Pred. No. 1.4e+03;
RESULT 849
ID AAM40399 standard; protein; 1150 AA.
DE Human polypeptide SEQ ID NO 3544.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 59.5; DB 4; Length 1150;
Best Local Similarity 28.4%; Pred. No. 2e+03;
RESULT 850
ID ADE59446 standard; protein; 1152 AA.
DE Human Protein XP_047123, SEQ ID NO 5341.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.3%; Score 59.5; DB 7; Length 1152;
Best Local Similarity 28.4%; Pred. No. 2e+03;
RESULT 851
ID AAY81947 standard; protein; 1330 AA.
DE Heterosigma akashiwo Na+-ATPase protein.
PN JP2000050874-A.
PD 22-FEB-2000.
PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.
Query Match 13.3%; Score 59.5; DB 3; Length 1330;
Best Local Similarity 25.9%; Pred. No. 2.3e+03;
RESULT 852
ID AEA20119 standard; protein; 1709 AA.
DE Novel human polypeptide SEQ ID NO 813.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 1709;
Best Local Similarity 28.4%; Pred. No. 3.2e+03;
RESULT 853
ID ABU00419 standard; protein; 105 AA.
DE Human novel polypeptide #512.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 59; DB 6; Length 105;
Best Local Similarity 26.8%; Pred. No. 1.1e+02;
RESULT 854
ID ADD14077 standard; protein; 146 AA.
DE Human src biomarker polypeptide SEQ ID NO:266.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 855
ID ADD44869 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 10300.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 856
ID ADD47797 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 13493.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 857
ID ADD48851 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 14562.

PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 858
ID ADJ69511 standard; protein; 146 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1317.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 859
ID ABM81767 standard; protein; 146 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82609, SEQ:4554.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 8; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 860
ID ADY14610 standard; protein; 146 AA.
DE PRO polypeptide SEQ ID NO 416.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 9; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 861
ID AAB32861 standard; protein; 153 AA.
DE Eucalyptus grandis transcription factor protein sequence #319.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 13.1%; Score 59; DB 3; Length 153;
Best Local Similarity 31.9%; Pred. No. 1.8e+02;
RESULT 862
ID AAW74475 standard; protein; 155 AA.
DE Amino acid sequence of human Cytochrome B5.
PN WO9836071-A1.
PD 20-AUG-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 13.1%; Score 59; DB 2; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 863
ID AAG73876 standard; protein; 155 AA.
DE Human colon cancer antigen protein SEQ ID NO:4640.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 4; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 864
ID ABP41469 standard; protein; 155 AA.
DE Human ovarian antigen HPDOC39, SEQ ID NO:2601.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 5; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 865
ID ABR41609 standard; protein; 155 AA.
DE Human dITHP electron transfer-associated protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.1%; Score 59; DB 6; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 866

ID AAB43457 standard; protein; 169 AA.
DE Human cancer associated protein sequence SEQ ID NO:902.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 3; Length 169;
Best Local Similarity 34.2%; Pred. No. 2e+02;
RESULT 867
ID AAY08599 standard; protein; 214 AA.
DE Anti-human TNF-alpha monoclonal antibody L-chain protein.
PN JP11127855-A.
PD 18-MAY-1999.
PA (NIHA) JAPAN ENERGY CORP.
Query Match 13.1%; Score 59; DB 2; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.7e+02;
RESULT 868
ID ADL70799 standard; protein; 214 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 72.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 13.1%; Score 59; DB 8; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.7e+02;
RESULT 869
ID AAB75036 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 870
ID AAB75038 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CE8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 871
ID AAB75034 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC2K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 872
ID AAB75037 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CD7K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 873
ID AAB75039 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC6K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 874
ID ADN04732 standard; protein; 227 AA.
DE Antipsoriatic protein sequence #547.
PN WO2004028479-A2.
PD 08-APR-2004.

PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 8; Length 227;
Best Local Similarity 33.3%; Pred. No. 2.9e+02;
RESULT 875
ID ADW18317 standard; protein; 246 AA.
DE Eucalyptus grandis transcription factor protein MYB family Seq 2104.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.1%; Score 59; DB 9; Length 246;
Best Local Similarity 31.9%; Pred. No. 3.2e+02;
RESULT 876
ID ABB59849 standard; protein; 600 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.1%; Score 59; DB 4; Length 600;
Best Local Similarity 21.9%; Pred. No. 9.8e+02;
RESULT 877
ID ABO78248 standard; protein; 641 AA.
DE Pseudomonas aeruginosa polypeptide #10423.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.1%; Score 59; DB 7; Length 641;
Best Local Similarity 31.6%; Pred. No. 1.1e+03;
RESULT 878
ID AAU74519 standard; protein; 1781 AA.
DE Lactobacillus reuteri glucosyltransferase A (gtfa) polypeptide.
PN WO200190372-A1.
PD 29-NOV-2001.
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
Query Match 13.1%; Score 59; DB 5; Length 1781;
Best Local Similarity 23.7%; Pred. No. 3.9e+03;
RESULT 879
ID ABG14083 standard; protein; 104 AA.
DE Novel human diagnostic protein #14074.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 104;
Best Local Similarity 30.0%; Pred. No. 1.2e+02;
RESULT 880
ID ADP74724 standard; protein; 137 AA.
DE Human porimin protein SEQ ID NO: 6.
PN WO2004047762-A2.
PD 10-JUN-2004.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 137;
Best Local Similarity 28.0%; Pred. No. 1.8e+02;
RESULT 881
ID AAB11523 standard; protein; 166 AA.
DE SEN virus protein fragment SEQ ID NO: 69.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.0%; Score 58.5; DB 3; Length 166;
Best Local Similarity 24.4%; Pred. No. 2.2e+02;
RESULT 882
ID AAU14973 standard; protein; 177 AA.
DE Novel bone marrow polypeptide #179.
PN WO200155442-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 177;
Best Local Similarity 28.0%; Pred. No. 2.4e+02;
RESULT 883
ID AAG68168 standard; protein; 207 AA.
DE Zmax1 signaling pathway analysis bait protein.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 13.0%; Score 58.5; DB 4; Length 207;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 884
ID ABR41135 standard; protein; 207 AA.
DE LRP5 related yeast two hybrid protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 207;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 885
ID ADB98802 standard; protein; 207 AA.
DE LRP5-related protein #9.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 207;
Best Local Similarity 26.2%; Pred. No. 2.9e+02;
RESULT 886
ID AAY66761 standard; protein; 208 AA.
DE Membrane-bound protein PRO1271.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 3; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 887
ID AAY94908 standard; protein; 208 AA.
DE Human secreted protein clone ci52_2 protein sequence SEQ ID NO:22.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 13.0%; Score 58.5; DB 3; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 888
ID AAE06585 standard; protein; 208 AA.
DE Human protein having hydrophobic domain, HP10753.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 889
ID AAU12426 standard; protein; 208 AA.
DE Human PRO1271 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 890
ID AAU14891 standard; protein; 208 AA.
DE Novel bone marrow polypeptide #97.
PN WO200155442-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 891
ID AAE01725 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:137.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 892
ID AAE01683 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:95.
PN WO200134767-A2.

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PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 893
ID AAE01724 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:136.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 894
ID AAE01723 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:135.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 895
ID AAE03766 standard; protein; 208 AA.
DE Human gene 3 encoded secreted protein HNTAC64, SEQ ID NO:36.
PN WO200132837-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 896
ID AAB88375 standard; protein; 208 AA.
DE Human membrane or secretory protein clone PSEC0111.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 897
ID AAG81329 standard; protein; 208 AA.
DE Human AFP protein sequence SEQ ID NO:176.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 898
ID AAB50924 standard; protein; 208 AA.
DE Human PRO1271 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 899
ID AAB65284 standard; protein; 208 AA.
DE Human PRO1271 (UNQ641) protein sequence SEQ ID NO:416.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 900
ID ABG63986 standard; protein; 208 AA.
DE Human albumin fusion protein #661.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 901
ID ABG63987 standard; protein; 208 AA.
DE Human albumin fusion protein #662.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 902
ID ABG63985 standard; protein; 208 AA.
DE Human albumin fusion protein #660.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 903
ID ABG65496 standard; protein; 208 AA.
DE Human albumin fusion protein #2171.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 904
ID ABG63988 standard; protein; 208 AA.
DE Human albumin fusion protein #663.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 905
ID ABUS8099 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 906
ID ABUS9177 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1271.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 907
ID ABUS2689 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 908
ID ABO17870 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 909
ID ABUS60608 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 910
ID ABU13990 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
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RESULT 911
ID ABU81124 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 912
ID ABU72575 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 913
ID ABU66824 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 914
ID ABU59905 standard; protein; 208 AA.
DE Novel secreted and transmembrane protein PRO1271.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 915
ID ABU59324 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 916
ID ABO26021 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 917
ID ABO25095 standard; protein; 208 AA.
DE Human secreted/transmembrane protein (PRO) #255.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 918
ID ABU59030 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 919
ID ABU92408 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 920
ID ABU59473 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1375.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 921
ID ABU67100 standard; protein; 208 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 510.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 922
ID ABU92239 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 923
ID ABU10945 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 924
ID ABU81697 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 925
ID ABU88636 standard; protein; 208 AA.
DE Human secreted and transmembrane polypeptide PRO1271.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 926
ID ABO34150 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 927
ID ADA6029 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 928
ID ADA76460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 929
ID ADA19110 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
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Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 930
ID ADA61733 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 931
ID ADB19518 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 932
ID ADB28059 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 933
ID ADA86538 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 934
ID ADB16102 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 935
ID ADA37927 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 936
ID ADA47888 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 937
ID ADA21613 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 938
ID ADA10400 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, PRO1271.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 939
ID ADA67683 standard; protein; 208 AA.
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DE Human PRO polypeptide #255.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 940
ID ADB30690 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 941
ID ADA85986 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 942
ID ADA17944 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 943
ID ADA97198 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 944
ID ADA79502 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 945
ID ADA87641 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 946
ID ADB16843 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 947
ID ADA28052 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 948
ID ADA91935 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082694-A1.
PD 01-MAY-2003.
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PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 949
ID ADB14998 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 950
ID ADB18959 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 951
ID ADA94174 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 952
ID ADB20070 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 953
ID ADB13382 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 954
ID ABO43403 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 955
ID ADA94632 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 956
ID ADA74636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 957
ID ADB24869 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 958
ID ADA82393 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 959
ID ADA75356 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 960
ID ADA85434 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 961
ID ADA84982 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 962
ID ADB30138 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 963
ID ADA80666 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 964
ID ADA75908 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 965
ID ADA38857 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 966
ID ADA47133 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 6; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 967
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ID ADB25429 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 968
ID ADA93605 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 969
ID ADB26955 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 970
ID ADB31242 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 971
ID ADA92978 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 972
ID ADA61170 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 973
ID ADB24317 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 974
ID ADA96646 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 975
ID ADA81218 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 976
ID ADA96094 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 977
ID ADB26403 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 978
ID ADB21888 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 6; Length 208;
RESULT 979
ID ADA77667 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 980
ID ADB18407 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 981
ID ADA87090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 982
ID ADA88193 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 983
ID ADA46581 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 984
ID ADB28611 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 985
ID ADB29163 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082706-A1.
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 986
ID ABO53236 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 987
ID ADA77115 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 988
ID ADA22539 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 989
ID ADA88745 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 990
ID ADA97750 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 991
ID ADB27507 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 992
ID ADB22440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 993
ID ABO22606 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 994
ID ADA06705 standard; protein; 208 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 995
ID ADA39398 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 996
ID ADA67131 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 997
ID ADB22992 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 998
ID ADB23765 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 999
ID ADA92487 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1000
ID ADB15550 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1001
ID ADB38802 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1002
ID ADB96424 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1003
ID ADB38250 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1004
ID ADB66722 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1005
ID ADB89802 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1006
ID ADB90534 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1007
ID ADB39635 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1008
ID ADB47258 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1009
ID ADB86865 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1010
ID ADB77470 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1011
ID ADB34627 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1012
ID ADB35731 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1013
ID ADB34075 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1014
ID ADB35179 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1015
ID ADB36283 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1016
ID ADB46678 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1017
ID ADC57896 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1018
ID ADC55260 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1019
ID ADC12127 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1020
ID ADC56549 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1021
ID ADC07604 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1022
ID ADC11594 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1023
ID ADC50551 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1024
ID ADC72098 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1025
ID ADC60077 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1026
ID ADC53084 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1027
ID ADC57438 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1028
ID ADC60629 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1029
ID ADC51104 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1030
ID ADC65631 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1031
ID ADC54729 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1032
ID ADC53690 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1033
ID ADC59213 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1034
ID ADC56091 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1035
ID ADC58661 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1036
ID ADC14716 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1037
ID ADD08248 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1038
ID ADD03335 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1039
ID ADC90327 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1040
ID ADC82073 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1041
ID ADC69746 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1042
ID ADC48635 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
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PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1043
  ID ADD10164 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194776-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1044
  ID ADD07715 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2002193299-A1.
  PD 19-DEC-2002.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1045
  ID ADD04739 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003087354-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1046
  ID ADC82606 standard; protein; 208 AA.
  DE Human PRO polypeptide #131.
  PN US2003059833-A1.
  PD 27-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1047
  ID ADC80695 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003092103-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1048
  ID ADD11202 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194774-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1049
  ID ADC48083 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194771-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1050
  ID ADD08786 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003073090-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1051
  ID ADC80143 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003087358-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1052
  ID ADD07035 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2002193300-A1.
  PD 19-DEC-2002.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1053
  ID ADD09612 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194775-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1054
  ID ADC83282 standard; protein; 208 AA.
  DE Human PRO polypeptide #131.
  PN US2003059783-A1.
  PD 27-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1055
  ID ADD41325 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003203438-A1.
  PD 30-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1056
  ID ADD52464 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194769-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1057
  ID ADD53204 standard; protein; 208 AA.
  DE Human PRO polypeptide #255.
  PN US2003194792-A1.
  PD 16-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1058
  ID ADD53756 standard; protein; 208 AA.
  DE Novel human secreted and transmembrane protein PRO1271.
  PN US2003203437-A1.
  PD 30-OCT-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1059
  ID ADD55389 standard; protein; 208 AA.
  DE Human PRO polypeptide #131.
  PN US2003077593-A1.
  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1060
  ID ADD56347 standard; protein; 208 AA.
  DE Human PRO polypeptide #131.
  PN US2003077594-A1.
  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
  RESULT 1061
  ID ADD51912 standard; protein; 208 AA.
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DE Human PRO polypeptide #255.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1062
ID ADD02711 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1063
ID ADD02145 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1064
ID ADD54327 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1065
ID ADD54785 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1066
ID ADD92644 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1067
ID ADD91540 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1068
ID ADE04154 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1069
ID ADE26939 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1070
ID ADE32451 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194765-A1.

PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1071
ID ADE22383 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1072
ID ADD79607 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1073
ID ADE42143 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1074
ID ADE17960 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1075
ID ADD92092 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1076
ID ADE33555 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1077
ID ADE34107 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1078
ID ADD80159 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      13.0%; Score 58.5; DB 7; Length 208;
  Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1079
ID ADD93196 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194768-A1.
PD 16-OCT-2003.
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[illegible]

Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1089			
ID	ADD80711 standard; protein;	208 AA.	
DE	Human PRO polypeptide #255.		
PN	US2003207418-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1090			
ID	ADD89739 standard; protein;	208 AA.	
DE	Human PRO polypeptide #255.		
PN	US2003199028-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1091			
ID	ADE41023 standard; protein;	208 AA.	
DE	Human PRO polypeptide #255.		
PN	US2003199031-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1092			
ID	ADE04822 standard; protein;	208 AA.	
DE	Human PRO polypeptide #255.		
PN	US2003199034-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1093			
ID	ADF60236 standard; protein;	208 AA.	
DE	Human contig polypeptide sequence SEQ ID NO:2603.		
PN	WO2003080795-A2.		
PD	02-OCT-2003.		
PA	(HYSE-) HYSEQ INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1094			
ID	ADE92951 standard; protein;	208 AA.	
DE	Human PRO polypeptide #255.		
PN	US2003194777-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1095			
ID	ADF67343 standard; protein;	208 AA.	
DE	Human PRO1271 amino acid sequence SEQ ID NO:416.		
PN	US2002198148-A1.		
PD	26-DEC-2002.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1096			
ID	ADG21660 standard; protein;	208 AA.	
DE	Novel human secreted and transmembrane protein PRO1271.		
PN	US2003207355-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1097			
ID	ADG23301 standard; protein;	208 AA.	
DE	Novel human secreted and transmembrane protein PRO1271.		
PN	US2003207384-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	
RESULT 1098			
ID	ADG23301 standard; protein;	208 AA.	
DE	Novel human secreted and transmembrane protein PRO1271.		
PN	US2003207384-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Query Match	13.0%;	Score 58.5; DB 7;	Length 208;
Best Local Similarity	28.0%;	Pred. No. 3e+02;	

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RESULT 1098
ID ADF97636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1099
ID ADG80700 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1100
ID ADG80148 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1101
ID ADH55440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1102
ID ADH55992 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1103
ID ADI35597 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1104
ID ADI64211 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1105
ID ADI65160 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1106
ID ADI63659 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1107
ID ADH82073 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003100087-A1.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1108
ID ADI00090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1109
ID ADH81521 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1110
ID ADM82690 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1111
ID ADN16089 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1112
ID ADN16718 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1113
ID ADN15537 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1114
ID ADN14985 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1115
ID ADC81247 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1116
ID ADD76695 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003100087-A1.
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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1117
ID ADE88821 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1127
ID ADE94841 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1128
ID ADE91252 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1129
ID ADF35542 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1130
ID ADE95393 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1131
ID ADE93503 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1132
ID ADF35084 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1133
ID ADE92399 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1134
ID ADE90700 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1135
ID ADE18512 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194794-A1.
PD 16-OCT-2003.

PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1117
ID ADD88059 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1118
ID ADD86463 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1119
ID ADE75911 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1120
ID ADE23487 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1121
ID ADE24039 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1122
ID ADE24682 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1123
ID ADD87507 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1124
ID ADE89373 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1125
ID ADE18512 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194794-A1.
PD 16-OCT-2003.
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Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1135
ID ADE91847 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1136
ID ADG11792 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1137
ID ADG02426 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1138
ID ADG22212 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1139
ID ADG20282 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1140
ID ADF98188 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1141
ID ADG24405 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1142
ID ADF98759 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1143
ID ADG03590 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1144
ID ADF99311 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1145
ID ADG16896 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1146
ID ADG05355 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1147
ID ADG19622 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1148
ID ADG13459 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1149
ID ADG08516 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1150
ID ADG15686 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1151
ID ADF97084 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1152
ID ADG06269 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1153
ID ADG03590 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1154
ID ADF99311 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1155
ID ADG16896 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
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ID ADG23853 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1154
ID ADG04142 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1155
ID ADG25043 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1156
ID ADG07340 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1157
ID ADG07892 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1158
ID ADG55387 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1159
ID ADG61051 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1160
ID ADG62155 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1161
ID ADG82356 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1162
ID ADG57595 standard; protein; 208 AA.

DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1163
ID ADG57043 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1164
ID ADG55939 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1165
ID ADG58699 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1166
ID ADG71065 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1167
ID ADG58147 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1168
ID ADG53731 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1169
ID ADG71617 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1170
ID ADG81804 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1171
ID ADH19662 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003228656-A1.

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PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1172
ID ADH30766 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US200307723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1173
ID ADH12133 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1174
ID ADG52555 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1175
ID ADG54283 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1176
ID ADG81252 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1177
ID ADG56491 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1178
ID ADH12757 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1179
ID ADH21155 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1180
ID ADG61603 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1181
ID ADH20195 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1182
ID ADH28690 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003202331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1183
ID ADG54835 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1184
ID ADG59875 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1185
ID ADI81299 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1186
ID ADG10042 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1187
ID ADI15513 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1188
ID ADG09390 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
RESULT 1189
ID ADI14845 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 8; Length 208;
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Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1190
ID ADI18440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1191
ID ADJ63721 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1192
ID ADL77250 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 732.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1193
ID ADL77251 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 733.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1194
ID ADL77253 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 735.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1195
ID ADL77252 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 734.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1196
ID ADL78763 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2245.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1197
ID ADJ77616 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1198
ID ADJ65738 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004214269-A1.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1199
ID ADM27874 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1200
ID ADM42598 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1201
ID ADM28460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1202
ID ADP07778 standard; protein; 208 AA.
DE Human secreted protein, seq id 261.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1203
ID ADP74722 standard; protein; 208 AA.
DE Human porimin protein SEQ ID NO: 4.
PN WO2004047762-A2.
PD 10-JUN-2004.
PA (CHIR ) CHIRON CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1204
ID ADI95942 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1205
ID ADI96494 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1206
ID ADS32446 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1207
ID ADT03430 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004214269-A1.
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PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1208
ID ADY63115 standard; protein; 208 AA.
DE Human clone PSEC0111 protein, SEQ ID 118.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1209
ID ADZ03481 standard; protein; 208 AA.
DE Human secreted/transmembrane PRO1271 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1210
ID AEA38633 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #199.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1211
ID AEB14227 standard; protein; 208 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 510.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1212
ID ABM84936 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5185.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 225;
Best Local Similarity 30.4%; Pred. No. 3.3e+02;
RESULT 1213
ID ABM84934 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5183.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 225;
Best Local Similarity 30.4%; Pred. No. 3.3e+02;
RESULT 1214
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 58.5; DB 5; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.4e+02;
RESULT 1215
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 58.5; DB 5; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.4e+02;
RESULT 1216
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 13.0%; Score 58.5; DB 7; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.4e+02;
RESULT 1217
ID ABB69469 standard; protein; 276 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35199.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 58.5; DB 4; Length 276;
Best Local Similarity 26.1%; Pred. No. 4.2e+02;
RESULT 1218
ID ADW17748 standard; protein; 288 AA.
DE Pinus radiata transcription factor protein MYB family Seq 1522.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.0%; Score 58.5; DB 9; Length 288;
Best Local Similarity 25.3%; Pred. No. 4.5e+02;
RESULT 1219
ID ADM03974 standard; protein; 302 AA.
DE Human protein of the invention SEQ ID NO:2659.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 58.5; DB 7; Length 302;
Best Local Similarity 29.4%; Pred. No. 4.7e+02;
RESULT 1220
ID ADE55614 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1433.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.3e+02;
RESULT 1221
ID ADE55610 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1429.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.3e+02;
RESULT 1222
ID AAG47665 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60101.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.0%; Score 58.5; DB 3; Length 330;
Best Local Similarity 36.0%; Pred. No. 5.3e+02;
RESULT 1223
ID ABB63026 standard; protein; 357 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15870.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 58.5; DB 4; Length 357;
Best Local Similarity 29.3%; Pred. No. 5.8e+02;
RESULT 1224
ID ADR20443 standard; protein; 374 AA.
DE Trichinella spiralis serine protease protein fragment 1.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 374;
Best Local Similarity 25.0%; Pred. No. 6.2e+02;
RESULT 1225
ID ADR20442 standard; protein; 421 AA.
DE Full length Trichinella spiralis serine protease protein.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 421;
Best Local Similarity 25.0%; Pred. No. 7.2e+02;
RESULT 1226
ID ADW17284 standard; protein; 494 AA.
DE Eucalyptus grandis transcription factor protein GRAS family Seq 1035.
PN WO200501050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.0%; Score 58.5; DB 9; Length 494;
Best Local Similarity 25.0%; Pred. No. 8.8e+02;
RESULT 1227
ID ABM88793 standard; protein; 1161 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7039.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.0%; Score 58.5; DB 7; Length 1161;
Best Local Similarity 27.7%; Pred. No. 2.6e+03;
RESULT 1228
ID AAW83310 standard; protein; 1451 AA.
DE LRP5 protein from isoform 2 (also isoform 4,5,6).
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1451;
Best Local Similarity 26.2%; Pred. No. 3.4e+03;
RESULT 1229
ID ADC86833 standard; protein; 1494 AA.
DE Human GPCR protein SEQ ID NO:1286.
PN EP1270724-A2.

PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO. Length 1494;
Query Match 13.0%; Score 58.5; DB 7;
Best Local Similarity 26.2%; Pred. No. 3.5e+03;
RESULT 1230
ID AAW83308 standard; protein; 1591 AA.
DE Mature LRP5 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1591;
Best Local Similarity 26.2%; Pred. No. 3.8e+03;
RESULT 1231
ID AAW83309 standard; protein; 1615 AA.
DE LRP5 protein from the longest open reading frame.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1232
ID AAG68169 standard; protein; 1615 AA.
DE Human Zmax1 protein SEQ ID NO:3.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1233
ID AAG68170 standard; protein; 1615 AA.
DE Human HBM protein SEQ ID NO:4.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1234
ID AAE21740 standard; protein; 1615 AA.
DE Human BSMR protein mutant, R494Q.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1235
ID AAE21741 standard; protein; 1615 AA.
DE Human BSMR protein mutant, A1330L.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1236
ID AAE21730 standard; protein; 1615 AA.
DE Human bone strength and mineralisation regulatory protein (BSMR).
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1237
ID AAU80879 standard; protein; 1615 AA.
DE Human Zmax1 polypeptide.
PN WO200192891-A2.

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PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
  Query Match      13.0%; Score 58.5; DB 5; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1238
ID AAU80880 standard; protein; 1615 AA.
DE Human high bone mass (HBM) polypeptide.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
  Query Match      13.0%; Score 58.5; DB 5; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1239
ID ABR41093 standard; protein; 1615 AA.
DE Human wild-type LRP5.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1240
ID ABR41094 standard; protein; 1615 AA.
DE Human LRP5 allelic variant HBM.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1241
ID ABR41131 standard; protein; 1615 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1242
ID ADB98058 standard; protein; 1615 AA.
DE Human LRP5.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1243
ID ADB98798 standard; protein; 1615 AA.
DE Human Zmax1(LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1244
ID ADB98059 standard; protein; 1615 AA.
DE LRP5 mutein.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1245
ID ADE82428 standard; protein; 1615 AA.
DE Human HBM gene.
PN WO200292015-A2.
PD 21-NOV-2002.

PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1246
ID ADE82427 standard; protein; 1615 AA.
DE Human Zmax1 gene.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1247
ID ADI27181 standard; protein; 1615 AA.
DE Human LRP binding family protein #12.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1248
ID ADQ20524 standard; protein; 1615 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3344.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1249
ID ADRI7561 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1250
ID ADRI6921 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1251
ID ADRI7560 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1252
ID ADRI6922 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1253
ID ABO84659 standard; protein; 1615 AA.
DE Human cancer-associated protein HP20-001.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1254
ID ADR47572 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US2004176582-A1.
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PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1255
ID ADR48212 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1256
ID ADR47573 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1257
ID ADR48211 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1258
ID ADR73482 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5, LRP5, protein.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SURR-) SURROMED INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1259
ID ADV97195 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5 (LRP5), SEQ:50.
PN US2005003390-A1.
PD 06-JAN-2005.
PA (AXEN/) AXENOVICH S A.
PA (STUL/) STULL R.
PA (GELM/) GELMAN M.
PA (CHUI/) CHUI K.
PA (NGDD/) NG D.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1260
ID AEB69940 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1261
ID AEB69301 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein, SEQ ID 3.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1262
ID AEB69302 standard; protein; 1615 AA.
DE Human High Bone Mass gene, mutant allele HBM protein, SEQ ID 4.

PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1263
ID ABM85665 standard; protein; 1627 AA.
DE Human protein sequence hCPI690976.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.0%; Score 58.5; DB 7; Length 1627;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1264
ID ABO84660 standard; protein; 1627 AA.
DE Human cancer-associated protein HP20-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1627;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1265
ID AAW83311 standard; protein; 1639 AA.
DE LRP5 isoform 3 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1639;
Best Local Similarity 26.2%; Pred. No. 4e+03;
RESULT 1266
ID ABR41133 standard; protein; 1665 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1267
ID ADB98800 standard; protein; 1665 AA.
DE Human Zmax1 (LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1268
ID ABG77164 standard; protein; 236 AA.
DE Germline protein sequence of anti-IGF-1R antibody AJ30/Jk1.
PN WO200253596-A2.
PD 11-JUL-2002.
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
Query Match 12.9%; Score 58; DB 5; Length 236;
Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1269
ID ADR28586 standard; protein; 236 AA.
DE Human anti-IGF-IR antibody heavy chain A30/Jk1 protein SEQ ID NO:52.
PN WO2004071529-A2.
PD 26-AUG-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 8; Length 236;
Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1270
ID ADX57906 standard; protein; 236 AA.
DE Human germline A30/Jk1 protein sequence SeqID6.
PN WO2005016967-A2.
PD 24-FEB-2005.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 9; Length 236;

Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1271
ID ADS43001 standard; protein; 375 AA.
DE Bacterial polypeptide #21431.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 375;
Best Local Similarity 24.2%; Pred. No. 7.1e+02;
RESULT 1272
ID ADS15092 standard; protein; 405 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 647.
PN WO2004093385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 405;
Best Local Similarity 38.6%; Pred. No. 7.8e+02;
RESULT 1273
ID ADX90494 standard; protein; 418 AA.
DE Plant full length insert polypeptide seqid 53158.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 418;
Best Local Similarity 31.7%; Pred. No. 8.1e+02;
RESULT 1274
ID AAU31533 standard; protein; 450 AA.
DE Novel human secreted protein #2024.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 4; Length 450;
Best Local Similarity 29.5%; Pred. No. 8.9e+02;
RESULT 1275
ID ABO78245 standard; protein; 469 AA.
DE Pseudomonas aeruginosa polypeptide #10420.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 12.9%; Score 58; DB 7; Length 469;
Best Local Similarity 38.6%; Pred. No. 9.4e+02;
RESULT 1276
ID AAW05408 standard; protein; 486 AA.
DE Mouse Hs1 protein.
PN WO9631625-A1.
PD 10-OCT-1996.
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match
Best Local Similarity 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1277
ID AAY03795 standard; protein; 486 AA.
DE Murine Lck binding protein, LckBP1.
PN US5891673-A.
PD 06-APR-1999.
PA (SYNT) SYNTAX USA INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1278
ID ABR44110 standard; protein; 486 AA.
DE Human protein expressed in haematopoietic cells.
PN EP1295895-A1.
PD 26-MAR-2003.
PA (INSR) INST ROUSSY GUSTAVE.

PA (UYPA-) UNIV PARIS SUD.
Query Match
Best Local Similarity 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1279
ID ABO07214 standard; protein; 486 AA.
DE Human p53 modifying protein, SEQ ID 174.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1280
ID ADD67624 standard; protein; 486 AA.
DE Human Ly1729p protein SEQ ID NO:101.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 12.9%; Score 58; DB 7; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1281
ID ADM67192 standard; protein; 486 AA.
DE Human haematopoietic cell specific Lyn substrate 1 protein SeqID 546.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1282
ID ADM67191 standard; protein; 486 AA.
DE Murine haematopoietic cell specific Lyn substrate 1 protein SeqID 545.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1283
ID ADN25984 standard; protein; 496 AA.
DE Bacterial polypeptide #8637.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 496;
Best Local Similarity 30.0%; Pred. No. 1e+03;
RESULT 1284
ID AEB41830 standard; protein; 499 AA.
DE L. pneumophila protein SEQ ID NO 6162.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 12.9%; Score 58; DB 9; Length 499;
Best Local Similarity 38.7%; Pred. No. 1e+03;
RESULT 1285
ID ABO58685 standard; protein; 501 AA.
DE Human genome derived single exon protein #4919.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 501;
Best Local Similarity 28.0%; Pred. No. 1e+03;
RESULT 1286
ID AEB38588 standard; protein; 507 AA.
DE L. pneumophila protein SEQ ID NO 2920.
PN WO2005049642-A2.
PD 02-JUN-2005.

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PA (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 12.9%; Score 58; DB 9; Length 507;
RESULT 1287
ID AAW90945 standard; protein; 540 AA.
DE Comamonas testosteroni R5 phenol hydroxylase protein #4.
PN JP2000069968-A.
PD 07-MAR-2000.
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
Query Match
Best Local Similarity 12.9%; Score 58; DB 3; Length 540;
RESULT 1288
ID ADJ49107 standard; protein; 628 AA.
DE Oil-associated gene related protein #507.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 628;
RESULT 1289
ID ADJ49064 standard; protein; 628 AA.
DE Oil-associated gene related protein #564.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 628;
RESULT 1290
ID AAM78503 standard; protein; 797 AA.
DE Human protein SEQ ID NO 1165.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 4; Length 797;
RESULT 1291
ID AAM40565 standard; protein; 801 AA.
DE Human polypeptide SEQ ID NO 5496.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 4; Length 801;
RESULT 1292
ID ABB11940 standard; peptide; 973 AA.
DE Human secreted protein homologue, SEQ ID NO:2310.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 4; Length 973;
RESULT 1293
ID AAM79487 standard; protein; 973 AA.
DE Human protein SEQ ID NO 3133.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 4; Length 973;
RESULT 1294
ID ADC31585 standard; protein; 1094 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1667.
PN WO2003048323-A2.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 7; Length 1094;
RESULT 1295
ID ADC31584 standard; protein; 1114 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1666.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 7; Length 1114;
RESULT 1296
ID ADQ66563 standard; protein; 1139 AA.
DE Novel human protein sequence #1536.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 12.9%; Score 58; DB 8; Length 1139;
RESULT 1297
ID ABP74029 standard; protein; 1177 AA.
DE Candida albicans essential protein SEQ ID NO 7866.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 5; Length 1177;
RESULT 1298
ID AAE29358 standard; protein; 1331 AA.
DE Plasmodium falciparum BBP-5 protein.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match
Best Local Similarity 12.9%; Score 58; DB 5; Length 1331;
RESULT 1299
ID AAM84121 standard; protein; 95 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:11714.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 4; Length 95;
RESULT 1300
ID AAU31789 standard; protein; 213 AA.
DE Novel human secreted protein #2280.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 4; Length 213;
RESULT 1301
ID ADL70801 standard; protein; 213 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 74.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 213;
RESULT 1302
ID ABM83745 standard; protein; 221 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3994.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 221;
RESULT 1303
ID ADE34554 standard; protein; 269 AA.
DE Human MHC class II HLA-DR2/Dw12 #SEQ ID 38.
PN WO2003048323-A2.
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PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (CARM/) CARMAN J.
PA (NADL/) NADLER S G.
PA (BOWE/) BOWEN M.
PA (NEUB/) NEUBAUER M.
PA (LUPP/) LU P.
Query Match 12.8%; Score 57.5; DB 7; Length 269;
Best Local Similarity 21.0%; Pred. No. 5.3e+02;
RESULT 1304
ID ADX91260 standard; protein; 273 AA.
DE Plant full length insert polypeptide seqid 53924.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 273;
Best Local Similarity 26.6%; Pred. No. 5.4e+02;
RESULT 1305
ID ABU15131 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #658.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 275;
Best Local Similarity 35.6%; Pred. No. 5.5e+02;
RESULT 1306
ID ABO62158 standard; protein; 281 AA.
DE Klebsiella pneumoniae polypeptide seqid 8675.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.8%; Score 57.5; DB 7; Length 281;
Best Local Similarity 22.2%; Pred. No. 5.6e+02;
RESULT 1307
ID AEA26355 standard; protein; 286 AA.
DE Stress tolerant plant-related transcription factor protein SeqID196.
PN WO2005047516-A2.
PD 26-MAY-2005.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 12.8%; Score 57.5; DB 9; Length 286;
Best Local Similarity 32.3%; Pred. No. 5.8e+02;
RESULT 1308
ID ABU31908 standard; protein; 308 AA.
DE Protein encoded by Prokaryotic essential gene #17435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 308;
Best Local Similarity 28.6%; Pred. No. 6.3e+02;
RESULT 1309
ID ADN22689 standard; protein; 546 AA.
DE Bacterial polypeptide #5342.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.8%; Score 57.5; DB 8; Length 546;
Best Local Similarity 33.8%; Pred. No. 1.3e+03;
RESULT 1310
ID ABB48487 standard; protein; 574 AA.
DE Listeria monocytogenes protein #1191.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 12.8%; Score 57.5; DB 5; Length 574;

Best Local Similarity 27.9%; Pred. No. 1.4e+03;
RESULT 1311
ID ADY09430 standard; protein; 715 AA.
DE Plant full length insert polypeptide seqid 65245.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 715;
Best Local Similarity 25.3%; Pred. No. 1.8e+03;
RESULT 1312
ID ABB60747 standard; protein; 722 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9033.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 57.5; DB 4; Length 722;
Best Local Similarity 21.0%; Pred. No. 1.8e+03;
RESULT 1313
ID AAW34501 standard; protein; 804 AA.
DE Obesity receptor protein splice variant.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.1e+03;
RESULT 1314
ID ADB12853 standard; protein; 804 AA.
DE Human leptin receptor, OB-RE , splice variant protein.
PN US2003073829-A1.
PD 17-APR-2003.
PA (ADHA/) ADHAM N.
PA (BORO/) BOROWSKY B.
PA (LEVE/) LEVENS N.
PA (SKOD/) SKODA R C.
Query Match 12.8%; Score 57.5; DB 7; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.1e+03;
RESULT 1315
ID AAW34502 standard; protein; 839 AA.
DE Obesity receptor protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 839;
Best Local Similarity 26.9%; Pred. No. 2.2e+03;
RESULT 1316
ID ADG63038 standard; protein; 867 AA.
DE Human Obr truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 867;
Best Local Similarity 26.9%; Pred. No. 2.3e+03;
RESULT 1317
ID ADG63030 standard; protein; 868 AA.
DE Human Obr truncated protein, delta 868.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 868;
Best Local Similarity 26.9%; Pred. No. 2.3e+03;
RESULT 1318
ID AAW50003 standard; protein; 896 AA.
DE Human OB-R variant Form 3.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;

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RESULT 1319
ID AAW24052 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1320
ID AAW14841 standard; protein; 896 AA.
DE Human haemopoietin receptor NR2.
PN WO9712037-A1.
PD 03-APR-1997.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1321
ID ABU87939 standard; protein; 896 AA.
DE Human WSX receptor splice variant 6.4.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1322
ID ABO53758 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1323
ID ADC08904 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN US2002193571-A1.
PD 19-DEC-2002.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1324
ID ADD95274 standard; protein; 896 AA.
DE Human leptin receptor OBR1.
PN WO2003072787-A2.
PD 04-SEP-2003.
PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS ) CENT NAT RECH SCI.
Query Match 12.8%; Score 57.5; DB 7; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1325
ID ADN04458 standard; protein; 896 AA.
DE Antipsoriatic protein sequence #422.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 8; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1326
ID ADR27661 standard; protein; 896 AA.
DE Human leptin receptor related protein OB-RGRP related sequence SEQ ID 10.
PN FR2850971-A1.
PD 13-AUG-2004.
PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 12.8%; Score 57.5; DB 8; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1327
ID AAW24052 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1328
ID AAR88912 standard; protein; 898 AA.
DE Haematopoietin receptor Hu-B1.219 Form 3 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 898;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1329
ID AAW50002 standard; protein; 904 AA.
DE Human OB-R variant Form 2.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 904;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1330
ID AAR88911 standard; protein; 908 AA.
DE Haematopoietin receptor Hu-B1.219 Form 2 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 908;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1331
ID AAW19536 standard; protein; 908 AA.
DE Variant form of human leptin receptor OB-R.
PN WO9726523-A2.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 908;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1332
ID AAW24053 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1333
ID ABU87940 standard; protein; 923 AA.
DE Human WSX receptor splice variant 12.1.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1334
ID ABO53759 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1335
ID ADC08905 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN US2002193571-A1.
PD 19-DEC-2002.
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PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 7; Length 923;
RESULT 1336 26.9%; Pred. No. 2.5e+03;
ID ADW88113 standard; protein; 923 AA.
DE Human WSK receptor variant 12.1 protein.
PN US2005019325-A1.
PD 27-JAN-2005.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 9; Length 923;
RESULT 1337 26.9%; Pred. No. 2.5e+03;
ID ADO23831 standard; protein; 925 AA.
DE Leptin receptor extracellular domain-GPI fusion protein.
PN WO2003034275-A2.
PD 24-APR-2003.
PA (ASTE-) ASTERION LTD.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 7; Length 925;
RESULT 1338 26.9%; Pred. No. 2.5e+03;
ID AAW38214 standard; protein; 958 AA.
DE Human OB-R variant Form 1.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 958;
RESULT 1339 26.9%; Pred. No. 2.6e+03;
ID AAW31911 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726370-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 958;
RESULT 1340 26.9%; Pred. No. 2.6e+03;
ID AAW19535 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726272-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 958;
RESULT 1341 26.9%; Pred. No. 2.6e+03;
ID AAW22773 standard; protein; 958 AA.
DE Human haematopoietin receptor variant Hu-B1.219 form 1.
PN WO9727286-A1.
PD 31-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 958;
RESULT 1342 26.9%; Pred. No. 2.6e+03;
ID AAR88910 standard; protein; 960 AA.
DE Haematopoietin receptor Hu-B1.219 Form 1 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 960;
RESULT 1343 26.9%; Pred. No. 2.6e+03;
ID ADG63037 standard; protein; 964 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 964;
RESULT 1344 26.9%; Pred. No. 2.7e+03;
ID ADG63031 standard; protein; 965 AA.
DE Human OB-R truncated protein, delta 965.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 965;
RESULT 1345 26.9%; Pred. No. 2.7e+03;
ID AAW34499 standard; protein; 970 AA.
DE Obesity receptor C protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 970;
RESULT 1346 26.9%; Pred. No. 2.7e+03;
ID AAW34497 standard; protein; 972 AA.
DE Obesity receptor A protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 972;
RESULT 1347 26.9%; Pred. No. 2.7e+03;
ID AAW34498 standard; protein; 999 AA.
DE Obesity receptor B protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 2; Length 999;
RESULT 1348 26.9%; Pred. No. 2.8e+03;
ID ADG63032 standard; protein; 1065 AA.
DE Human OB-R truncated protein, delta 1065.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 1065;
RESULT 1349 26.9%; Pred. No. 3e+03;
ID ADG63039 standard; protein; 1067 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 1067;
RESULT 1350 26.9%; Pred. No. 3e+03;
ID ADG63033 standard; protein; 1115 AA.
DE Human OB-R truncated protein, delta 1115.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 1115;
RESULT 1351 26.9%; Pred. No. 3.2e+03;
ID AEA19287 standard; protein; 1152 AA.
DE Mouse B220.
PN WO2005049865-A2.
PD 02-JUN-2005.
PA (REPR-) REPROCELL INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 9; Length 1152;
RESULT 1352 21.7%; Pred. No. 3.3e+03;
ID ADG63040 standard; protein; 1155 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 12.8%; Score 57.5; DB 8; Length 1155;

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Best Local Similarity 26.9%; Pred. No. 3.3e+03;
RESULT 1353
ID ABO84453 standard; protein; 1157 AA.
DE Mouse cancer-associated protein MP13-011.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1157;
Best Local Similarity 21.7%; Pred. No. 3.3e+03;
RESULT 1354
ID ADG63041 standard; protein; 1161 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1161;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1355
ID AAW24051 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1356
ID AAW19116 standard; protein; 1165 AA.
DE Human Ob receptor.
PN WO9719952-A1.
PD 05-JUN-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1357
ID AAY13474 standard; protein; 1165 AA.
DE Peptide Seq ID No: 4 of WO9233493.
PN WO9233493-A1.
PD 14-MAY-1999.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1358
ID AAE12551 standard; protein; 1165 AA.
DE Human Ob receptor (Obr) protein mutant (Y1141F).
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1359
ID AAE12609 standard; protein; 1165 AA.
DE Human Ob receptor (Obr) protein.
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1360
ID AAE25455 standard; protein; 1165 AA.
DE Human Ob receptor (Obr) protein.
PN US6395498-B1.
PD 28-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1361
ID AAE25774 standard; protein; 1165 AA.
DE Human obesity receptor (Obr) mutant protein, Y1079F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1362
ID AAE25765 standard; protein; 1165 AA.
DE Human obesity receptor (Obr) protein.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1363
ID AAE25772 standard; protein; 1165 AA.
DE Human obesity receptor (Obr) mutant protein, Y1141F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1364
ID AAE25773 standard; protein; 1165 AA.
DE Human obesity receptor (Obr) mutant protein, Y986F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1365
ID AAE23859 standard; protein; 1165 AA.
DE Human Ob receptor (obr) protein.
PN US6380363-B1.
PD 30-APR-2002.
PA (TART/) TARTAGLIA L A.
PA (TEPP/) TEPPER R I.
PA (CULP/) CULPEPPER J A.
PA (WHIT/) WHITE D W.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1366
ID ABU87938 standard; protein; 1165 AA.
DE Human DNA full length WSX receptor.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1367
ID ABP72720 standard; protein; 1165 AA.
DE Human leptin receptor long form.
PN WO2003017825-A2.
PD 06-MAR-2003.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1368
ID ABO53757 standard; protein; 1165 AA.
DE Human full length WSX receptor variant 13.2.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1369
ID ADC08903 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN US2002193571-A1.
PD 19-DEC-2002.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1370
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ID ADE62888 standard; protein; 1165 AA.
DE Human Protein P48357, SEQ ID NO 8822.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1371
ID ADD46275 standard; protein; 1165 AA.
DE Human Protein P48357, SEQ ID NO 11950.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1372
ID ADG63035 standard; protein; 1165 AA.
DE Human Obr mutant protein, Y986F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1373
ID ADG62979 standard; protein; 1165 AA.
DE Human Obr protein from clone famj5312.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1374
ID ADG63036 standard; protein; 1165 AA.
DE Human Obr mutant protein, Y1141F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1375
ID ADG63034 standard; protein; 1165 AA.
DE Human Obr mutant protein, Y1079F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1376
ID ADW88111 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2 protein.
PN US2005019325-A1.
PD 27-JAN-2005.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 9; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1377
ID AEB32310 standard; protein; 1165 AA.
DE Human protein #12.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 12.8%; Score 57.5; DB 9; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1378
ID AEB32324 standard; protein; 1167 AA.
DE Human protein #26.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 12.8%; Score 57.5; DB 9; Length 1167;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1379
ID AAW34500 standard; protein; 1220 AA.
DE Obesity receptor D protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1220;
Best Local Similarity 26.9%; Pred. No. 3.6e+03;
RESULT 1380
ID AAW62544 standard; protein; 1221 AA.
DE Human ob-receptor replacement mutant.
PN WO9824881-A1.
PD 11-JUN-1998.
PA (MERI ) MERCK & CO INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1221;
Best Local Similarity 26.9%; Pred. No. 3.6e+03;
RESULT 1381
ID ADL16234 standard; protein; 1291 AA.
DE Mouse protein tyrosine phosphatase #7.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Query Match 12.8%; Score 57.5; DB 7; Length 1291;
Best Local Similarity 21.7%; Pred. No. 3.8e+03;
RESULT 1382
ID ADM67208 standard; protein; 1343 AA.
DE Murine adipocyte specific leukocyte common antigen protein SeqID 562.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1343;
Best Local Similarity 21.7%; Pred. No. 4e+03;
RESULT 1383
ID AAW52217 standard; protein; 105 AA.
DE Antibody LD1-84-VL chain sequence.
PN WO9749809-A1.
PD 31-DEC-1997.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
Query Match 12.7%; Score 57; DB 2; Length 105;
Best Local Similarity 35.6%; Pred. No. 1.9e+02;
RESULT 1384
ID ADV66220 standard; protein; 135 AA.
DE S. mansoni protein SEQ ID 1638.
PN WO2005023979-A2.
PD 17-MAR-2005.
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
Query Match 12.7%; Score 57; DB 9; Length 135;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
RESULT 1385
ID AAB16367 standard; protein; 136 AA.
DE Eucalyptus grandis diphenol oxidase protein sequence SEQ ID NO:293.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 12.7%; Score 57; DB 3; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.6e+02;
RESULT 1386
ID ADD41543 standard; protein; 136 AA.
DE Diphenol oxidase #4.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 12.7%; Score 57; DB 7; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.6e+02;
RESULT 1387
ID AAY34312 standard; protein; 147 AA.
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DE Igm antibody CEM 10.12 G5 kappa chain sequence.
PN WO9945031-A2.
PD 10-SEP-1999.
PA (ABGE-) ABGENIX INC. 12.7%; Score 57; DB 2; Length 147;
Query Match 28.4%; Pred. No. 2.9e+02;
Best Local Similarity 28.4%; Pred. No. 2.9e+02;
RESULT 1388
ID ADP44641 standard; protein; 213 AA.
DE Human anti-CD20 light chain protein.
PN WO2004050041-A2.
PD 17-JUN-2004.
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1389
ID ADU80277 standard; protein; 213 AA.
DE CD20 binding AME 33 complete light chain variable protein.
PN WO2004103404-A1.
PD 02-DEC-2004.
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1390
ID AEA60641 standard; protein; 213 AA.
DE Human butyrylcholinesterase variant protein SEQ ID NO:198.
PN US2005136044-A1.
PD 23-JUN-2005.
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
Query Match 12.7%; Score 57; DB 9; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1391
ID ABO73390 standard; protein; 218 AA.
DE Pseudomonas aeruginosa polypeptide #5565.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 218;
Best Local Similarity 24.5%; Pred. No. 4.7e+02;
RESULT 1392
ID AAR59416 standard; protein; 219 AA.
DE 6D9 antibody light chain.
PN JP06220072-A.
PD 09-AUG-1994.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 2; Length 219;
Best Local Similarity 28.4%; Pred. No. 4.7e+02;
RESULT 1393
ID AEB08093 standard; protein; 220 AA.
DE Murine Ig kappa light chain constant domain, SEQ ID NO: 55.
PN WO2005058251-A2.
PD 30-JUN-2005.
PA (DEND-) DENDREON CORP.
Query Match 12.7%; Score 57; DB 9; Length 220;
Best Local Similarity 28.4%; Pred. No. 4.7e+02;
RESULT 1394
ID ADZ57707 standard; protein; 236 AA.
DE Anti-cMet antibody 8.90.3 light chain protein.
PN GB2404660-A.
PD 09-FEB-2005.
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
Query Match 12.7%; Score 57; DB 9; Length 236;
Best Local Similarity 26.9%; Pred. No. 5.2e+02;
RESULT 1395
ID ADX95267 standard; protein; 321 AA.
DE Plant full length insert polypeptide seqid 57931.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.7%; Score 57; DB 8; Length 321;
Best Local Similarity 29.7%; Pred. No. 7.6e+02;
RESULT 1396
ID ADT57341 standard; protein; 370 AA.
DE Plant polypeptide, SEQ ID 7418.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 12.7%; Score 57; DB 8; Length 370;
Best Local Similarity 29.7%; Pred. No. 9.1e+02;
RESULT 1397
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 12.7%; Score 57; DB 8; Length 454;
Best Local Similarity 32.8%; Pred. No. 1.2e+03;
RESULT 1398
ID AAG64459 standard; protein; 573 AA.
DE Mouse 6D9 catalytic antibody.
PN JP2001128681-A.
PD 15-MAY-2001.
PA (NISB) JAPAN TOBACCO INC.
PA (SEIB-) SEIBUTSU BUNSHI KOGAKU KENKYUSHO KK.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 4; Length 573;
Best Local Similarity 28.4%; Pred. No. 1.6e+03;
RESULT 1399
ID ABO77277 standard; protein; 576 AA.
DE Pseudomonas aeruginosa polypeptide #9452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 576;
Best Local Similarity 38.2%; Pred. No. 1.6e+03;
RESULT 1400
ID ADC08221 standard; protein; 676 AA.
DE Rice protein sequence Seq ID526 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 676;
Best Local Similarity 45.5%; Pred. No. 1.9e+03;
RESULT 1401
ID ADC07938 standard; protein; 729 AA.
DE Rice protein sequence Seq ID204 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 729;
Best Local Similarity 45.5%; Pred. No. 2.1e+03;
RESULT 1402
ID AAO15273 standard; protein; 757 AA.
DE Human nervous serine protease inhibitor (PII2) 83-27.
PN CN1333249-A.
PD 30-JAN-2002.
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
Query Match 12.7%; Score 57; DB 5; Length 757;
Best Local Similarity 28.0%; Pred. No. 2.2e+03;
RESULT 1403
ID ABB64716 standard; protein; 971 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20940.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.7%; Score 57; DB 4; Length 971;
Best Local Similarity 35.2%; Pred. No. 3.1e+03;
RESULT 1404
ID ADR18920 standard; protein; 1225 AA.
DE Human tracheobronchial mucin protein, MUC5A.

PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 1225;
Best Local Similarity 27.7%; Pred. No. 4.1e+03;
RESULT 1405
ID ADD93316 standard; protein; 1302 AA.
DE Zebrafish Flt1 protein required for angiogenesis.
PN WO2003079776-A2.
PD 02-OCT-2003.
PA (ARTE-) ARTEMIS PHARM GMBH.
Query Match 12.7%; Score 57; DB 7; Length 1302;
Best Local Similarity 30.0%; Pred. No. 4.4e+03;
RESULT 1406
ID ABR53378 standard; protein; 1411 AA.
DE Protein sequence #SEQ ID 1621.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 6; Length 1411;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
RESULT 1407
ID ADK63342 standard; protein; 1411 AA.
DE Disease treating protein complex-derived protein #982.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 7; Length 1411;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
RESULT 1408
ID ADR18918 standard; protein; 2202 AA.
DE Mature Human mucin-like protein, SCS0005, SEQ ID 8.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2202;
Best Local Similarity 27.7%; Pred. No. 8.6e+03;
RESULT 1409
ID ADR18917 standard; protein; 2227 AA.
DE Human mucin-like protein, SCS0005, SEQ ID 7.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2227;
Best Local Similarity 27.7%; Pred. No. 8.7e+03;
RESULT 1410
ID ADR18919 standard; protein; 2233 AA.
DE His-tagged Human mucin-like protein, SCS0005, SEQ ID 9.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2233;
Best Local Similarity 27.7%; Pred. No. 8.7e+03;
RESULT 1411
ID ADV24899 standard; protein; 3869 AA.
DE Anabaena microcystin polyketide synthase mcyD protein.
PN WO2004104211-A2.
PD 02-DEC-2004.
PA (HELS-) HELSINGIN YLIOPISTO.
PA (UYLI-) UNIV LIEGE.
PA (CNRD) CONSIGLIO NAZ DELLE RICERCHE.
Query Match 12.7%; Score 57; DB 9; Length 3869;
Best Local Similarity 35.4%; Pred. No. 1.7e+04;
RESULT 1412
ID ADP79571 standard; protein; 107 AA.
DE Humanised 2H7.v16 variant light chain variable domain SEQ ID NO:2.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1413
ID ADS33301 standard; protein; 107 AA.

DE Anti-CD20 humanised antibody hu2H7v16, light chain variable domain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1414
ID ADW03407 standard; protein; 107 AA.
DE Humanized anti-CD20 antibody light chain variable region - SEQ ID 13.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1415
ID ADW21304 standard; protein; 107 AA.
DE Mouse anti-CD20 antibody 2H7 VL, humanized clone v16.
PN WO2005005462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1416
ID ADX00802 standard; protein; 107 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 1.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1417
ID ADY62622 standard; protein; 107 AA.
DE Humanized 2H7 antibody variable light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1418
ID AEB27725 standard; protein; 107 AA.
DE Humanized 2H7 antibody light chain variable region sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1419
ID ABB17635 standard; peptide; 107 AA.
DE Variable light peptide sequence of humanized 2H7 antibody.
PN WO2005061542-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1420
ID ADA89110 standard; protein; 109 AA.
DE MS-Pro-28-VL amino acid sequence SEQ ID NO:98.
PN WO2002102973-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
Query Match 12.6%; Score 56.5; DB 6; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.2e+02;
RESULT 1421
ID ADG74361 standard; protein; 109 AA.
DE MSPRO light chain variable region protein, SEQ ID No 98.
PN WO2002102972-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
PA (MORP-) MORPHOSYS AG.
Query Match 12.6%; Score 56.5; DB 7; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.2e+02;
RESULT 1422
ID ADI26478 standard; protein; 114 AA.

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DE H. pylori HpU-18-L SEQ ID NO:14.
PN WO2004009805-A1.
PD 29-JAN-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 114;
Best Local Similarity 38.9%; Pred. No. 2.4e+02;
RESULT 1423
ID ABO58078 standard; protein; 169 AA.
DE Human genome derived single exon protein #4312.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.6%; Score 56.5; DB 8; Length 169;
Best Local Similarity 24.2%; Pred. No. 3.9e+02;
RESULT 1424
ID ADP55680 standard; protein; 175 AA.
DE Human PRO protein sequence SEQ ID NO:1656.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 175;
Best Local Similarity 29.3%; Pred. No. 4.1e+02;
RESULT 1425
ID ADY22634 standard; protein; 186 AA.
DE Plant full length insert polypeptide seqid 70418.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.6%; Score 56.5; DB 8; Length 186;
Best Local Similarity 29.1%; Pred. No. 4.4e+02;
RESULT 1426
ID ABM84939 standard; protein; 221 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5188.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 221;
Best Local Similarity 32.7%; Pred. No. 5.4e+02;
RESULT 1427
ID ABO69554 standard; protein; 235 AA.
DE Pseudomonas aeruginosa polypeptide #1729.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 56.5; DB 7; Length 235;
Best Local Similarity 28.2%; Pred. No. 5.9e+02;
RESULT 1428
ID ADN25938 standard; protein; 273 AA.
DE Bacterial polypeptide #8591.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 56.5; DB 8; Length 273;
Best Local Similarity 27.7%; Pred. No. 7.1e+02;
RESULT 1429
ID ADC19732 standard; protein; 324 AA.
DE H. influenzae Orf15 polypeptide SEQ ID NO:29.
PN WO2003055905-A2.
PD 10-JUL-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
Query Match 12.6%; Score 56.5; DB 7; Length 324;
Best Local Similarity 34.3%; Pred. No. 8.8e+02;
RESULT 1430
ID ADT55522 standard; protein; 335 AA.
DE Plant polypeptide, SEQ ID 5599.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 12.6%; Score 56.5; DB 8; Length 335;
Best Local Similarity 36.0%; Pred. No. 9.2e+02;
RESULT 1431
ID ABB58822 standard; protein; 351 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3258.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.6%; Score 56.5; DB 4; Length 351;
Best Local Similarity 25.3%; Pred. No. 9.7e+02;
RESULT 1432
ID ADA55440 standard; protein; 412 AA.
DE Human protein, SEQ ID 3008.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 12.6%; Score 56.5; DB 6; Length 412;
Best Local Similarity 22.0%; Pred. No. 1.2e+03;
RESULT 1433
ID ABB11538 standard; peptide; 416 AA.
DE Human TRAP150 homologue, SEQ ID NO:1908.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 416;
Best Local Similarity 23.3%; Pred. No. 1.2e+03;
RESULT 1434
ID AAW59836 standard; protein; 438 AA.
DE Maize Id protein.
PN WO9837201-A1.
PD 27-AUG-1998.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 12.6%; Score 56.5; DB 2; Length 438;
Best Local Similarity 39.6%; Pred. No. 1.3e+03;
RESULT 1435
ID ADY72479 standard; protein; 475 AA.
DE HIV-2/VCP clone 8c.3 gp120 protein SEQ ID NO:29.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 475;
Best Local Similarity 30.6%; Pred. No. 1.4e+03;
RESULT 1436
ID ADY72487 standard; protein; 482 AA.
DE HIV-2/VCP gp120 protein with a V3(6,6) deletion.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 482;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1437
ID ADY72491 standard; protein; 484 AA.
DE HIV-2/VCP gp120 protein p16.9 clone.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 484;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1438
ID ADY72473 standard; protein; 485 AA.
DE HIV-2/VCP clone p16.9 gp120 protein SEQ ID NO:23.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 485;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
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RESULT 1439
ID ADW69549 standard; protein; 500 AA.
DE HIV-1 gp120 protein, U-228cl.
PN WO2004110384-A2.
PD 23-DEC-2004.
PA (VAXG-) VAXGEN INC.
Query Match 12.6%; Score 56.5; DB 9; Length 500;
Best Local Similarity 23.2%; Pred. No. 1.5e+03;
RESULT 1440
ID ADY72455 standard; protein; 501 AA.
DE HIV-2/VCP gp120 protein SEQ ID NO:5.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 501;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1441
ID ADY72481 standard; protein; 503 AA.
DE HIV-2/VCP gp120 protein.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 503;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1442
ID ADX94611 standard; protein; 553 AA.
DE Plant full length insert polypeptide seqid 57275.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABR/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.6%; Score 56.5; DB 8; Length 553;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;
RESULT 1443
ID AAB31664 standard; protein; 610 AA.
DE Amino acid sequence of a codon optimised TGEV S-gene.
PN CA2272793-A1.
PD 11-DEC-2000.
PA (UYGU-) UNIV GUELPH.
Query Match 12.6%; Score 56.5; DB 4; Length 610;
Best Local Similarity 29.0%; Pred. No. 2e+03;
RESULT 1444
ID ADB65251 standard; protein; 629 AA.
DE Human protein encoded by clone TESTI20049410.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.6%; Score 56.5; DB 7; Length 629;
Best Local Similarity 22.0%; Pred. No. 2e+03;
RESULT 1445
ID ADS21458 standard; protein; 708 AA.
DE Bacterial polypeptide #10491.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 56.5; DB 8; Length 708;
Best Local Similarity 22.7%; Pred. No. 2.4e+03;
RESULT 1446
ID ADY72478 standard; protein; 713 AA.
DE HIV-2/VCP clone 8c.3 env protein SEQ ID NO:28.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 713;
Best Local Similarity 30.6%; Pred. No. 2.4e+03;
RESULT 1447
ID ADY72472 standard; protein; 723 AA.
DE HIV-2/VCP clone p16.9 env protein SEQ ID NO:22.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 723;
Best Local Similarity 30.6%; Pred. No. 2.4e+03;
RESULT 1448
ID ADY72454 standard; protein; 739 AA.
DE HIV-2/VCP env protein SEQ ID NO:4.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 739;
Best Local Similarity 30.6%; Pred. No. 2.5e+03;
RESULT 1449
ID ABG15572 standard; protein; 804 AA.
DE Novel human diagnostic protein #15563.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 804;
Best Local Similarity 31.6%; Pred. No. 2.8e+03;
RESULT 1450
ID AAG90560 standard; protein; 811 AA.
DE C glutamicum protein fragment SEQ ID NO: 4314.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 12.6%; Score 56.5; DB 4; Length 811;
Best Local Similarity 24.7%; Pred. No. 2.8e+03;
RESULT 1451
ID ADL65931 standard; protein; 811 AA.
DE C. glutamicum RXA-associated protein #144.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI) BASF AG.
Query Match 12.6%; Score 56.5; DB 7; Length 811;
Best Local Similarity 24.7%; Pred. No. 2.8e+03;
RESULT 1452
ID ABY00038 standard; protein; 1447 AA.
DE Transmissible gastroenteritis virus spike (S) protein, SEQ:6057.
PN WO2004092360-A2.
PD 28-OCT-2004.
PA (CHIR) CHIRON CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 1447;
Best Local Similarity 29.0%; Pred. No. 5.8e+03;
RESULT 1453
ID ABG12703 standard; protein; 1468 AA.
DE Novel human diagnostic protein #12694.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 1468;
Best Local Similarity 31.1%; Pred. No. 5.9e+03;
RESULT 1454
ID AAP80474 standard; protein; 1483 AA.
DE Sequence of protein of transmissible gastroenteritis virus (TGEV) encoded on peplomer gene.
PN EP278541-A.
PD 17-AUG-1988.
PA (DUIN) DUPHAR INT RES BV.
Query Match 12.6%; Score 56.5; DB 1; Length 1483;
Best Local Similarity 29.0%; Pred. No. 6e+03;
RESULT 1455
ID ABG23183 standard; protein; 1513 AA.
DE Novel human diagnostic protein #23174.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 1513;
Best Local Similarity 31.1%; Pred. No. 5.9e+03;
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Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1473
ID ADC26154 standard; protein; 214 AA.
DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.
PN WO2003068801-A2.
PD 21-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 7; Length 214;
Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1474
ID ADC26156 standard; protein; 214 AA.
DE Anti-VEGF Y0101 antibody mutant light chain protein 1.
PN WO2003068801-A2.
PD 21-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 7; Length 214;
Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1475
ID ADL93656 standard; protein; 233 AA.
DE Human CD44-binding antibody light chain HAE-F1-kappa-light SEQ ID NO:151.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.5%; Score 56; DB 8; Length 233;
Best Local Similarity 28.1%; Pred. No. 6.6e+02;
RESULT 1476
ID ADS84458 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab412 light chain SEQ ID NO:97.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1477
ID ADS84476 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab484 light chain SEQ ID NO:115.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1478
ID ADS84464 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 29.7%; Pred. No. 6.7e+02;
RESULT 1479
ID ADR68618 standard; protein; 234 AA.
DE Human antibody Ab484 light chain polypeptide seqid 115.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1480
ID ADR68600 standard; protein; 234 AA.
DE Human antibody Ab412 light chain polypeptide seqid 97.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;

RESULT 1481
ID ADR68606 standard; protein; 234 AA.
DE Human antibody Ab430 light chain polypeptide seqid 103.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 29.7%; Pred. No. 6.7e+02;
RESULT 1482
ID AAU74297 standard; protein; 236 AA.
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.
PN WO200187981-A2.
PD 22-NOV-2001.
PA (NIBS) JAPAN TOBACCO INC.
Query Match 12.5%; Score 56; DB 5; Length 236;
Best Local Similarity 26.9%; Pred. No. 6.7e+02;
RESULT 1483
ID ABB81107 standard; protein; 237 AA.
DE Anti-VEGF light chain fragment.
PN WO200261090-A2.
PD 08-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 5; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1484
ID ABP51952 standard; protein; 237 AA.
DE Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
PN WO200248376-A2.
PD 20-JUN-2002.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 5; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1485
ID ADO14128 standard; protein; 237 AA.
DE Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.
PN WO2004042017-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1486
ID ADO14131 standard; protein; 237 AA.
DE Plasmid pXVG11VNERK expression cassette light chain protein SEQ ID NO:11.
PN WO2004042017-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1487
ID ADQ90703 standard; protein; 237 AA.
DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1488
ID ADQ90701 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1489
ID ADQ90705 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:9.
PN WO2004065417-A2.
PD 05-AUG-2004.

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PA (GETH ) GENENTECH INC.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1490
ID ADQ90709 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:13.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH ) GENENTECH INC.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1491
ID ADQ90723 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:27.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH ) GENENTECH INC.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1492
ID ADQ90721 standard; protein; 237 AA.
DE Anti-VEGF antibody light chain protein SEQ ID NO:25.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH ) GENENTECH INC.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1493
ID ADQ90707 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:11.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH ) GENENTECH INC.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1494
ID ADY06952 standard; protein; 237 AA.
DE Plant full length insert polypeptide seqid 62767.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match      12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 31.0%; Pred. No. 6.8e+02;
RESULT 1495
ID ABU97115 standard; protein; 250 AA.
DE Recombinant anti-infective bursal disease virus-antibody fragment #1.
PN WO200298921-A1.
PD 12-DEC-2002.
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
Query Match      12.5%; Score 56; DB 6; Length 250;
Best Local Similarity 26.8%; Pred. No. 7.3e+02;
RESULT 1496
ID ABM69176 standard; protein; 258 AA.
DE Photorhabdus luminescens protein sequence #2273.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match      12.5%; Score 56; DB 6; Length 258;
Best Local Similarity 25.5%; Pred. No. 7.5e+02;
RESULT 1497
ID ADE57818 standard; protein; 261 AA.
DE Human Protein P01919, SEQ ID NO 3683.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match      12.5%; Score 56; DB 7; Length 261;
Best Local Similarity 30.8%; Pred. No. 8e+02;
RESULT 1498
ID ADE62851 standard; protein; 261 AA.
DE Human Protein P01919, SEQ ID NO 8785.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match      12.5%; Score 56; DB 7; Length 261;
Best Local Similarity 30.8%; Pred. No. 7.7e+02;
RESULT 1499
ID ADQ17236 standard; protein; 261 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 52.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match      12.5%; Score 56; DB 8; Length 261;
Best Local Similarity 30.8%; Pred. No. 7.7e+02;
RESULT 1500
ID AAY68284 standard; peptide; 269 AA.
DE Class II beta chain protein DQ-beta SEQ ID NO:116.
PN US6011146-A.
PD 04-JAN-2000.
PA (INSP ) INST PASTEUR.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
Query Match      12.5%; Score 56; DB 3; Length 269;
Best Local Similarity 30.8%; Pred. No. 8e+02;
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:54:14 ; Search time 39.1837 Seconds
(without alignments)
196.443 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KGPLMCNPSNSNANCEPSL.....RASSPHFDSEENKRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	17.5	281	2 T51961	ATAF1-like protein
2	73	16.3	413	2 S01076	aspartate transami
3	70	15.6	490	2 S52830	HMS1 protein - yea
4	70	15.6	1011	2 T13669	neuromusculin - fr
5	68	15.1	2201	2 A32160	tenascin-C - human
6	67	14.9	296	2 AH1173	conserved hypothet
7	66	14.7	575	2 A54861	tenascin - rat (fr
8	66	14.7	1217	2 T00270	hypothetical prote
9	65.5	14.6	620	2 T49067	transcription fact
10	65.5	14.6	656	2 B49423	semaphorin I - fru
11	65	14.5	652	2 H96924	probable phosphohy
12	64.5	14.4	330	2 T43061	hypothetical prote
13	64.5	14.4	461	2 T25671	hypothetical prote
14	64.5	14.4	475	2 T39486	hypothetical prote
15	64.5	14.4	503	2 T38303	SWI/SNF complex tr
16	64	14.3	228	2 T16678	hypothetical prote
17	64	14.3	992	2 A42318	glycogen phosphory
18	64	14.3	1500	2 T03824	probable immediate
19	63	14.0	418	2 E86395	hypothetical prote
20	63	14.0	1165	1 S45879	chitin synthase (E
21	63	14.0	2051	2 T13164	plexin B - fruit f
22	62.5	13.9	296	2 AI1530	conserved hypothet
23	62.5	13.9	413	2 S29027	aspartate transami
24	62.5	13.9	646	2 JQ2150	B west mating prot
25	62.5	13.9	1748	1 JN0786	integrin beta-4 ch
26	62.5	13.9	1811	2 T00035	nonstructural poly
27	62	13.8	971	2 S50912	probable membrane
28	61.5	13.7	417	2 AG1934	folylpolyglutamate
29	61.5	13.7	487	2 T49424	hypothetical prote

30	61.5	13.7	647	2 JQ2149	B west mating prot
31	61.5	13.7	1034	2 S49947	SMT4 protein - Yea
32	61	13.6	326	2 G84748	hypothetical prote
33	61	13.6	412	2 S13035	aspartate transami
34	61	13.6	413	2 S29028	aspartate transami
35	61	13.6	413	2 JT0439	aspartate transami
36	61	13.6	1810	1 A32230	tenascin precursor
37	61	13.6	2019	1 JQ1322	tenascin precursor
38	60.5	13.5	444	2 D97142	surface-layer rela
39	60.5	13.5	661	2 S37592	beta-fructofuranos
40	60.5	13.5	661	2 S37591	beta-fructofuranos
41	60.5	13.5	661	2 S37590	beta-fructofuranos
42	60.5	13.5	937	2 A56517	nucleoporin Nup98
43	60.5	13.5	992	2 S49835	hypothetical prote
44	60	13.4	292	2 T19669	hypothetical prote
45	60	13.4	292	2 G88783	protein C33A12.16
46	60	13.4	577	2 T32336	hypothetical prote
47	59.5	13.3	557	2 JC5487	cellulase (EC 3.2.
48	59.5	13.3	821	2 T41364	hypothetical prote
49	59	13.1	284	2 T06129	zinc finger protei
50	59	13.1	412	2 A26341	aspartate transami
51	59	13.1	433	2 S31436	Ig upsilon chain -
52	59	13.1	493	2 I39541	cytolytic enteroto
53	59	13.1	554	2 G96598	protein F20N2.6 [i
54	59	13.1	677	1 A45264	system b(0,+) amin
55	59	13.1	741	2 JS0606	homeobox protein A
56	59	13.1	763	2 S17998	gene COX1 intron 4
57	59	13.1	838	2 E89473	protein F52D2.6 [i
58	59	13.1	1006	2 T41104	probable transcrip
59	59	13.1	2352	2 T43431	alpha-glucan synth
60	58.5	13.0	508	2 T19350	hypothetical prote
61	58.5	13.0	640	2 S23008	insulin-like growt
62	58.5	13.0	1615	2 JE0372	low density lipopr
63	58.5	13.0	1748	1 JQ1555	genome polyprotein
64	58	12.9	261	2 I68718	MHC class II histo
65	58	12.9	375	2 A64300	aspartate transami
66	58	12.9	405	2 A83038	hypothetical prote
67	58	12.9	465	2 S03325	transforming prote
68	58	12.9	486	2 S07633	hematopoietic line
69	58	12.9	486	2 I49760	LckBp1 protein - m
70	58	12.9	528	2 S63009	hypothetical prote
71	58	12.9	795	2 T31180	hypothetical prote
72	58	12.9	1666	2 T43169	hypothetical prote
73	57.5	12.8	176	2 I53630	cell surface glyco
74	57.5	12.8	269	2 I54432	MHC class II histo
75	57.5	12.8	275	1 F65090	3',5'-cyclic-nucle
76	57.5	12.8	275	1 G85963	3',5'-cyclic-nucle
77	57.5	12.8	275	1 H91118	3',5'-cyclic-nucle
78	57.5	12.8	413	2 S51667	serine/threonine k
79	57.5	12.8	546	2 T32382	hypothetical prote
80	57.5	12.8	574	2 AC1414	ABC transporter re
81	57.5	12.8	640	2 B84887	probable SCARECROW
82	57.5	12.8	959	2 T25704	hypothetical prote
83	57.5	12.8	1291	1 A28334	protein-tyrosine-p
84	57.5	12.8	1807	2 JC6319	integrin beta-4 ch
85	57.5	12.8	3005	2 S33642	homeotic protein z
86	57	12.7	219	2 S52028	Ig kappa chain - m
87	57	12.7	307	2 A45600	asparagine-rich bl
88	57	12.7	446	2 F84506	En/Spm-like transp
89	57	12.7	471	2 AH1810	isochorismate synt
90	57	12.7	619	1 KSNCL0	laccase (EC 1.10.3
91	57	12.7	619	1 KSNCLT	laccase (EC 1.10.3
92	57	12.7	813	2 T04220	H+-transporting AT
93	57	12.7	1042	2 T29307	hypothetical prote
94	57	12.7	1411	2 S55123	hypothetical prote
95	57	12.7	2761	2 T21064	hypothetical prote
96	56.5	12.6	169	2 T31484	hypothetical prote
97	56.5	12.6	180	1 HLHUC3	MHC class II histo
98	56.5	12.6	251	2 S40995	hypothetical prote
99	56.5	12.6	263	2 T46093	hypothetical prote
100	56.5	12.6	457	2 S18239	glycerol-3-phospha
101	56.5	12.6	569	2 B84904	probable laccase (
102	56.5	12.6	740	2 H82807	beta-glucosidase X

103	56.5	12.6	768	2	JC6564	cellobiose oxidase	176	55	12.2	601	2	T00119	probable transcrip
104	56.5	12.6	874	2	AC2287	hypothetical prote	177	55	12.2	650	2	S23217	beta-fructofuranos
105	56.5	12.6	891	1	RDBHP	nitrate reductase	178	55	12.2	708	2	S52317	quinohemoprotein e
106	56.5	12.6	1018	2	T30986	period protein - C	179	55	12.2	956	1	QQBK2	UL105 protein - hu
107	56.5	12.6	1125	2	T39052	hypothetical serin	180	55	12.2	1052	1	A44937	kinetoplast-associ
108	56.5	12.6	1447	1	VGIHE3	E2 glycoprotein pr	181	55	12.2	1191	2	T13850	gene u-shaped prot
109	56.5	12.6	1447	1	VGIHE2	E2 glycoprotein pr	182	55	12.2	1194	2	E96624	hypothetical prote
110	56.5	12.6	4351	2	T00252	MEGF1 protein - ra	183	55	12.2	1245	2	G86404	probable P-glycopr
111	56.5	12.6	5138	2	B96695	hypothetical prote	184	55	12.2	1280	2	A39117	170K lectin precur
112	56	12.5	238	2	A45544	BoLA-DQ beta-1 - b	185	55	12.2	1450	2	C86880	hypothetical prote
113	56	12.5	247	2	I45942	MHC class II - bov	186	55	12.2	2843	1	RBHUAP	adenomatous polypo
114	56	12.5	259	2	S64423	probable membrane	187	54.5	12.1	155	2	T49557	hypothetical prote
115	56	12.5	261	1	HLHU2C	MHC class II histo	188	54.5	12.1	219	2	I45937	MHC cell surface g
116	56	12.5	261	2	I45928	MHC class II - bov	189	54.5	12.1	232	2	I47094	MHC class II OLA-D
117	56	12.5	447	2	A84718	hypothetical prote	190	54.5	12.1	237	2	S68702	tryptase (EC 3.4.2
118	56	12.5	468	2	T22397	hypothetical prote	191	54.5	12.1	261	2	I45943	MHC class II - bov
119	56	12.5	492	2	I39591	hemolysin - Aeromo	192	54.5	12.1	323	2	T06506	glutenin low molec
120	56	12.5	518	2	T23745	hypothetical prote	193	54.5	12.1	348	2	S57601	ribonuclease H (EC
121	56	12.5	555	2	C83444	probable AMP-bindin	194	54.5	12.1	361	2	A91037	probable peptidase
122	56	12.5	703	2	A97312	membrane associate	195	54.5	12.1	361	2	C85881	hypothetical prote
123	56	12.5	711	2	D83897	catalase katB [imp	196	54.5	12.1	373	2	D71636	glycerol-3-phospha
124	56	12.5	714	2	S56208	hypothetical prote	197	54.5	12.1	396	2	S01660	tubulin alpha-2 ch
125	56	12.5	729	2	T46328	probable adenosine	198	54.5	12.1	448	2	S40439	tubulin alpha-1 ch
126	56	12.5	731	2	S56028	protein YKR018c ho	199	54.5	12.1	449	2	S55911	hypothetical prote
127	56	12.5	953	2	T01093	luminidependens pr	200	54.5	12.1	449	2	T21415	hypothetical prote
128	56	12.5	1161	2	B70172	DNA polymerase III	201	54.5	12.1	477	2	S53362	mucin 5AC (clone J
129	56	12.5	1308	2	B32494	transposable eleme	202	54.5	12.1	482	2	T02538	hypothetical prote
130	55.5	12.4	218	2	B49346	butyrate-acetoacet	203	54.5	12.1	506	2	D84609	hypothetical prote
131	55.5	12.4	276	2	A69437	dehydrase homolog	204	54.5	12.1	528	1	A31854	lanosterol 14alpha
132	55.5	12.4	288	2	A90135	SAM-dependent meth	205	54.5	12.1	681	1	A36500	transferrin precur
133	55.5	12.4	417	2	B97249	fusion HD-GYP doma	206	54.5	12.1	760	2	S70294	FUN21 protein - ye
134	55.5	12.4	441	2	S29921	hypothetical prote	207	54.5	12.1	774	2	A86454	hypothetical prote
135	55.5	12.4	501	2	S51160	nitrate reductase	208	54.5	12.1	811	1	POLJSP	gag polyprotein -
136	55.5	12.4	544	2	C96943	uncharacterized me	209	54.5	12.1	859	1	VCLJCT	env polyprotein pr
137	55.5	12.4	646	2	JN0473	p-selectin precurs	210	54.5	12.1	859	2	S24571	env protein - huma
138	55.5	12.4	683	2	T03146	probable glycoprot	211	54.5	12.1	916	2	S07554	nitrate reductase
139	55.5	12.4	699	2	I37369	epican - human	212	54.5	12.1	1034	2	AB2013	hypothetical prote
140	55.5	12.4	704	1	S39004	finger protein MSN	213	54.5	12.1	1036	2	A29832	HPI layer surface
141	55.5	12.4	858	1	A42239	adenylate cyclase	214	54.5	12.1	1106	2	T25065	hypothetical prote
142	55.5	12.4	884	2	S66308	nitrate reductase	215	54.5	12.1	1133	2	T01757	hypothetical prote
143	55.5	12.4	886	2	A59223	nitrate reductase	216	54.5	12.1	1241	2	JU0466	potassium transpor
144	55.5	12.4	912	1	RDBHNS	nitrate reductase	217	54.5	12.1	1599	2	T16210	hypothetical prote
145	55.5	12.4	915	1	RDBHNS	nitrate reductase	218	54.5	12.1	1776	1	RRWPM	genome polyprotein
146	55.5	12.4	1016	2	T30990	period protein - C	219	54.5	12.1	2524	2	A35844	Xotch protein - Af
147	55.5	12.4	1056	2	A53767	mucin MUC5B, trach	220	54.5	12.1	6658	2	T13931	projectin - fruit
148	55.5	12.4	1874	1	JQ0533	genome polyprotein	221	54	12.0	115	2	AB2223	hypothetical prote
149	55	12.2	183	2	A32339	MHC class II histo	222	54	12.0	140	2	S20914	lysozyme (EC 3.2.1
150	55	12.2	183	2	I54288	MHC class II DQ3.1	223	54	12.0	140	2	S41577	lysozyme (EC 3.2.1
151	55	12.2	183	2	I79496	MHC HLA-DQ-beta ch	224	54	12.0	140	2	S41574	lysozyme (EC 3.2.1
152	55	12.2	218	2	G71260	probable ribulose-	225	54	12.0	140	2	S41573	lysozyme (EC 3.2.1
153	55	12.2	224	2	A31459	MHC class II histo	226	54	12.0	214	2	S45465	heat shock protein
154	55	12.2	233	2	E83580	conserved hypothe	227	54	12.0	221	2	S25168	CHT28 protein - ch
155	55	12.2	261	1	HLHU1C	MHC class II histo	228	54	12.0	223	1	CSNCM	peptidylprolyl iso
156	55	12.2	261	1	HLHUDB	MHC class II histo	229	54	12.0	237	2	C86309	Similar to Ubiquit
157	55	12.2	261	2	I55996	MHC class II histo	230	54	12.0	260	2	I45938	MHC cell surface g
158	55	12.2	261	2	B37044	MHC class II histo	231	54	12.0	261	2	I68732	probable hydrolase
159	55	12.2	261	2	I54480	HLA DQ-beta - huma	232	54	12.0	276	2	H96985	hypothetical prote
160	55	12.2	261	2	B32527	class II histocomp	233	54	12.0	360	2	S48365	retinoid X recepto
161	55	12.2	268	2	D29312	MHC class II histo	234	54	12.0	422	2	I50516	mammalian swi/snf
162	55	12.2	287	2	T26411	hypothetical prote	235	54	12.0	425	2	T50184	hypothetical prote
163	55	12.2	358	2	I38429	connexin40 - human	236	54	12.0	447	2	T13204	hemolysin - Aeromo
164	55	12.2	359	2	E86706	hypothetical prote	237	54	12.0	485	2	S26575	cellulase (EC 3.2.
165	55	12.2	363	2	JC7750	CVC domain-contain	238	54	12.0	504	2	S54744	hypothetical prote
166	55	12.2	406	2	S60962	hypothetical prote	239	54	12.0	513	2	T41011	thyroid hormone re
167	55	12.2	413	2	S21560	aspartate transami	240	54	12.0	614	2	A32608	hypothetical zinc
168	55	12.2	443	2	F87488	prolyl-tRNA synthe	241	54	12.0	636	2	T41673	hypothetical prote
169	55	12.2	458	2	S50919	hypothetical prote	242	54	12.0	713	2	B75489	hypothetical prote
170	55	12.2	486	2	A25976	aerolysin precursor	243	54	12.0	771	2	T38616	hypothetical prote
171	55	12.2	571	1	HNNZP2	hemagglutinin-neur	244	54	12.0	802	2	T21315	hypothetical prote
172	55	12.2	571	1	HNNZT2	hemagglutinin-neur	245	54	12.0	849	2	T01286	probable RNA-bindin
173	55	12.2	582	2	T38743	hypothetical zinc	246	54	12.0	851	2	S12159	env protein - huma
174	55	12.2	586	2	JC7277	Sarcophaga-derived	247	54	12.0	890	2	T11805	nitrate reductase
175	55	12.2	593	2	T38547	probable cell divi	248	54	12.0	920	2	S52301	nitrate reductase

249	54	12.0	938	2	T39006	related to yeast z
250	54	12.0	964	2	T41547	hypothetical prote
251	54	12.0	978	2	T16948	hypothetical prote
252	54	12.0	989	2	A54505	serine-repeat anti
253	54	12.0	997	2	B71617	SERA antigen/papai
254	54	12.0	1224	2	T07446	DNA-directed RNA p
255	54	12.0	1446	2	T30916	carboxypeptidase D
256	54	12.0	1742	2	S24600	profectin - fruit
257	54	12.0	1746	1	S19694	tenascin precursor
258	54	12.0	1945	2	T13937	plexin A - fruit f
259	54	12.0	2718	2	A23475	G surface protein
260	53.5	11.9	114	2	A34353	anti-peptide Fab'
261	53.5	11.9	122	2	A11116	hypothetical prote
262	53.5	11.9	125	2	S40315	Ig kappa chain - h
263	53.5	11.9	175	2	T23437	hypothetical prote
264	53.5	11.9	261	2	F96722	hypothetical prote
265	53.5	11.9	264	2	S65070	chitinase (EC 3.2.
266	53.5	11.9	289	2	A48913	KRAB zinc finger p
267	53.5	11.9	308	2	B71697	probable proteinas
268	53.5	11.9	357	2	S09269	Ig alpha chain C r
269	53.5	11.9	403	2	E42521	A39R protein - vac
270	53.5	11.9	427	2	G82827	6-phosphofructokin
271	53.5	11.9	448	2	T22194	hypothetical prote
272	53.5	11.9	451	2	S13337	tubulin alpha-2 ch
273	53.5	11.9	455	2	T32189	zinc finger protei
274	53.5	11.9	474	2	A90520	ABC transporter pe
275	53.5	11.9	482	2	B83113	catalase PA4236 [i
276	53.5	11.9	517	2	S77255	hypothetical prote
277	53.5	11.9	617	2	S19254	nitrate reductase
278	53.5	11.9	642	2	S55521	beta-fructofuranos
279	53.5	11.9	661	2	T16597	hypothetical prote
280	53.5	11.9	678	2	H88187	protein C18H9.8 [i
281	53.5	11.9	751	2	T15230	hypothetical prote
282	53.5	11.9	823	2	H83724	hypothetical prote
283	53.5	11.9	825	2	T47164	hypothetical prote
284	53.5	11.9	900	2	S47029	nitrate reductase
285	53.5	11.9	909	2	JN0665	nitrate reductase
286	53.5	11.9	936	2	T26521	hypothetical prote
287	53.5	11.9	1131	2	T38744	hypothetical prote
288	53.5	11.9	1239	1	A32579	neuroglial - fruit
289	53.5	11.9	1513	2	T44045	hypothetical prote
290	53.5	11.9	1520	2	T44231	hypothetical prote
291	53.5	11.9	1712	2	C71618	hypothetical prote
292	53.5	11.9	2399	2	H71879	toxin-like outer m
293	53	11.8	140	2	A83285	hypothetical prote
294	53	11.8	144	2	T41370	hypothetical prote
295	53	11.8	203	2	T23943	hypothetical prote
296	53	11.8	207	2	T34054	hypothetical prote
297	53	11.8	232	2	B90129	26S proteasome SU
298	53	11.8	263	2	D83085	conserved hypothet
299	53	11.8	302	2	E64800	probable glutamate
300	53	11.8	302	2	A85566	probable periplasm
301	53	11.8	302	2	F90715	probable periplasm
302	53	11.8	310	2	JL0119	Fc gamma (IgG) rec
303	53	11.8	317	2	JL0118	Fc gamma (IgG) rec
304	53	11.8	323	2	S06946	endo-beta-N-acetyl
305	53	11.8	339	2	A42259	hypothetical prote
306	53	11.8	341	2	S31236	hypothetical prote
307	53	11.8	350	2	B82281	early switch prote
308	53	11.8	352	2	T23464	hypothetical prote
309	53	11.8	355	1	A55473	early switch prote
310	53	11.8	355	2	T07160	glutamate-ammonia
311	53	11.8	360	2	T06786	6a-hydroxymaackiai
312	53	11.8	367	2	T00815	probable Tail-like
313	53	11.8	413	1	XNPGDC	aspartate transami
314	53	11.8	417	2	B55473	early switch prote
315	53	11.8	426	2	C55473	early switch prote
316	53	11.8	428	2	A53689	transcription fact
317	53	11.8	436	2	B86469	protein F12K21.16
318	53	11.8	443	2	T14916	mitosis-specific c
319	53	11.8	445	2	D84385	oligopeptide ABC t
320	53	11.8	461	2	T11819	glycerol-3-phospha
321	53	11.8	484	2	T16695	hypothetical prote

322	53	11.8	504	2	S00390	Ig gamma chain (cl
323	53	11.8	530	2	F89581	protein xol-1 (limp
324	53	11.8	533	1	TVFVFP	protein-tyrosine k
325	53	11.8	536	2	S66716	glutamate-tRNA lig
326	53	11.8	634	2	S31925	beta-fructofuranos
327	53	11.8	642	1	S34416	transcription fact
328	53	11.8	649	2	AH3546	outer membrane pro
329	53	11.8	660	2	T00902	hypothetical prote
330	53	11.8	666	2	I52648	class A helix-loop
331	53	11.8	667	2	A41311	transcription fact
332	53	11.8	687	2	S69723	hypothetical prote
333	53	11.8	744	2	S68115	catalase (EC 1.11.
334	53	11.8	782	1	G64157	probable organic s
335	53	11.8	838	2	T04449	hypothetical prote
336	53	11.8	852	2	S41886	DNA repair protein
337	53	11.8	858	1	VCLJG2	env polyprotein pr
338	53	11.8	911	2	T08108	nitrate reductase
339	53	11.8	917	2	B96807	nitrate reductase
340	53	11.8	917	2	S35228	nitrate reductase
341	53	11.8	969	2	T23256	hypothetical prote
342	53	11.8	1121	2	T52631	1-phosphatidylinos
343	53	11.8	1159	2	S62562	probable nuclear p
344	53	11.8	1337	1	I38670	protein-tyrosine-p
345	53	11.8	1344	2	H84557	hypothetical prote
346	53	11.8	1365	2	T00833	RNA-directed DNA p
347	53	11.8	1806	2	T23298	hypothetical prote
348	53	11.8	4688	2	F82885	hypothetical prote
349	52.5	11.7	99	2	D70582	probable PG protei
350	52.5	11.7	210	2	T49785	hypothetical prote
351	52.5	11.7	222	2	S22517	S-allele-associate
352	52.5	11.7	257	1	S50294	hypothetical prote
353	52.5	11.7	261	2	G90612	cytochrome c oxida
354	52.5	11.7	272	2	T09132	26S proteasome bet
355	52.5	11.7	304	2	A97768	probable protease
356	52.5	11.7	327	1	JQ0965	chitinase (EC 3.2.
357	52.5	11.7	357	2	C69223	anion permease - M
358	52.5	11.7	361	2	A41535	glutamyl-peptide
359	52.5	11.7	414	2	A70214	hypothetical prote
360	52.5	11.7	419	2	T18420	hypothetical prote
361	52.5	11.7	449	2	A48466	tubulin alpha chai
362	52.5	11.7	457	2	T15271	hypothetical prote
363	52.5	11.7	462	2	S44490	RXR type hormone r
364	52.5	11.7	470	2	T10193	glycerol-3-phospha
365	52.5	11.7	472	2	S51768	glycerol-3-phospha
366	52.5	11.7	491	1	CSRZ	catalase (EC 1.11.
367	52.5	11.7	499	1	S30007	probable UTP-gluc
368	52.5	11.7	536	2	T04222	hypothetical prote
369	52.5	11.7	556	2	S51858	probable membrane
370	52.5	11.7	795	2	T21487	hypothetical prote
371	52.5	11.7	798	2	B27079	fibronectin recept
372	52.5	11.7	803	2	S45916	hypothetical prote
373	52.5	11.7	837	2	S45624	ROP1 protein - yea
374	52.5	11.7	844	2	T00529	hypothetical prote
375	52.5	11.7	852	1	VCLJGG	env polyprotein pr
376	52.5	11.7	891	2	G89957	hypothetical prote
377	52.5	11.7	985	2	I51549	receptor tyrosine
378	52.5	11.7	1015	2	A42915	type II cAMP-depen
379	52.5	11.7	1017	2	T42384	inositol-1,4,5-tri
380	52.5	11.7	1036	1	A34755	nitrogen regulator
381	52.5	11.7	1106	2	T19948	hypothetical prote
382	52.5	11.7	1146	2	S64402	probable transcrip
383	52.5	11.7	1211	2	S54500	alpha,alpha-trehal
384	52.5	11.7	1367	1	IGHUR1	insulin-like growt
385	52.5	11.7	1445	2	A59437	KRAA1204 protein [
386	52.5	11.7	1449	1	A43573	E2 glycoprotein pr
387	52.5	11.7	1449	1	VGIHFS	E2 glycoprotein pr
388	52.5	11.7	1449	2	S47423	E2 glycoprotein pr
389	52.5	11.7	1806	2	AF1717	probable peptidogl
390	52.5	11.7	3014	1	JC5620	genome polyprotein
391	52	11.6	133	2	S57885	T-cell receptor al
392	52	11.6	167	2	I58352	p16INK4a - mouse
393	52	11.6	194	1	YQEC7P	fimbrial protein 9
394	52	11.6	215	2	JE0243	Ig kappa chain NIG

395	52	11.6	239	2	T34305	hypothetical prote
396	52	11.6	287	2	A45854	leucocyte common a
397	52	11.6	289	2	T25277	hypothetical prote
398	52	11.6	291	2	T01241	probable MYB famil
399	52	11.6	301	2	C69143	hypothetical prote
400	52	11.6	305	2	AD3378	hypothetical prote
401	52	11.6	373	2	T10341	late expression fa
402	52	11.6	426	2	T20253	hypothetical prote
403	52	11.6	437	2	S55392	mah ptein - fruit
404	52	11.6	471	2	D90094	hypothetical prote
405	52	11.6	505	2	F71218	hypothetical prote
406	52	11.6	514	2	T11249	cytochrome-c oxida
407	52	11.6	516	2	F82070	2-isopropylmalate
408	52	11.6	533	2	H86282	protein F10B6.34 [
409	52	11.6	572	2	S77249	hypothetical prote
410	52	11.6	597	2	T23961	hypothetical prote
411	52	11.6	611	2	T21747	hypothetical prote
412	52	11.6	638	2	B83890	hypothetical prote
413	52	11.6	681	2	S33316	structural protein
414	52	11.6	681	2	A45705	type I transembra
415	52	11.6	729	2	T52187	probable transposa
416	52	11.6	799	1	TVRTTB	nerve growth facto
417	52	11.6	855	2	A45713	Env transmembrane
418	52	11.6	865	2	E84718	hypothetical prote
419	52	11.6	903	2	E88221	protein T0IH3.2 [i
420	52	11.6	926	2	T48391	protein kinase-lik
421	52	11.6	1273	1	TDRTL	leucocyte common a
422	52	11.6	1398	2	S56814	microtubule-intera
423	52	11.6	1444	1	A30588	140K adhesin precu
424	52	11.6	2958	2	S64921	probable membrane
425	52	11.6	4981	2	T18489	hypothetical prote
426	51.5	11.5	98	2	PH1069	Ig light chain V r
427	51.5	11.5	102	2	S35882	AL0 protein - Indi
428	51.5	11.5	113	2	G71071	hypothetical prote
429	51.5	11.5	124	2	S40336	Ig kappa chain V-J
430	51.5	11.5	143	2	A95253	PTS system, IIA co
431	51.5	11.5	145	2	T16598	hypothetical prote
432	51.5	11.5	146	2	D42402	cell surface glyco
433	51.5	11.5	148	2	G98117	hypothetical prote
434	51.5	11.5	194	2	H22845	hypothetical prote
435	51.5	11.5	207	2	G69381	flagellin (flaB1-2
436	51.5	11.5	210	2	A85018	probable copper-co
437	51.5	11.5	211	2	E71334	hypothetical prote
438	51.5	11.5	257	2	I54285	MHC class II histo
439	51.5	11.5	261	2	A26344	carbonate dehydrat
440	51.5	11.5	262	2	G81954	cytochrome C1 prec
441	51.5	11.5	262	2	T34547	hypothetical prote
442	51.5	11.5	266	2	D81011	ubiquinol-cytochro
443	51.5	11.5	278	2	D36791	hypothetical prote
444	51.5	11.5	280	2	AF3144	non-heme chloroper
445	51.5	11.5	312	2	C84511	hypothetical prote
446	51.5	11.5	312	2	C75124	hypothetical prote
447	51.5	11.5	313	2	T49129	hypothetical prote
448	51.5	11.5	320	2	A40216	flavonol 4'-sulfo
449	51.5	11.5	324	2	E85513	probable integrase
450	51.5	11.5	324	2	G90662	probable integrase
451	51.5	11.5	326	2	F98143	non-heme chloroper
452	51.5	11.5	332	2	AH2533	hypothetical prote
453	51.5	11.5	344	2	T29264	hypothetical prote
454	51.5	11.5	376	2	T05420	cyclin delta-3 - A
455	51.5	11.5	377	2	T31604	hypothetical prote
456	51.5	11.5	387	2	D88968	protein T27B7.3 [i
457	51.5	11.5	395	2	S51449	probable membrane
458	51.5	11.5	446	2	S46786	serine-trna ligase
459	51.5	11.5	447	2	T06004	1-aminocyclopropan
460	51.5	11.5	465	2	B71716	transhydrogenase c
461	51.5	11.5	484	2	D64214	hypothetical prote
462	51.5	11.5	492	2	T09756	catalase (EC 1.11.
463	51.5	11.5	511	1	VGVN	spike glycoprotein
464	51.5	11.5	513	2	S58200	probable membrane
465	51.5	11.5	527	2	JE0373	low density lipopr
466	51.5	11.5	537	2	S26857	isocitrate lyase (
467	51.5	11.5	538	2	S62566	PHD finger protein

468	51.5	11.5	551	2	S05667	glucan 1,4-alpha-m
469	51.5	11.5	570	2	S56132	cellulase (EC 3.2.
470	51.5	11.5	576	2	S75958	hypothetical prote
471	51.5	11.5	576	2	T38293	hypothetical serin
472	51.5	11.5	578	1	BVBVD1	GCD1 protein - yea
473	51.5	11.5	578	2	S66353	L-ascorbate oxidas
474	51.5	11.5	610	2	S50539	hypothetical prote
475	51.5	11.5	618	2	T49177	hypothetical prote
476	51.5	11.5	620	2	JC4925	XmnI methyltransfe
477	51.5	11.5	648	2	B81686	conserved hypothet
478	51.5	11.5	717	1	S29923	transforming prote
479	51.5	11.5	766	2	B85440	receptor kinase-li
480	51.5	11.5	792	2	T26050	hypothetical prote
481	51.5	11.5	854	2	AC2309	hypothetical prote
482	51.5	11.5	862	2	I49583	differentiation an
483	51.5	11.5	868	2	A46512	CD22 homolog/B lym
484	51.5	11.5	911	2	T08105	nitrate reductase
485	51.5	11.5	959	2	B44402	nuclear pore compl
486	51.5	11.5	965	2	T12545	hypothetical prote
487	51.5	11.5	1007	2	G96606	disease resistance
488	51.5	11.5	1107	2	S61667	probable membrane
489	51.5	11.5	1142	2	S59359	GIN4 protein - Yea
490	51.5	11.5	1335	2	H86489	protein T32E20.13
491	51.5	11.5	1338	2	T18416	hypothetical prote
492	51.5	11.5	1518	2	A44811	glucosyltransferas
493	51.5	11.5	1528	2	S13743	DNA strand transfe
494	51.5	11.5	3635	2	T10053	laminin alpha 5 ch
495	51.5	11.5	4753	1	A47437	LDL-receptor-relat
496	51.5	11.5	5005	2	F82884	hypothetical prote
497	51.5	11.5	26926	1	I38344	titin, cardiac mus
498	51	11.4	160	2	C64171	hypothetical prote
499	51	11.4	174	2	T48419	hypothetical prote
500	51	11.4	191	2	E75132	molybdopterin-guan
501	51	11.4	205	2	B31906	hypothetical prote
502	51	11.4	221	2	T03954	hypothetical prote
503	51	11.4	253	2	T40687	hypothetical prote
504	51	11.4	287	2	C82158	ROK family protein
505	51	11.4	290	2	G72858	AcOrf-70 protein -
506	51	11.4	319	2	AD1108	other proteins hom
507	51	11.4	322	2	T25416	hypothetical prote
508	51	11.4	329	2	H83907	cytochrome aa3 qui
509	51	11.4	331	2	F86142	F633.5 protein - A
510	51	11.4	333	2	AF0407	lipoprotein (impor
511	51	11.4	352	2	G85606	hypothetical prote
512	51	11.4	352	2	F90797	hypothetical prote
513	51	11.4	388	2	S59860	hypothetical prote
514	51	11.4	397	2	I39184	bomapin - human
515	51	11.4	402	2	A84581	probable disease r
516	51	11.4	407	2	C45600	asparagine-rich bl
517	51	11.4	417	2	A45794	tubulin alpha chai
518	51	11.4	430	2	T23899	hypothetical prote
519	51	11.4	430	2	I39727	mannopine biosynth
520	51	11.4	470	2	T25578	hypothetical prote
521	51	11.4	481	2	F97472	hypothetical prote
522	51	11.4	488	2	E70234	conserved hypothet
523	51	11.4	512	2	H86216	protein T23G18.16
524	51	11.4	555	2	H96762	hypothetical prote
525	51	11.4	578	2	S55102	PSP2 protein - yea
526	51	11.4	580	2	T46024	hypothetical prote
527	51	11.4	642	2	S53434	plasma protein S p
528	51	11.4	684	2	S45758	proliferating-cell
529	51	11.4	710	2	T41352	probable transcrip
530	51	11.4	714	2	C90100	hypothetical prote
531	51	11.4	732	2	F84394	helicase [imported
532	51	11.4	753	2	A27041	tyrosine kinase-re
533	51	11.4	758	2	S47866	SPR21 protein - ye
534	51	11.4	773	2	D89010	protein R08F11.7 [
535	51	11.4	795	2	T20939	hypothetical prote
536	51	11.4	798	2	S01659	integrin beta-1 ch
537	51	11.4	799	1	IJMSFB	fibronectin recept
538	51	11.4	799	2	JC4126	integrin beta olig
539	51	11.4	805	2	T21957	hypothetical prote
540	51	11.4	807	2	T02916	hypothetical prote

541	51	11.4	839	1	TQZMCA	probable transposase	614	50.5	11.2	827	2	T04789	hypothetical prote
542	51	11.4	874	2	S62486	probable leucyl tr	615	50.5	11.2	869	2	S53098	envelope polypept
543	51	11.4	879	2	S64755	hypothetical prote	616	50.5	11.2	904	1	RDNTNS	nitrate reductase
544	51	11.4	882	2	C83234	hypothetical prote	617	50.5	11.2	904	1	RDNTNT	nitrate reductase
545	51	11.4	890	2	A98017	probable 2-compone	618	50.5	11.2	911	1	RDTONH	nitrate reductase
546	51	11.4	890	2	C85861	probable 2-compone	619	50.5	11.2	926	1	RDSPNH	nitrate reductase
547	51	11.4	890	2	F64991	yojN protein - Esc	620	50.5	11.2	960	2	T50383	homolog to yeast c
548	51	11.4	900	2	T19689	hypothetical prote	621	50.5	11.2	964	2	JC5545	integrin beta-4 pr
549	51	11.4	995	2	S67564	hypothetical prote	622	50.5	11.2	974	1	A40213	optic lobe develop
550	51	11.4	1021	2	S64506	hypothetical prote	623	50.5	11.2	1050	2	T27753	hypothetical prote
551	51	11.4	1034	2	A36108	protein kinase BUB	624	50.5	11.2	1070	2	T34385	hypothetical prote
552	51	11.4	1041	2	D82792	integrin alpha-V c	625	50.5	11.2	1087	2	S58147	protein kinase - f
553	51	11.4	1079	2	PC7034	conserved hypotHet	626	50.5	11.2	1148	2	T09073	splicing factor Si
554	51	11.4	1092	2	JX0312	Na+ bicarbonate co	627	50.5	11.2	1195	2	S61886	chitin synthase (B
555	51	11.4	1097	2	S17308	differentiation-st	628	50.5	11.2	1228	2	G90581	hypothetical prote
556	51	11.4	1112	2	S28289	leukemia inhibitor	629	50.5	11.2	1292	2	T09229	galactose binding
557	51	11.4	1187	1	TVHUY2	hypothetical prote	630	50.5	11.2	1325	2	S62497	probable nucleopor
558	51	11.4	1205	2	T41987	protein-tyrosine k	631	50.5	11.2	1466	2	A36426	SPA2 protein - yea
559	51	11.4	1209	2	T46027	hypothetical prote	632	50.5	11.2	1607	2	T04583	TMV resistance pro
560	51	11.4	1247	2	F86405	hypothetical prote	633	50.5	11.2	1692	2	A33988	adenylate cyclase
561	51	11.4	1265	2	T51498	probable P-glycopr	634	50.5	11.2	1708	2	F69189	protoporphyrin IX
562	51	11.4	1379	1	S01254	hypothetical prote	635	50.5	11.2	1875	2	A36429	integrin beta-4 ch
563	51	11.4	1385	2	A88554	hepatocyte growth	636	50.5	11.2	2167	2	S50658	bud emergence prot
564	51	11.4	1391	2	B88554	protein C38C10.5a	637	50.5	11.2	3623	2	T08618	intrinsic factor-B
565	51	11.4	1424	2	T03851	protein C38C10.5b	638	50	11.1	115	2	T51208	hypothetical prote
566	51	11.4	1604	2	B86287	thyroid hormone re	639	50	11.1	118	2	F58932	ribosomal protein
567	51	11.4	1839	2	S77626	F9L1.23 protein -	640	50	11.1	165	2	A82246	probable phosphata
568	51	11.4	2197	2	B71600	mannuronan C-5-epi	641	50	11.1	175	1	CYBOAB	alpha-crystallin c
569	51	11.4	3124	2	A40020	variant-specific s	642	50	11.1	175	1	CYHUAB	alpha-crystallin c
570	50.5	11.2	125	2	A53627	collagen alpha 1(X	643	50	11.1	175	2	A53871	alpha-crystallin c
571	50.5	11.2	233	2	T00202	fibroblast growth	644	50	11.1	191	2	T19668	hypothetical prote
572	50.5	11.2	254	2	S20741	occlusion-derived	645	50	11.1	202	1	DHRT	IG delta chain C r
573	50.5	11.2	264	2	H90102	chitinase (EC 3.2.	646	50	11.1	215	2	JE0242	IG kappa chain NIG
574	50.5	11.2	280	2	F81984	translational init	647	50	11.1	217	2	T50521	hypothetical prote
575	50.5	11.2	281	2	A97604	hypothetical prote	648	50	11.1	243	2	T24981	hypothetical prote
576	50.5	11.2	281	2	AB2826	probable oxidoredu	649	50	11.1	245	2	T41291	conserved hypotHet
577	50.5	11.2	283	2	S73523	aldo/keto reductas	650	50	11.1	261	2	A60404	MHC class II histo
578	50.5	11.2	324	1	UBCHA8	probable lipoprote	651	50	11.1	261	2	B60404	MHC class II histo
579	50.5	11.2	325	2	G70334	tubulin alpha-8 ch	652	50	11.1	270	2	T43491	hypothetical prote
580	50.5	11.2	332	2	S49758	hypothetical prote	653	50	11.1	271	2	C82841	cysteine proteinas
581	50.5	11.2	338	2	S73441	probable membrane	654	50	11.1	311	2	A69095	cobalt transport A
582	50.5	11.2	340	2	T48288	MG032 homolog B01	655	50	11.1	321	2	AG2936	transglycosylase A
583	50.5	11.2	342	2	S57814	hypothetical prote	656	50	11.1	321	2	H98345	hypothetical prote
584	50.5	11.2	361	1	F65012	oxidase like prote	657	50	11.1	327	1	HLHUCD	hypothetical prote
585	50.5	11.2	361	2	S67590	hypothetical prote	658	50	11.1	345	2	AI2217	T-cell surface gly
586	50.5	11.2	361	2	AH1469	mannose-1-phosphat	659	50	11.1	354	2	JT0594	low specificity L-
587	50.5	11.2	376	2	B96714	internalin protein	660	50	11.1	368	2	S46601	site-specific DNA-
588	50.5	11.2	420	2	T47998	hypothetical prote	661	50	11.1	370	2	A96547	hypothetical prote
589	50.5	11.2	427	2	AH2141	pectinacetylestera	662	50	11.1	374	2	T24162	hypothetical prote
590	50.5	11.2	446	2	H90094	type I restriction	663	50	11.1	379	2	T04762	chitinase homolog
591	50.5	11.2	454	2	S65970	hypothetical prote	664	50	11.1	397	1	Z6BPT9	ribonucleoside-tri
592	50.5	11.2	455	2	T49176	replicative DNA he	665	50	11.1	410	2	G90362	hypothetical prote
593	50.5	11.2	459	2	T11489	hypothetical prote	666	50	11.1	416	2	B86384	probable zinc fing
594	50.5	11.2	492	2	T09754	hypothetical prote	667	50	11.1	418	2	A37344	acrosin (EC 3.4.21
595	50.5	11.2	494	2	S62697	catalase (EC 1.11.	668	50	11.1	431	2	F90316	dsrP protein, prob
596	50.5	11.2	541	2	T33312	catalase (EC 1.11.	669	50	11.1	436	1	A70409	hypothetical prote
597	50.5	11.2	550	2	G86225	hypothetical prote	670	50	11.1	438	1	HVRKC2	IG mu chain C regi
598	50.5	11.2	561	2	T23564	hypothetical prote	671	50	11.1	456	2	T33822	hypothetical prote
599	50.5	11.2	567	2	B84650	probable selenium-	672	50	11.1	459	2	A25928	cellulase (EC 3.2.
600	50.5	11.2	568	2	T28041	hypothetical prote	673	50	11.1	473	2	B85187	glycoprotein homol
601	50.5	11.2	592	2	S25705	hypothetical prote	674	50	11.1	494	2	A48657	monophenol monooxy
602	50.5	11.2	610	2	S05807	IG mu chain - shee	675	50	11.1	497	2	S74404	o-succinylbenzoate
603	50.5	11.2	624	2	A84150	SAN1 protein - Yea	676	50	11.1	497	2	T15812	hypothetical prote
604	50.5	11.2	660	2	S71276	beta-fructofuranos	677	50	11.1	505	2	S39962	hypothetical prote
605	50.5	11.2	664	2	B86257	beta-fructosidase	678	50	11.1	512	2	AF3628	nitrate reductase
606	50.5	11.2	683	1	A41785	system b(0,+) amin	679	50	11.1	513	2	T37806	probable flavoprot
607	50.5	11.2	687	2	S56939	probable membrane	680	50	11.1	520	2	C64213	ribose transport s
608	50.5	11.2	688	2	T32750	hypothetical prote	681	50	11.1	522	2	S77073	hypothetical prote
609	50.5	11.2	720	2	E72074	1,4-alpha-glucan b	682	50	11.1	524	2	G64243	hypothetical prote
610	50.5	11.2	720	2	G86549	glucan branching e	683	50	11.1	524	2	S46007	hypothetical prote
611	50.5	11.2	743	2	C56695	transducin-like en	684	50	11.1	568	2	B86400	T17H3.1 protein -
612	50.5	11.2	769	2	T08431	gene bobby sox pro	685	50	11.1	584	1	ALBY	alpha-glucosidase
613	50.5	11.2	795	2	E86247	receptor-like prot	686	50	11.1	584	2	S64627	alpha-glucosidase

687	50	11.1	584	2	S46183	alpha-glucosidase	760	49.5	11.0	264	2	S11650	class II histocomp
688	50	11.1	592	1	S13391	endo-1,4-beta-xyla	761	49.5	11.0	264	2	A30529	H-2 class II histo
689	50	11.1	603	2	S61504	glycogen(starch) s	762	49.5	11.0	264	2	I48422	MHC class II histo
690	50	11.1	605	2	T07123	nine-cis-epoxycaro	763	49.5	11.0	267	2	AC3232	conjugal transfer
691	50	11.1	621	2	T20307	hypothetical prote	764	49.5	11.0	269	2	S61633	YNT20 protein - Ye
692	50	11.1	631	2	S67268	hypothetical prote	765	49.5	11.0	278	2	B65006	hypothetical prote
693	50	11.1	672	2	T20310	hypothetical prote	766	49.5	11.0	293	2	G86901	hypothetical prote
694	50	11.1	676	1	KXHUS	plasma protein S p	767	49.5	11.0	317	2	F70185	phosphomevalonate
695	50	11.1	682	2	T18847	hypothetical prote	768	49.5	11.0	319	2	F75420	hypothetical prote
696	50	11.1	710	2	S30154	low-temperature-in	769	49.5	11.0	324	2	S56694	chitinase (EC 3.2.
697	50	11.1	747	1	QRECFE	ferrichrome-iron r	770	49.5	11.0	325	2	A69930	conserved hypothet
698	50	11.1	747	2	B85499	outer membrane rec	771	49.5	11.0	326	2	A28129	sporulation-specif
699	50	11.1	747	2	B90648	outer membrane rec	772	49.5	11.0	328	2	E82324	immunogenic protei
700	50	11.1	750	2	S67100	protein-tyrosine-p	773	49.5	11.0	335	2	G82708	malate dehydrogena
701	50	11.1	758	1	S45477	SEC18 protein - ye	774	49.5	11.0	342	2	S63654	hypothetical COI i
702	50	11.1	758	2	S65169	hypothetical prote	775	49.5	11.0	361	2	T14800	hypothetical prote
703	50	11.1	771	1	WMVZ9J	ribonucleoside-dip	776	49.5	11.0	371	2	A61275	tubulin alpha-2 ch
704	50	11.1	771	1	WZVZH4	ribonucleoside-dip	777	49.5	11.0	376	2	S45763	hypothetical prote
705	50	11.1	771	2	T28496	ribonucleoside-dip	778	49.5	11.0	387	2	AG3218	acetyloronithine de
706	50	11.1	771	2	B36843	ribonucleoside-dip	779	49.5	11.0	411	1	UBCHA	tubulin alpha chai
707	50	11.1	771	2	H72157	L4L protein - vari	780	49.5	11.0	418	2	JC7872	stearyl-CoA 9-des
708	50	11.1	798	2	F96714	probable protease	781	49.5	11.0	426	2	H97765	proline-tRNA ligas
709	50	11.1	813	2	A40601	ferripyoverdine re	782	49.5	11.0	432	2	G71695	conserved hypothet
710	50	11.1	815	2	H83345	ferripyoverdine re	783	49.5	11.0	434	2	AE0226	tubulin alpha chai
711	50	11.1	857	1	QQBE1L	glycoprotein B - h	784	49.5	11.0	444	2	A56635	tubulin alpha chai
712	50	11.1	879	2	B84765	hypothetical prote	785	49.5	11.0	444	2	S25004	tubulin alpha chai
713	50	11.1	961	2	A55380	faciogenital dyspl	786	49.5	11.0	448	1	UBCHA5	tubulin alpha-5 ch
714	50	11.1	974	2	S15038	cell division cont	787	49.5	11.0	448	2	A25873	tubulin alpha chai
715	50	11.1	1009	2	S61174	hypothetical prote	788	49.5	11.0	448	2	I77427	tubulin alpha chai
716	50	11.1	1046	2	T30199	chitinase (EC 3.2.	789	49.5	11.0	449	2	S00253	tubulin alpha chai
717	50	11.1	1048	2	S64758	SCD25 protein (ver	790	49.5	11.0	449	2	I77428	tubulin alpha chai
718	50	11.1	1139	1	E64234	cytadherence-acces	791	49.5	11.0	450	2	S43138	tubulin alpha chai
719	50	11.1	1145	2	T33606	hypothetical prote	792	49.5	11.0	451	1	UBPGA	tubulin alpha chai
720	50	11.1	1206	2	T30555	nitric-oxide synth	793	49.5	11.0	451	1	UBRTA	tubulin alpha chai
721	50	11.1	1323	2	S27224	N-methyl-D-asparta	794	49.5	11.0	451	2	A23035	tubulin alpha-3 ch
722	50	11.1	1323	2	I78557	N-methyl-D-asparta	795	49.5	11.0	451	2	C24903	tubulin alpha-1 ch
723	50	11.1	1356	1	C45219	N-methyl-D-asparta	796	49.5	11.0	451	2	JC4133	tubulin alpha chai
724	50	11.1	1827	1	UUHU	sucrose alpha-gluc	797	49.5	11.0	451	2	I77403	tubulin alpha-1 ch
725	50	11.1	2279	2	T42531	acetyl-CoA carboxy	798	49.5	11.0	451	2	A24903	tubulin alpha-1 ch
726	50	11.1	2280	2	T38906	acetyl-CoA carboxy	799	49.5	11.0	451	2	B24903	tubulin alpha-2 ch
727	50	11.1	2327	2	T31733	hypothetical prote	800	49.5	11.0	451	2	I77424	tubulin alpha chai
728	50	11.1	2655	2	D96595	probable acetyl-Co	801	49.5	11.0	451	2	I77425	tubulin alpha chai
729	50	11.1	3328	2	T30835	breast cancer tumo	802	49.5	11.0	452	2	A60671	tubulin alpha chai
730	50	11.1	3329	2	T42205	breast cancer susc	803	49.5	11.0	452	2	S11207	tubulin alpha chai
731	50	11.1	3343	2	S44887	ZK112.7 protein -	804	49.5	11.0	477	2	JS0597	t-plasminogen acti
732	50	11.1	4131	2	T21085	hypothetical prote	805	49.5	11.0	477	2	F64805	RhsA protein (impo
733	50	11.1	4725	1	A44357	dynein heavy chain	806	49.5	11.0	479	2	F82328	aspartokinase III,
734	49.5	11.0	92	2	S37512	Ig kappa chain V r	807	49.5	11.0	480	2	S38134	probable xanthine
735	49.5	11.0	102	2	B83934	hypothetical prote	808	49.5	11.0	493	2	F95940	hypothetical prote
736	49.5	11.0	119	2	D84845	hypothetical prote	809	49.5	11.0	495	2	T33065	hypothetical prote
737	49.5	11.0	165	2	S68776	myogenin - rainbow	810	49.5	11.0	522	2	T19762	hypothetical prote
738	49.5	11.0	187	2	I84461	MHC HLA-SB beta ch	811	49.5	11.0	529	2	T00677	hypothetical prote
739	49.5	11.0	187	2	T51876	hypothetical prote	812	49.5	11.0	542	2	AH2191	probable purine nu
740	49.5	11.0	207	2	AG2553	hypothetical prote	813	49.5	11.0	543	2	S56830	beta-fructofuranos
741	49.5	11.0	222	2	F96918	beta-phosphoglucom	814	49.5	11.0	562	2	S57951	hypothetical prote
742	49.5	11.0	224	1	HLHUS1	MHC class II histo	815	49.5	11.0	608	2	T18437	noncapsid protein
743	49.5	11.0	224	2	I68751	MHC class II lymph	816	49.5	11.0	620	1	UYVPAP	probable serine pr
744	49.5	11.0	229	2	A28909	MHC class II histo	817	49.5	11.0	632	2	D84921	similar to axi 1 p
745	49.5	11.0	232	1	HLMSE2	H-2 class II histo	818	49.5	11.0	638	2	E84799	beta-fructofuranos
746	49.5	11.0	233	2	I55654	MHC class II prote	819	49.5	11.0	639	2	S71268	tumor cell suppres
747	49.5	11.0	237	2	A21200	H-2 class II histo	820	49.5	11.0	645	2	A49013	cysteine proteinas
748	49.5	11.0	241	2	I48657	I-E(b-beta) protei	821	49.5	11.0	658	2	T08153	envelope protein -
749	49.5	11.0	243	2	A53506	folate receptor ty	822	49.5	11.0	669	2	A46511	catalase (EC 1.11.
750	49.5	11.0	244	2	C90580	DNA processing pro	823	49.5	11.0	686	2	D69647	protein F23N19.3 l
751	49.5	11.0	258	1	HLHUPB	MHC class II histo	824	49.5	11.0	728	2	A96652	probable membrane
752	49.5	11.0	258	1	HLHUS2	MHC class II histo	825	49.5	11.0	760	2	S19374	amine oxidase (cop
753	49.5	11.0	258	2	I54458	MHC class II histo	826	49.5	11.0	762	2	A54411	glucose-6-phosphat
754	49.5	11.0	261	2	AH2960	HLA-DPB1 - human	827	49.5	11.0	763	2	A47563	cellobiose oxidase
755	49.5	11.0	261	2	AH2960	ABC transporter, m	828	49.5	11.0	770	2	S60676	beta-1 integrin su
756	49.5	11.0	261	2	F98322	nitrate transport	829	49.5	11.0	773	2	I46059	nerve growth facto
757	49.5	11.0	261	2	T11525	cytochrome-c oxida	830	49.5	11.0	790	1	TVHUTT	gastric mucin MUC5
758	49.5	11.0	264	1	HLMSE1	H-2 class II histo	831	49.5	11.0	850	2	S56015	nitrate reductase
759	49.5	11.0	264	1	HLMSEB	H-2 class II histo	832	49.5	11.0	859	2	S70584	

833	49.5	11.0	859	2	AB2217	hypothetical prote	906	49	10.9	362	2	T52038	probable phytochel
834	49.5	11.0	868	1	JC4283	nitrate reductase	907	49	10.9	363	2	S56273	probable membrane
835	49.5	11.0	877	2	C46356	env polypeptide n	908	49	10.9	377	2	S67448	hypothetical prote
836	49.5	11.0	942	2	T37539	probable guanine n	909	49	10.9	385	2	A86165	protein F15K9.6 [i
837	49.5	11.0	985	2	B86084	hypothetical prote	910	49	10.9	389	2	S08031	nucleosid prote
838	49.5	11.0	997	2	S44457	period clock prote	911	49	10.9	393	1	HVRK01	Ig mu chain C regi
839	49.5	11.0	1028	2	G96769	unknown protein F9	912	49	10.9	410	2	I50494	serine proteinase
840	49.5	11.0	1030	2	T16114	hypothetical prote	913	49	10.9	426	2	I36948	Ig epsilon-chain -
841	49.5	11.0	1043	2	F97302	hypothetical prote	914	49	10.9	427	1	T49031	acid phosphatase (
842	49.5	11.0	1082	2	T31112	ATPase 2 (EC 3.6.1	915	49	10.9	428	2	S22377	aspartate transami
843	49.5	11.0	1131	2	S22266	FUN30 protein - ye	916	49	10.9	438	1	HVRK05	Ig mu chain C regi
844	49.5	11.0	1181	2	C86349	F8K7.4 protein - A	917	49	10.9	444	2	C84789	hypothetical prote
845	49.5	11.0	1237	2	A54080	protein-tyrosine-p	918	49	10.9	444	2	JC1141	metacyclic-form-sp
846	49.5	11.0	1377	2	B86034	rhsA protein in rh	919	49	10.9	461	1	HVRK01	Ig mu chain C regi
847	49.5	11.0	1377	2	C65159	rhsA protein precu	920	49	10.9	461	2	A31820	thyroid hormone re
848	49.5	11.0	1394	2	H91236	RhsH core protein	921	49	10.9	462	2	H64145	hypothetical prote
849	49.5	11.0	1397	2	A85570	rhcC protein in rh	922	49	10.9	472	2	E81784	glutamate-ammonia
850	49.5	11.0	1397	2	C64805	rhcC protein precu	923	49	10.9	472	2	F81208	neuroblast prolif
851	49.5	11.0	1399	2	A99720	RhsC core protein	924	49	10.9	474	2	A40721	testosterone 7alph
852	49.5	11.0	1402	2	F84480	probable retroelem	925	49	10.9	492	2	A34272	conserved hypothet
853	49.5	11.0	1409	2	F91187	rhsA core protein	926	49	10.9	510	2	T44810	nitrate reductase
854	49.5	11.0	1411	2	E65145	rhsB protein precu	927	49	10.9	510	2	H69893	NADH2 dehydrogenas
855	49.5	11.0	1590	2	B86398	protein T7N9.24 [i	928	49	10.9	513	2	F83162	carboxypeptidase C
856	49.5	11.0	1661	2	T31330	head-activator bin	929	49	10.9	513	2	E71683	cholesterol monoox
857	49.5	11.0	1677	2	T46095	hypothetical prote	930	49	10.9	523	1	S61713	xylan 1,4-beta-xyl
858	49.5	11.0	1677	2	T14267	hypothetical prote	931	49	10.9	526	1	A34164	receiver-like prot
859	49.5	11.0	1711	2	T21432	Xin protein, stage	932	49	10.9	536	2	G64752	hypothetical prote
860	49.5	11.0	1908	2	T42707	hypothetical prote	933	49	10.9	552	2	T04653	regulatory protein
861	49.5	11.0	2123	2	F86348	hypothetical prote	934	49	10.9	558	2	T02704	hypothetical prote
862	49.5	11.0	2330	1	RRIWMV	genome polypeptide	935	49	10.9	562	2	S16594	hypothetical prote
863	49.5	11.0	2331	2	S44054	probable polypeptide	936	49	10.9	605	2	T27397	hypothetical prote
864	49.5	11.0	2559	2	T09144	probable guanine n	937	49	10.9	611	2	T03890	hypothetical prote
865	49.5	11.0	2957	2	T33152	hypothetical prote	938	49	10.9	613	2	T15489	hypothetical prote
866	49.5	11.0	4307	2	T20721	hypothetical prote	939	49	10.9	623	2	T39001	probable exonuclea
867	49	10.9	55	2	AD1852	Ig kappa chain V r	940	49	10.9	626	2	H96810	probable RNA-bindi
868	49	10.9	77	2	G28840	hypothetical prote	941	49	10.9	649	2	S67787	hypothetical prote
869	49	10.9	89	2	F69268	hypothetical prote	942	49	10.9	651	2	T12083	beta-fructofuranos
870	49	10.9	101	1	ARRA3	allergen Ra3 - com	943	49	10.9	667	2	AD0295	probable formyl tr
871	49	10.9	107	2	S57444	Ig kappa chain V-J	944	49	10.9	675	1	KQMS	plasma protein S p
872	49	10.9	111	1	CCTO	cytochrome c [vali	945	49	10.9	700	1	HYHUMB	mepirin A (EC 3.4.2
873	49	10.9	128	2	T40464	probable RNA bindi	946	49	10.9	712	1	VCLJSA	env polypeptide pr
874	49	10.9	130	2	A82853	hypothetical prote	947	49	10.9	713	2	JN0133	WD-40 repeat regul
875	49	10.9	135	1	CBRT5M	cytochrome b5, out	948	49	10.9	779	2	C96805	hypothetical prote
876	49	10.9	157	2	S73704	hypothetical prote	949	49	10.9	802	2	T21464	hypothetical prote
877	49	10.9	158	2	B86169	hypothetical prote	950	49	10.9	843	2	S44868	kinesin heavy chai
878	49	10.9	173	2	JC5971	alpha-b crystallin	951	49	10.9	848	2	S48273	probable transcrip
879	49	10.9	213	2	G86195	hypothetical prote	952	49	10.9	849	2	I50617	protein-tyrosine k
880	49	10.9	226	2	AH1138	conserved hypothet	953	49	10.9	859	1	VCLJST	env polypeptide pr
881	49	10.9	228	2	B90369	hypothetical prote	954	49	10.9	860	1	C35905	endopeptidase Clp
882	49	10.9	234	2	D84768	hypothetical prote	955	49	10.9	874	2	JC4930	S-layer protein pr
883	49	10.9	239	2	S14470	asparagine-rich pr	956	49	10.9	876	2	G90592	hypothetical prote
884	49	10.9	247	1	QBEF1	HXLf3 protein prec	957	49	10.9	886	2	A57172	probable hormone r
885	49	10.9	259	2	F42528	B25R protein - vac	958	49	10.9	887	2	T11566	envelope glycoprot
886	49	10.9	263	2	G82259	probable rare lipo	959	49	10.9	905	2	G83314	NADH dehydrogenase
887	49	10.9	274	2	I50682	tenascin - chicken	960	49	10.9	927	2	F82818	conserved hypothet
888	49	10.9	285	1	YXECIC	isochorismatase (E	961	49	10.9	944	2	T41711	probable alpha-tre
889	49	10.9	285	2	F85558	isochorismatase (E	962	49	10.9	953	2	A86351	hypothetical prote
890	49	10.9	285	2	B90708	isochorismatase (E	963	49	10.9	1031	1	A38713	kinesin heavy chai
891	49	10.9	289	2	T12682	hypothetical prote	964	49	10.9	1089	2	T21582	hypothetical prote
892	49	10.9	294	2	S39606	class I histocompa	965	49	10.9	1143	2	T10636	hypothetical prote
893	49	10.9	294	2	G84504	probable VSF-1-lik	966	49	10.9	1191	1	A44051	DNA-binding protei
894	49	10.9	295	2	T22039	hypothetical prote	967	49	10.9	1193	2	G71605	hypothetical prote
895	49	10.9	301	2	S51439	hypothetical prote	968	49	10.9	1217	2	F97177	alpha-glucosidase
896	49	10.9	311	2	F83695	hypothetical prote	969	49	10.9	1250	2	S14177	SCD25 protein (ver
897	49	10.9	319	2	A72284	oligopeptide ABC t	970	49	10.9	1391	2	T20406	hypothetical prote
898	49	10.9	328	2	I51215	inhibin alpha-subu	971	49	10.9	1441	2	A86685	prophage p11 prote
899	49	10.9	328	2	T25231	hypothetical prote	972	49	10.9	1456	1	A36563	mannose receptor p
900	49	10.9	337	2	T15071	hypothetical prote	973	49	10.9	1463	2	C86482	protein F5J5.1 [im
901	49	10.9	343	2	S44834	F54H12.3 protein -	974	49	10.9	1524	2	S68553	surface layer prot
902	49	10.9	343	2	T27230	hypothetical prote	975	49	10.9	1844	2	D71612	hypothetical prote
903	49	10.9	354	1	S00574	alkanal monooxygen	976	49	10.9	2274	2	T30258	adenomatous polypo
904	49	10.9	356	2	B84495	En/Spm-like transp	977	49	10.9	2301	1	GNNVTN	genome polypeptide
905	49	10.9	358	2	F84053	transcription regu	978	49	10.9	2670	2	T37919	GCN1 homolog - fis

979 49 10.9 2704 2 S09118 G surface protein
980 49 10.9 3848 2 T17414 TipC protein - sli
981 49 10.9 4572 2 S57908 hypothetical 527K
982 49 10.9 6642 2 T29757 protein UNC-99 - C
983 48.5 10.8 108 2 S30521 Ig kappa chain V r
984 48.5 10.8 110 2 S22890 T-cell receptor al
985 48.5 10.8 111 2 S57889 T cell receptor Er
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987 48.5 10.8 122 2 AE1477 hypothetical prote
988 48.5 10.8 128 2 S40345 Ig kappa chain V-J
989 48.5 10.8 132 2 S23374 T-cell receptor al
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1001 48.5 10.8 274 2 T16003 hypothetical prote
1002 48.5 10.8 276 2 JC4161 probable chloride
1003 48.5 10.8 300 2 JC4367 NAD(P) - arginine AD
1004 48.5 10.8 302 1 ORBP15 replication protei
1005 48.5 10.8 319 2 AH2062 aldo/keto reductas
1006 48.5 10.8 320 2 S59947 chitinase (EC 3.2.
1007 48.5 10.8 320 2 C72421 oligopeptide ABC t
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1015 48.5 10.8 372 2 I52196 homeobox transcrip
1016 48.5 10.8 380 2 T09661 ascorbate oxidase
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1018 48.5 10.8 421 2 A56550 Krox-20 - African
1019 48.5 10.8 428 2 S22379 aspartate transami
1020 48.5 10.8 433 2 S77340 hypothetical prote
1021 48.5 10.8 446 2 T03021 mitosis-specific c
1022 48.5 10.8 446 2 A26724 tubulin alpha-2 ch
1023 48.5 10.8 453 2 T48240 chromosome replica
1024 48.5 10.8 458 2 AC1632 glycerol-3-phospha
1025 48.5 10.8 459 2 E86446 F13K23.11 protein
1026 48.5 10.8 462 2 B86262 deoxyribodipyrimid
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1028 48.5 10.8 473 2 S22321 catalase (EC 1.11.
1029 48.5 10.8 482 2 S60757 nuclear protein BB
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1031 48.5 10.8 489 2 A49388 differentiated ker
1032 48.5 10.8 502 2 A48679 cytochrome-c oxida
1033 48.5 10.8 514 2 T11859 cytochrome-c prote
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1035 48.5 10.8 524 2 T27177 hypothetical prote
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1042 48.5 10.8 608 2 T14731 peptide transporte
1043 48.5 10.8 624 2 T48587 gene NS-1 protein
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1045 48.5 10.8 650 2 S75072 transketolase I UU
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1047 48.5 10.8 665 2 T46570 hypothetical prote
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1060 48.5 10.8 798 2 A28193 integrin beta-1 ch
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1080 48.5 10.8 1364 2 T00250 MEGF2 protein - hu
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1083 48.5 10.8 1487 1 CGHU6C collagen alpha 1(I
1084 48.5 10.8 1560 2 T00080 hypothetical prote
1085 48.5 10.8 1589 2 T13826 translation initia
1086 48.5 10.8 1630 2 A53577 ascites sialoglyco
1087 48.5 10.8 1770 2 S56221 hypothetical prote
1088 48.5 10.8 1804 2 H96597 hypothetical prote
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1090 48.5 10.8 2386 1 FNHU fibronectin precur
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1096 48 10.7 112 1 CCRZ cytochrome c [vali
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1101 48 10.7 126 2 C53116 Ig epsilon chain C
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1105 48 10.7 151 2 S21987 probable heme-bind
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1108 48 10.7 160 2 T29392 hypothetical prote
1109 48 10.7 165 2 H90355 transposase all756
1110 48 10.7 189 2 AI2534 prolactin - green
1111 48 10.7 198 1 A60620 ribonuclease (EC 3
1112 48 10.7 213 1 JX0295 hypothetical prote
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1114 48 10.7 219 2 PC4203 conserved hypothet
1115 48 10.7 226 2 AG1496 Ig epsilon chain C
1116 48 10.7 227 2 PH1215 Ig gamma chain (cl
1117 48 10.7 228 2 S03050 hypothetical prote
1118 48 10.7 236 2 T45067 cellulase (EC 3.2.
1119 48 10.7 242 2 S60143 Ig epsilon chain C
1120 48 10.7 243 2 PH1216 hypothetical prote
1121 48 10.7 246 2 T32510 Ig epsilon chain C
1122 48 10.7 258 1 DHMS coat protein - sha
1123 48 10.7 262 1 JQ1738 hypothetical prote
1124 48 10.7 263 2 T43629

1125	48	10.7	278	2	S29615	whiG protein - Str	1198	48	10.7	534	2	T23305	hypothetical prote
1126	48	10.7	280	2	E96589	hypothetical prote	1199	48	10.7	543	2	T48239	hypothetical prote
1127	48	10.7	285	2	I51412	hypothetical trans	1200	48	10.7	546	2	AF2268	type II site-speci
1128	48	10.7	289	2	S48664	distal-less 3 prot	1201	48	10.7	553	2	A47504	epoxide hydrolase
1129	48	10.7	289	2	I53082	homeoprotein - rat	1202	48	10.7	554	2	A47503	epoxide hydrolase
1130	48	10.7	291	1	DHMS2	Ig delta chain C r	1203	48	10.7	566	2	S50979	RHC21 protein - Ye
1131	48	10.7	294	2	G85474	homeodomain-like p	1204	48	10.7	573	2	B86247	hypothetical prote
1132	48	10.7	301	2	T06112	homeotic protein T	1205	48	10.7	578	2	T41715	hypothetical prote
1133	48	10.7	307	2	AF32339	conserved hypothet	1206	48	10.7	582	2	S37047	beta-fructofuranos
1134	48	10.7	309	2	B84550	hypothetical prote	1207	48	10.7	587	2	D84426	hypothetical prote
1135	48	10.7	316	2	A71129	hypothetical prote	1208	48	10.7	591	2	T48395	Gr2-like protein -
1136	48	10.7	317	2	T24468	hypothetical prote	1209	48	10.7	595	2	B86798	prophage pi3 prote
1137	48	10.7	318	1	S75765	stearyl-CoA 9-des	1210	48	10.7	601	2	S27777	80K protein (allel
1138	48	10.7	319	2	AE1469	other protein homo	1211	48	10.7	604	2	T08302	hypothetical prote
1139	48	10.7	321	2	S75026	hypothetical prote	1212	48	10.7	605	2	H88640	protein F52C12.2 [
1140	48	10.7	334	2	T47693	hypothetical prote	1213	48	10.7	607	2	T24172	hypothetical prote
1141	48	10.7	342	2	T29557	hypothetical prote	1214	48	10.7	614	2	T29937	hypothetical prote
1142	48	10.7	348	2	E83920	hypothetical prote	1215	48	10.7	621	2	S35092	hypothetical prote
1143	48	10.7	351	2	T32093	hypothetical prote	1216	48	10.7	625	2	T06184	plakoglobin - mous
1144	48	10.7	355	2	C39725	hypothetical prote	1217	48	10.7	642	2	T15708	hypothetical prote
1145	48	10.7	363	2	A56940	integral membrane	1218	48	10.7	644	2	JQ0160	3-isopropylmalate
1146	48	10.7	367	2	AF1188	hypothetical prote	1219	48	10.7	656	2	T38741	major facilitator
1147	48	10.7	369	1	S57525	alcohol dehydrogen	1220	48	10.7	670	2	T28391	ORF MSV230 hypothe
1148	48	10.7	369	2	B71624	hypothetical prote	1221	48	10.7	703	2	T12696	NADH2 dehydrogenas
1149	48	10.7	375	2	T39329	hypothetical prote	1222	48	10.7	717	2	T06041	hypothetical prote
1150	48	10.7	377	2	F72165	Al7L protein - var	1223	48	10.7	717	2	E86812	sugar hydrolase [i
1151	48	10.7	377	2	T28558	hypothetical prote	1224	48	10.7	719	2	T00266	hypothetical prote
1152	48	10.7	377	2	H36849	Al6L protein - var	1225	48	10.7	724	2	D96949	secreted protein c
1153	48	10.7	379	2	H82284	queine tRNA-ribos	1226	48	10.7	731	2	B86132	hypothetical prote
1154	48	10.7	380	1	S73751	high affinity tran	1227	48	10.7	732	1	EKHUX	protein-glutamine
1155	48	10.7	392	2	T19869	hypothetical prote	1228	48	10.7	735	2	G91290	hypothetical prote
1156	48	10.7	394	2	AH1858	3-dehydroquinat s	1229	48	10.7	745	2	D86461	Fl4M2.9 protein -
1157	48	10.7	408	2	T38386	hypothetical wd-40	1230	48	10.7	758	2	S54522	hypothetical prote
1158	48	10.7	408	2	T34467	hypothetical prote	1231	48	10.7	792	1	A39914	dipeptidyl-peptida
1159	48	10.7	409	2	S40740	cyclin A homolog -	1232	48	10.7	872	2	S73785	DNA polymerase III
1160	48	10.7	412	2	G82406	long-chain fatty a	1233	48	10.7	914	1	S07047	iodide peroxidase
1161	48	10.7	417	2	S44062	phosphoglycerate k	1234	48	10.7	915	2	T03589	probable aspartate
1162	48	10.7	417	2	H96733	hypothetical prote	1235	48	10.7	919	2	T16459	hypothetical prote
1163	48	10.7	417	2	T33376	hypothetical prote	1236	48	10.7	940	2	D89723	protein F39D8.1b [
1164	48	10.7	418	2	T25092	hypothetical prote	1237	48	10.7	945	2	T21998	hypothetical prote
1165	48	10.7	420	2	C86197	hypothetical prote	1238	48	10.7	961	2	S67568	probable membrane
1166	48	10.7	421	2	T33523	hypothetical prote	1239	48	10.7	962	2	JC5808	G protein-coupled
1167	48	10.7	426	2	H71636	3-oxoacyl-[acyl-ca	1240	48	10.7	992	2	T38817	hypothetical prote
1168	48	10.7	428	1	EHHU	Ig epsilon chain C	1241	48	10.7	1035	2	T13962	sodium bicarbonate
1169	48	10.7	430	2	JC5125	aspartate transami	1242	48	10.7	1062	2	G86325	hypothetical prote
1170	48	10.7	430	2	D70193	hypothetical prote	1243	48	10.7	1070	2	F90106	TAP100 protein [im
1171	48	10.7	430	2	A65215	hypothetical 49.4	1244	48	10.7	1079	2	T14031	sodium bicarbonate
1172	48	10.7	435	2	E86266	protein F3F19.23 [1245	48	10.7	1093	1	S50614	regulatory protein
1173	48	10.7	435	2	S52203	vsf-1 protein - to	1246	48	10.7	1096	2	A96607	protein disease re
1174	48	10.7	436	2	T07816	S-locus-specific g	1247	48	10.7	1172	2	AD2310	hypothetical prote
1175	48	10.7	437	2	S11925	S-locus-specific g	1248	48	10.7	1215	2	C84848	hypothetical prote
1176	48	10.7	438	1	S11225	transcription fact	1249	48	10.7	1261	2	ES9430	PrPL1-associated R
1177	48	10.7	440	2	C71863	probable aminotran	1250	48	10.7	1341	2	S66835	probable membrane
1178	48	10.7	440	2	E64570	nifs-like protein	1251	48	10.7	1480	2	T05566	hypothetical prote
1179	48	10.7	440	2	T26471	hypothetical prote	1252	48	10.7	1583	2	F86366	protein F26F24.8 [
1180	48	10.7	458	2	A56055	CAP59 protein - Cr	1253	48	10.7	1606	2	T34073	paranemin - chicke
1181	48	10.7	459	1	S31083	glycerol-3-phospha	1254	48	10.7	1635	2	AI0452	hemolysin [importe
1182	48	10.7	462	2	T17480	endo-xylanase homo	1255	48	10.7	1795	2	T30332	avirulence protein
1183	48	10.7	479	1	S15031	paired box transcr	1256	48	10.7	1840	2	T29091	transitin - chicke
1184	48	10.7	482	2	S55950	hypothetical prote	1257	48	10.7	2004	2	T30185	hypothetical prote
1185	48	10.7	484	2	G82825	leucine aminopepti	1258	48	10.7	2109	1	ZLVNNU	genome polypeptide
1186	48	10.7	485	2	D88548	protein ZK507.6 [i	1259	48	10.7	2303	1	GNNYTM	genome polypeptide
1187	48	10.7	501	2	T39801	hypothetical sh3-c	1260	48	10.7	2485	1	H71621	serine/threonine-s
1188	48	10.7	503	2	A84434	Mutator-like trans	1261	48	10.7	2630	2	T08868	polyprotein P1 - A
1189	48	10.7	505	2	T15159	hypothetical prote	1262	48	10.7	2902	2	C71953	toxin-like outer m
1190	48	10.7	506	2	A99252	hypothetical prote	1263	48	10.7	4563	1	LPHUB	apolipoprotein B-1
1191	48	10.7	506	2	AC3034	hypothetical prote	1264	48	10.7	4639	1	A54794	dynein heavy chain
1192	48	10.7	515	2	AF2321	hypothetical prote	1265	48	10.7	6831	2	A88852	protein unc-22 [im
1193	48	10.7	517	2	I40798	hypothetical prote	1266	48	10.7	6839	2	S57242	twitchin [esimilari
1194	48	10.7	525	2	T47409	cellulase (EC 3.2.	1267	48	10.7	7160	2	T27935	hypothetical prote
1195	48	10.7	525	2	T23304	hypothetical prote	1268	47.5	10.6	76	2	B88318	protein age-1 [imp
1196	48	10.7	532	2	C97228	hypothetical prote	1269	47.5	10.6	85	2	A42056	ribosomal protein
1197	48	10.7	532	2	T49467	probable peptide A	1270	47.5	10.6	92	2	S37516	Ig kappa chain V r
						related to COP1-in							

1417 47.5 10.6 991 2 A46421 kainate-selective
1418 47.5 10.6 1015 2 T13062 CLOCK protein - fr
1419 47.5 10.6 1023 2 T13068 CLOCK protein - fr
1420 47.5 10.6 1027 2 T13071 CLOCK protein - fr
1421 47.5 10.6 1164 2 S71792 phosphatidylinosit
1422 47.5 10.6 1164 2 G71827 hypothetical prote
1423 47.5 10.6 1166 2 S70413 DNA-directed RNA p
1424 47.5 10.6 1178 2 S78475 mannosylphosphoryl
1425 47.5 10.6 1284 2 T40879 probable helicase
1426 47.5 10.6 1308 2 A90428 serine proteinase,
1427 47.5 10.6 1388 2 T00063 hypothetical prote
1428 47.5 10.6 1433 2 S54587 CAT8 protein - yea
1429 47.5 10.6 1457 2 T14577 protein kinase Yak
1430 47.5 10.6 1459 2 T30196 kinesin motor prot
1431 47.5 10.6 1460 2 D81675 polymorphic membra
1432 47.5 10.6 1639 2 S05603 major merozoite su
1433 47.5 10.6 1663 1 C3RT complement C3 prec
1434 47.5 10.6 1664 2 T18216 integrin-like prot
1435 47.5 10.6 1687 2 T30244 phosphodiesterase
1436 47.5 10.6 1719 2 T30174 exoribonuclease, v
1437 47.5 10.6 1856 2 C95008 immunoglobulin A1
1438 47.5 10.6 2055 2 T00093 hypothetical prote
1439 47.5 10.6 2131 2 S01446 hypothetical prote
1440 47.5 10.6 2163 2 S50675 pre-mRNA splicing
1441 47.5 10.6 2194 1 GNNYE7 genome polyprotein
1442 47.5 10.6 2229 2 T16199 hypothetical prote
1443 47.5 10.6 2338 2 I73957 kinase-related pro
1444 47.5 10.6 2391 2 T18410 carbamoyl-phosphat
1445 47.5 10.6 2477 1 SJCHA spectrin alpha cha
1446 47.5 10.6 2477 2 S14428 fibronectin precur
1447 47.5 10.6 2529 2 B64635 toxin-like outer m
1448 47.5 10.6 2869 2 T18518 apolipoprotein(a)
1449 47.5 10.6 2893 2 A64556 toxin-like outer m
1450 47.5 10.6 3176 2 CGHU3A collagen alpha 3(V
1451 47 10.5 78 2 C84636 hypothetical prote
1452 47 10.5 80 2 T10087 metallothionein -
1453 47 10.5 82 2 I57802 Ig lambda2-like ch
1454 47 10.5 98 1 KRSHH4 keratin high-sulfu
1455 47 10.5 98 2 I47086 BIIIB4 high-sulfur
1456 47 10.5 108 1 K1HUWS Ig kappa chain V-I
1457 47 10.5 110 2 B30583 T-cell receptor de
1458 47 10.5 111 1 CCED cytochrome c - Eur
1459 47 10.5 111 1 CCPO cytochrome c - cuc
1460 47 10.5 111 1 CCRM cytochrome c - cuc
1461 47 10.5 112 2 T04008 cytochrome c - Ara
1462 47 10.5 113 2 A29281 T-cell receptor al
1463 47 10.5 117 2 S46376 Ig kappa chain V-J
1464 47 10.5 131 2 S45059 AC1 protein (clone
1465 47 10.5 138 2 S24087 envelope protein -
1466 47 10.5 139 2 T25747 hypothetical prote
1467 47 10.5 146 2 I37296 dopamine transport
1468 47 10.5 152 2 S14236 Ig gamma-1 chain C
1469 47 10.5 157 2 H69849 hypothetical prote
1470 47 10.5 165 2 B72727 hypothetical prote
1471 47 10.5 178 2 F82808 toluene tolerance
1472 47 10.5 183 2 A37410 H-2 class II histo
1473 47 10.5 190 2 A13086 transcription regu
1474 47 10.5 199 2 A33653 tubulin alpha chai
1475 47 10.5 201 2 H98199 probable transcrip
1476 47 10.5 221 2 T43159 ubiquitin-protein
1477 47 10.5 222 2 T37522 conserved hypothet
1478 47 10.5 227 2 T37499 probable ubiquitin
1479 47 10.5 228 2 I58170 LERK-7 precursor -
1480 47 10.5 234 2 AH2634 hypothetical prote
1481 47 10.5 237 2 F97416 hypothetical prote
1482 47 10.5 239 2 A97358 glucose-inhibited
1483 47 10.5 245 2 I55951 MHC class II E-bet
1484 47 10.5 258 2 B90121 proliferating cell
1485 47 10.5 259 2 E84427 hypothetical prote
1486 47 10.5 263 2 B84778 hypothetical prote
1487 47 10.5 264 2 A60497 H-2 class II histo
1488 47 10.5 266 2 C95288 probable ABC trans
1489 47 10.5 275 2 T32010 hypothetical prote

1490 47 10.5 279 2 T26555 hypothetical prote
1491 47 10.5 282 2 H65116 hypothetical prote
1492 47 10.5 283 2 A59238 dUTP diphosphatase
1493 47 10.5 286 2 T18957 hypothetical prote
1494 47 10.5 286 2 T49876 hypothetical prote
1495 47 10.5 292 2 F70594 hypothetical prote
1496 47 10.5 293 2 JQ1675 frxC protein - Chl
1497 47 10.5 293 2 T06100 adenyl-yl-sulfate k
1498 47 10.5 298 2 I51410 transcription fact
1499 47 10.5 299 2 T25610 hypothetical prote
1500 47 10.5 300 2 S65554 protochlorophyllid

ALIGNMENTS

RESULT 1

T51961
ATAF1-like protein [imported] - Picea mariana (fragment)
C;Species: Picea mariana
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51961
R;Perry, D.J.; Bousquet, J.
Genetics 149, 1089-1098, 1998
A;Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, characteriz
A;Reference number: Z25268; MUID:98278823; PMID:9611216
A;Accession: T51961
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-281 <PER>
A;Cross-references: UNIPROT:O65061; UNIPARC:UPI00000AA7FF; EMBL:AF051222; PIDN:AAC32123.J
C;Genetics:
A;Note: Sb29

Query Match 17.5%; Score 78.5; DB 2; Length 281;
Best Local Similarity 29.0%; Pred. No. 0.53;
Matches 31; Conservative 14; Mismatches 27; Indels 35; Gaps 8;

QY 5 MCNPSNSN---ANCEF---SLKNISD-----IHP--ESFNLQW----- 35
Db 146 LCVSPMNSNICQLNLDFFQNSTTFFSDSTLKAPVQNTTFNPISISSINHQTNCNSTDLMS 205
QY 36 -FFND-SCAPPTGFNKPTS-NDTWASGWRASSFHFDFSEENKHLIHF 79
Db 206 GLHNDSSCKSPSPSEPISEKEEVQSSFRLENF---SQEQQSLFNF 249

RESULT 2

S01076
aspartate transaminase (EC 2.6.1.1), cytosolic - mouse
N;Alternate names: aspartate aminotransferase, cytosolic
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S01076; B25349
R;Obaru, K.; Tsuzuki, T.; Setoyama, C.; Shimada, K.
J. Mol. Biol. 200, 13-22, 1988
A;Title: Structural organization of the mouse aspartate aminotransferase isoenzyme genes
A;Reference number: S01076; MUID:88245178; PMID:3379636
A;Accession: S01076
A;Molecule type: DNA
A;Residues: 1-413 <OBA>
A;Cross-references: UNIPROT:P05201; UNIPARC:UPI000016CC1D; EMBL:X07302; NID:g50032; PIDN
A;Note: the authors translated the codon AAT for residue 291 as Ile
R;Obaru, K.; Nomiya, H.; Shimada, K.; Nagashima, F.; Morino, Y.
J. Biol. Chem. 261, 16976-16983, 1986
A;Title: Cloning and sequence analysis of mRNA for mouse aspartate aminotransferase isoe
A;Reference number: A92571; MUID:87057413; PMID:3782150
A;Accession: B25349
A;Molecule type: mRNA
A;Residues: 1-290,'I',292-413 <OB2>
A;Cross-references: UNIPARC:UPI0000001834; GB:J02623; NID:g466500; PIDN:AAA37263.1; PID:
C;Genetics:
A;Introns: 40/1; 100/3; 142/1; 179/3; 214/3; 265/1; 320/2; 368/1

C;Superfamily: aspartate aminotransferase
C;Keywords: aminotransferase; cytosol; phosphoprotein; pyridoxal phosphate
P;259/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 16.3%; Score 73; DB 2; Length 413;
Best Local Similarity 26.2%; Pred. No. 3.2;
Matches 21; Conservative 7; Mismatches 26; Indels 26; Gaps 3;

QY 3 PLMCNSPSNSNANCEFSLKNISDIHP-----ESFNLQWFFND-----SC 41
Db 133 PIYVSSFTWENHNAVFSAGFKDIRPYCYWDAEKRGLDLQGFLENAPESIFVLHAC 192

QY 42 APPTGFNKPTSNDTMASGWR 61
Db 193 A-----HNPTGDTPTPEQWK 207

RESULT 3
S52830
HMS1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9916.09; protein YMR070W
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52830; S59820
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S52814
A;Accession: S52830
A;Molecule type: DNA
A;Residues: 1-490 <PRA>
A;Cross-references: UNIPROT:P54785; UNIPARC:UPI000012F3CA; EMBL:Z48952; NID:g763008; PID
A;Experimental source: strain AB972
R;Madison, J.; Winston, F.
submitted to the EMBL Data Library, April 1995
A;Reference number: S59820
A;Accession: S59820
A;Molecule type: DNA
A;Residues: 1-490 <MAD>
A;Cross-references: UNIPARC:UPI000012F3CA; EMBL:U25279; NID:g805129; PIDN:AAC49982.1; PI
C;Genetics:
A;Gene: SGD:MOT3; HMS1
A;Cross-references: MIPS:YMR070W; SGD:S0004674
A;Map position: 13R

Query Match 15.6%; Score 70; DB 2; Length 490;
Best Local Similarity 34.0%; Pred. No. 8;
Matches 16; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 7 NSPSPNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTS 53
Db 139 NSTSNNNNNNNNNNNNNIHPNQFTAAANMNSNAAAAYSFPTAN 185

RESULT 4
T13669
neuromusculin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13669
R;Kania, A.; Han, P.L.; Kim, Y.T.; Bellen, H.
Neuron 11, 673-687, 1993
A;Title: Neuromusculin, a Drosophila gene expressed in peripheral neuronal precursors an
A;Reference number: Z17697; MUID:94000831; PMID:8398154
A;Accession: T13669
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1011 <KAN>
A;Cross-references: UNIPROT:Q24273; UNIPARC:UPI0000043BE8; EMBL:L23146; NID:g385073; PID
C;Genetics:
A;Gene: nrm
A;Cross-references: FlyBase:FBgn0005629

Query Match 15.6%; Score 70; DB 2; Length 1011;

Best Local Similarity 28.3%; Pred. No. 17;
Matches 28; Conservative 12; Mismatches 19; Indels 40; Gaps 7;

QY 4 LMCN-----SPS-----NSN-----ANCEFSLKNISDIHP-----ESFNLQWFFNDS 40
Db 494 LFCNVLDANPSVLTQVRWYANSTLLKELPDCEETREDLCHIDPSKLLLESIGRGFFYNYS 553

QY 41 CAPPTGFNKPTSNDTMASGWRASSPHFDSEENKRLIHF 79
Db 554 C---EGFN-----AAGWGPRS-----EDKELLVHY 575

RESULT 5
A32160
tenascin-C - human
N;Alternate names: hexabrachion
C;Species: Homo sapiens (man)
C;Date: 31-Jul-1989 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I38337; A32160; S14015; S16166; S50208; S49354
R;Gherzi, R.; Carnemolla, B.; Siri, A.; Ponassi, M.; Balza, E.; Zardi, L.
J. Biol. Chem. 270, 3429-3434, 1995
A;Title: Human tenascin gene. Structure of the 5'-region, identification, and characteri:
A;Reference number: A55974; MUID:95155442; PMID:7531707
A;Accession: I38337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2201 <RES>
A;Cross-references: UNIPROT:P24821; UNIPARC:UPI0000034A0E; EMBL:X78565; NID:g556844; PID
R;Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989
A;Title: An alternatively spliced region of the human hexabrachion contains a repeat of 1
A;Reference number: A32160; MUID:89160821; PMID:2466295
A;Accession: A32160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 431-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'L', <GUL>
A;Cross-references: UNIPARC:UPI000016AAC6; GB:M24630; NID:g514363; PIDN:AAA52703.1; PID:
R;Siri, A.; Carnemolla, B.; Saginati, M.; Leprini, A.; Casari, G.; Baralle, F.; Zardi, L.
Nucleic Acids Res. 19, 525-531, 1991
A;Title: Human tenascin: primary structure, pre-mRNA splicing patterns and localization
A;Reference number: S14015; MUID:91187670; PMID:1707164
A;Accession: S14015
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243, 245-369, 'V', 371-679, 'R', 681-1676, 'I', 1678-2139, 'TR', 2142, 2144-2201 <SI
A;Cross-references: UNIPARC:UPI0000155D15; EMBL:X56160; NID:g37226; PIDN:CAA39628.1; PID
R;Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.
J. Biol. Chem. 266, 2818-2823, 1991
A;Title: The complete cDNA sequence of human hexabrachion (tenascin). A multidomain prot
A;Reference number: S16166; MUID:91131572; PMID:1704365
A;Accession: S16166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'LH', 2055-2201 <NIE>
A;Cross-references: UNIPARC:UPI000016AAC5; EMBL:M55618; NID:g184483; PIDN:AAA88083.1; PI
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by 1
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50208
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 46-125 <GLJ>
A;Cross-references: UNIPARC:UPI0000177AF4; EMBL:X80280
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: GDB:HXB
A;Cross-references: GDB:120073; OMIM:187380
A;Map position: 9q33-q33
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: alternative splicing; extracellular matrix
F;408-434/Domain: EGF homology <EGF>
F;622-703/Domain: fibronectin type III repeat homology <FN3A>

Db 31 CNSNSQVRN^{IS}DLRFLID-DDDSFDLLYPFSENE^SFCIPPDATKREMSGDFTPASGIS 89
Qy 62 ASSFHFDSEENK^HRLI 77
Db 90 GDCVNEDETEKNTNGVL 105

RESULT 10
B49423
semaphorin I - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
C;Accession: B49423
R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone
A;Reference number: A49423; MUID:94094332; PMID:8269517
A;Accession: B49423
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-656 <KOL>
A;Cross-references: UNIPARC:UPI000017BED0; GB:L26082
C;Genetics:
A;Gene: semal
A;Cross-references: FlyBase:FBgn0011259

Query Match 14.6%; Score 65.5; DB 2; Length 656;
Best Local Similarity 31.8%; Pred. No. 33;
Matches 21; Conservative 7; Mismatches 27; Indels 11; Gaps 2;

Qy 7 NSPNS---NANCERSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSN^{DT}MASGWRAS 63
Db 202 NTPSNSIPGS^{AV}CA^FALQ^{DI}ADTFEGQ^FKEQTGINSN^WLPVNAKVPDP-----RPG 253

Qy 64 SFHFD^S 69
Db 254 SCHNDS 259

RESULT 11
H96924
probable phosphohydrolases, Icc family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H96924
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H96924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-652 <KUR>
A;Cross-references: UNIPROT:Q97MJ1; UNIPARC:UPI00000C9DB9; GB:AE001437; PIDN:AAK78187.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0205

Query Match 14.5%; Score 65; DB 2; Length 652;
Best Local Similarity 26.3%; Pred. No. 37;
Matches 25; Conservative 5; Mismatches 25; Indels 40; Gaps 3;

Qy 10 SNSNANCFSLK-----NISDI-----HPESFNLQWFFNDSCAPPT----- 45
Db 33 ANSNNNAISLAGSSGSD^{PS}DI^{VL}SPGSD^{PP}SELN^{FN}WYSNN^{SN}ATPTVEALKSDANDS 92

Qy 46 -----GFNKPTSN^{DT}MASGWRAS 64
Db 93 DFPANKCST^{FT}GKTSQGNL^NFTSNKVS^{VS}GLKPSS 127

RESULT 12
T43061
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43061
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43061
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-330 <YOS>
A;Cross-references: UNIPROT:O14470; UNIPARC:UPI0000169115; EMBL:D89227; NID:g1749661; PFI
A;Experimental source: strain PR745

Query Match 14.4%; Score 64.5; DB 2; Length 330;
Best Local Similarity 30.0%; Pred. No. 20;
Matches 27; Conservative 5; Mismatches 33; Indels 25; Gaps 6;

Qy 15 NCE-----FSLKNIS-DIHPESFNLQWF---FNDS---CAPPTGFN----KPTSN----- 53
Db 26 NCSQTWYHNLK^NKKYD^{IC}PC^{NY}KQGRFSS^{SN}SD^{FL}CMDAIDFNHDEK^{PW}SNQETLL 85

Qy 54 ---DTMASGWRASSPHFDSEENK^HRLIHF 79
Db 86 LEA^IETYGDD^NQIALH^VGSRTKEQCL^IHF 115

RESULT 13
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25671
R;Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid D2092.
A;Reference number: Z20067
A;Accession: T25671
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-461 <GAT>
A;Cross-references: UNIPROT:P91197; UNIPARC:UPI00000611E5; EMBL:U88167; PIDN:AAB42223.1;
A;Experimental source: strain Bristol N2; clone D2092
C;Genetics:
A;Gene: CESP:D2092.3
A;Map position: 1
A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor

Query Match 14.4%; Score 64.5; DB 2; Length 461;
Best Local Similarity 26.5%; Pred. No. 29;
Matches 18; Conservative 12; Mismatches 27; Indels 11; Gaps 2;

Qy 1 KGPLMCN^{SP}SN^{SN}ANCF^{SL}KNIS^{DI}HPES^{FN}LQWFFNDSCAPPTGFNKPTSN^{DT}MASGW 60
Db 378 KNPLDCN^{LP}SN-HAGYEAQ^{IL}LH^{SV}TELRRVAF-----YNKEEH^{DE}RIQT^DW 426

Qy 61 RASSPHFD 68
Db 427 RFAAMVVD 434

RESULT 14
T39486
hypothetical protein SPBC15D4.10c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39486
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997

A;Reference number: Z21858
A;Accession: T39486
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-475 <LYN>
A;Cross-references: UNIPROT:O74315; UNIPARC:UPI000006A222; EMBL:AL031349; PIDN:CAA20485
A;Experimental source: strain 972h-; cosmid c15D4
C;Genetics:
A;Gene: SPDB:SPBC15D4.10c
A;Map position: 2
A;Introns: 419/1

Query Match 14.4%; Score 64.5; DB 2; Length 475;
Best Local Similarity 30.3%; Pred. No. 30;
Matches 27; Conservative 7; Mismatches 32; Indels 23; Gaps 5;

QY 7 NSPSNS---NANCEFSLKNISD-----IHPESEFNLQ---WFFNDS---CAPPT 45
Db 318 NQPQSAFQNLNTQFSLPNSQPVFGHTSLTQPVNPNNGFTVQPPATFMQQQGPFPVPNT 377

QY 46 GFNKPSTNDTMASGWRASSFHFDSSEENKH 74
Db 378 TPESPFAVNT--SKISASGFSNDNPANKN 404

RESULT 15
T38303
SWI/SNF complex transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38303
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21785
A;Accession: T38303
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-503 <SKE>
A;Cross-references: UNIPROT:O14470; UNIPARC:UPI000006C8C4; EMBL:Z99163; PIDN:CAB16236.1;
A;Experimental source: strain 972h-; cosmid c23H3
C;Genetics:
A;Gene: SPDB:SPAC23H3.10
A;Map position: 1

Query Match 14.4%; Score 64.5; DB 2; Length 503;
Best Local Similarity 30.0%; Pred. No. 32;
Matches 27; Conservative 5; Mismatches 33; Indels 25; Gaps 6;

QY 15 NCE----FSLKNIS-DIHPESEFNLQWF---FNDS---CAPPTGFN---KPTSN----- 53
Db 199 NCSQTWYHNLKNKKYDPCNCKYQGRFSSSFSSDFLCMDAIDFNHDEEKPSNQETLLL 258

QY 54 ----DTMASGWRASSFHFDSSEENKRLIHF 79
Db 259 LEAITYGDDWNQIALHVGSRTKEQCLIHF 288

Search completed: December 22, 2005, 03:06:18
Job time : 59.1837 secs

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